

100	105	110	115	
gtg gcc aag acc tct gct gca cag gct atc cat cca gga tgc ggt ttt Val Ala Lys Thr Ser Ala Ala Gln Ala Ile His Pro Gly Cys Gly Phe				559
116 121 126 131				
ctt tca gaa aac atg gaa ttt gct gaa ctt tgt aag caa gaa gga att Leu Ser Glu Asn Met Glu Phe Ala Glu Leu Cys Lys Gln Glu Gly Ile				607
132 137 142 147				
att ttt ata ggc cct cct cca tct gca att aga gac atg ggt ata aag Ile Phe Ile Gly Pro Pro Ser Ala Ile Arg Asp Met Gly Ile Lys				655
148 153 158 163				
agc aca tcc aaa tcc ata atg gct gct gga gta cct gtt gtg gag Ser Thr Ser Lys Ser Ile Met Ala Ala Gly Val Pro Val Val Glu				703
164 169 174 179				
ggt tat cat ggt gag gac caa tca gac cag tgc ctg aag gaa cac gcc Gly Tyr His Gly Glu Asp Gln Ser Asp Gln Cys Leu Lys Glu His Ala				751
180 185 190 195				
agg aga att ggc tat cct gtc atg att aaa gcc gtc cg ^g ggt gga gga Arg Arg Ile Gly Tyr Pro Val Met Ile Lys Ala Val Arg Gly Gly				799
196 201 206 211				
gga aaa gga atg agg att gtt aga tca gaa caa gaa ttt caa gaa cag Gly Lys Gly Met Arg Ile Val Arg Ser Glu Gln Glu Phe Gln Glu Gln				847
212 217 222 227				
tta gag tca gca cgg aga gaa gct aag aag tct ttc aat gat gat gct Leu Glu Ser Ala Arg Arg Glu Ala Lys Lys Ser Phe Asn Asp Asp Ala				895
228 233 238 243				
atg ctg atc gag aag ttt gta gac aca ccg agg cat gta gaa gtc cag Met Leu Ile Glu Lys Phe Val Asp Thr Pro Arg His Val Glu Val Gln				943
244 249 254 259				
gtg ttt ggt gat cac cat ggc aat gct gtg tac ttg ttt gaa aga gac Val Phe Gly Asp His His Gly Asn Ala Val Tyr Leu Phe Glu Arg Asp				991
260 265 270 275				
tgt agt gtg cag agg cga cat cag aag atc att gag gag gcc cca gc ^g Cys Ser Val Gln Arg Arg His Gln Lys Ile Ile Glu Glu Ala Pro Ala				1039
276 281 286 291				
cct ggt att aaa tct gaa gta aga aaa aag ctg gga gaa gct gca gtc Pro Gly Ile Lys Ser Glu Val Arg Lys Lys Leu Gly Glu Ala Ala Val				1087
292 297 302 307				
aga gct gct aaa gct gta aat tat gtt gga gca ggg act gtg gag ttt Arg Ala Ala Lys Ala Val Asn Tyr Val Gly Ala Gly Thr Val Glu Phe				1135
308 313 318 323				
att atg gac tca aaa cat aat ttc tgt ttc atg gag atg aat aca agg Ile Met Asp Ser Lys His Asn Phe Cys Phe Met Glu Met Asn Thr Arg				1183
324 329 334 339				

ctg caa gtg gaa cat cct gtt act gag atg atc aca gga act gac ttg			1231
Leu Gln Val Glu His Pro Val Thr Glu Met Ile Thr Gly Thr Asp Leu			
340 345 350 355			
gtg gag tgg cag ctt aga att gca gca gga gag aag att cct ttg agc			1279
Val Glu Trp Gln Leu Arg Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser			
356 361 366 371			
cag gaa gaa ata act ctg cag ggc cat gcc ttc gaa gct aga ata tat			1327
Gln Glu Glu Ile Thr Leu Gln Gly His Ala Phe Glu Ala Arg Ile Tyr			
372 377 382 387			
gca gaa gat cct agc aat aac ttc atg cct gtg gca ggc cca tta gtg			1375
Ala Glu Asp Pro Ser Asn Asn Phe Met Pro Val Ala Gly Pro Leu Val			
388 393 398 403			
cac ctc tct act cct cga gca gac cct tcc acc agg att gaa act gga			1423
His Leu Ser Thr Pro Arg Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly			
404 409 414 419			
gta cggtt gaa gac gaa gtt tcc gtg cat tat gac ccc atg att gcg			1471
Val Arg Gln Gly Asp Glu Val Ser Val His Tyr Asp Pro Met Ile Ala			
420 425 430 435			
aag ctg gtc gtg tgg gca gca gat cgc cag gcg gca ttg aca aaa ctg			1519
Lys Leu Val Val Trp Ala Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu			
436 441 446 451			
agg tac agc ctt cgt cag tac aat att gtt gga ctg ccc acc aac att			1567
Arg Tyr Ser Leu Arg Gln Tyr Asn Ile Val Gly Leu Pro Thr Asn Ile			
452 457 462 467			
gac ttc tta ctc aac ctg tct ggc cac cca gag ttt gaa gct ggg aac			1615
Asp Phe Leu Leu Asn Leu Ser Gly His Pro Glu Phe Glu Ala Gly Asn			
468 473 478 483			
gtg cac act gat ttc atc cct caa cac cac aaa cag ttg ttg ctc agt			1663
Val His Thr Asp Phe Ile Pro Gln His His Lys Gln Leu Leu Leu Ser			
484 489 494 499			
cgg aag gct gca gcc aaa gag tct tta tgc cag gca gcc ctg ggt ctc			1711
Arg Lys Ala Ala Ala Lys Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu			
500 505 510 515			
atc ctc aag gag aaa gcc atg acc gac act ttc act ctt cag gca cat			1759
Ile Leu Lys Glu Lys Ala Met Thr Asp Thr Phe Thr Leu Gln Ala His			
516 521 526 531			
gat caa ttc tct cca ttt tcg tct agc agt gga aga aga ctg aat atc			1807
Asp Gln Phe Ser Pro Phe Ser Ser Ser Gly Arg Arg Leu Asn Ile			
532 537 542 547			
tcg tat acc aga aac atg act ctt aaa gat ggt aaa aac aat gta gcc			1855
Ser Tyr Thr Arg Asn Met Thr Leu Lys Asp Gly Lys Asn Asn Val Ala			
548 553 558 563			

ata gct gta acg tat aac cat gat ggg tct tat agc atg cag aat taa		1903
Ile Ala Val Thr Tyr Asn His Asp Gly Ser Tyr Ser Met Gln Asn *		
564	569	574
		579
agataaaaact ttccaagtcc ttggtaatct ttacagcgag ggagactgca cttacctgaa		1963
atgttctgtt aatggagttg ctagtaaagc gaagctgatt atcctggaaa acactattta		2023
cctatttcc aaggaaggaa gtattgagat tgacattcca gtccccaaat acttatcttc		2083
tgtgagctca caaaaaaaaaaaaaa		2108

;

<210> 90
<211> 2498
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (530)..(2356)

<400> 90		
gcaggtaccg cgtccggaaat tcccgggtcg acgatttcgt gtgactggaa tccagcttaa		60
ccccaaacaac catctacagc tgtattcttg ttcccttgat ggcacaatta aactgtggga		120
ctatatagat ggcatctaa taaagacttt catagttgga tgtaaacttc atgccttctt		180
tactcttgcc caagctgagg attctgtctt tgttatagtg aataaagaaaa aaccagatat		240
atttcagctg gtttcagtga aactgccaaa atcctaagc caggaagtag aagccaagga		300
gctgtccttt gttttggatt acataaacca gtcacccaaag tgcattgcct ttggaaacga		360
gggagtatat gttgctgcag tacggaaatt ttacttgtct gtttattttt tcaaaaagaa		420
aacaacatca aggttactt tatcatcatc aagaaataag aagcatgcta aaaaccattt		480
tacgtgtgta gcatgtcacc ccacggaaaga ccgcatacgca tctggtcac	atg gat	535
	Met Asp	
	1	

ggc caa att cgt ctt tgg agg aat ttt tat gat gat aag aaa tat acg		583
Gly Gln Ile Arg Leu Trp Arg Asn Phe Tyr Asp Asp Lys Lys Tyr Thr		
3	8	13
		18

tac aca tgt tta cat tgg cac cat gat atg gtt atg gat ttg gct ttt		631
Tyr Thr Cys Leu His Trp His His Asp Met Val Met Asp Leu Ala Phe		
19	24	29
		34

tca gtg aca ggc acc agt ctg ctg agt ggc ggt cgt gaa tct gta ctt		679
Ser Val Thr Gly Thr Ser Leu Leu Ser Gly Gly Arg Glu Ser Val Leu		
35	40	45
		50

gta gag tgg cgc gat gca aca gag aag aat aag gag ttt ctc ccg cgt		727	
Val Glu Trp Arg Asp Ala Thr Glu Lys Asn Lys Glu Phe Leu Pro Arg			
51	56	61	66
tta gga gct act att gaa cat atc tca gtc tcg cct gca gga gat tta		775	
Leu Gly Ala Thr Ile Glu His Ile Ser Val Ser Pro Ala Gly Asp Leu			
67	72	77	82
ttc tgc act tct cac tct gat aat aag ata ata att att cac cga aac		823	
Phe Cys Thr Ser His Ser Asp Asn Lys Ile Ile Ile His Arg Asn			
83	88	93	98
ctt gaa gca tcc gca gta att caa ggc cta gtg aaa gat agg agt atc		871	
Leu Glu Ala Ser Ala Val Ile Gln Gly Leu Val Lys Asp Arg Ser Ile			
99	104	109	114
ttc act ggt ttg atg att gat cca aga act aaa gct ttg gtt ttg aat		919	
Phe Thr Gly Leu Met Ile Asp Pro Arg Thr Lys Ala Leu Val Leu Asn			
115	120	125	130
gga aaa cct ggc cac ctg cag ttt tat tct ctc cag agt gat aaa cag		967	
Gly Lys Pro Gly His Leu Gln Phe Tyr Ser Leu Gln Ser Asp Lys Gln			
131	136	141	146
tta tac aat tta gat att ata cag caa gaa tat att aat gat tat ggt		1015	
Leu Tyr Asn Leu Asp Ile Ile Gln Gln Glu Tyr Ile Asn Asp Tyr Gly			
147	152	157	162
ctg atc caa att gaa cta aca aag gct gca ttt ggc tgc ttt ggt aac		1063	
Leu Ile Gln Ile Glu Leu Thr Lys Ala Ala Phe Gly Cys Phe Gly Asn			
163	168	173	178
tgg ctt gca aca gtg gaa cag cgg caa gaa aag gaa act gag ctt gaa		1111	
Trp Leu Ala Thr Val Glu Gln Arg Gln Glu Lys Glu Thr Glu Leu Glu			
179	184	189	194
ttg caa atg aaa ctg tgg atg tat aat aag aaa aca caa ggg ttt att		1159	
Leu Gln Met Lys Leu Trp Met Tyr Asn Lys Lys Thr Gln Gly Phe Ile			
195	200	205	210
ctt aac act aaa att aac atg cca cac gaa gac tgc att aca gct ctc		1207	
Leu Asn Thr Lys Ile Asn Met Pro His Glu Asp Cys Ile Thr Ala Leu			
211	216	221	226
tgt ttc tgt aat gca gaa aaa tct gaa cag ccc acc ttg gtt aca gct		1255	
Cys Phe Cys Asn Ala Glu Lys Ser Glu Gln Pro Thr Leu Val Thr Ala			
227	232	237	242
agc aaa gat ggt tac ttc aaa gta tgg ata tta aca gat gac tct gac		1303	
Ser Lys Asp Gly Tyr Phe Lys Val Trp Ile Leu Thr Asp Asp Ser Asp			
243	248	253	258
ata tac aaa aaa gct gtt ggc tgg acc tgt gac ttt gtt ggt agt tat		1351	
Ile Tyr Lys Lys Ala Val Gly Trp Thr Cys Asp Phe Val Gly Ser Tyr			
259	264	269	274
cac aag tat caa gca act aac tgt tgt ttc tcc gaa gat ggt tct tta		1399	

His Lys Tyr Gln Ala Thr Asn Cys Cys Phe Ser Glu Asp Gly Ser Leu			
275	280	285	290
ctc gca gtt agt ttt gag gaa ata gtc aca ata tgg gat tct gta aca			1447
Leu Ala Val Ser Phe Glu Glu Ile Val Thr Ile Trp Asp Ser Val Thr			
291	296	301	306
tgg gaa ctt aaa tgt aca ttt tgc caa cga gct ggg aaa ata agg cac			1495
Trp Glu Leu Lys Cys Thr Phe Cys Gln Arg Ala Gly Lys Ile Arg His			
307	312	317	322
ctt tgc ttt ggg aga ttg acg tgt tca aag tat cta ctt ggt gct act			1543
Leu Cys Phe Gly Arg Leu Thr Cys Ser Lys Tyr Leu Leu Gly Ala Thr			
323	328	333	338
gaa aat ggc att ctt tgc tgt tgg aat ctg ctg agc tgt gca ttg gag			1591
Glu Asn Gly Ile Leu Cys Cys Trp Asn Leu Leu Ser Cys Ala Leu Glu			
339	344	349	354
tgg aat gca aaa tta aat gtt aga gtt atg gaa ccc gat cct aat tca			1639
Trp Asn Ala Lys Leu Asn Val Arg Val Met Glu Pro Asp Pro Asn Ser			
355	360	365	370
gag aat att gct gca atc tct cag tct tca gtg ggt tca gac ttg ttt			1687
Glu Asn Ile Ala Ala Ile Ser Gln Ser Ser Val Gly Ser Asp Leu Phe			
371	376	381	386
gta ttt aaa cct agt gag cca agg cca ttg tat att caa aag ggt atc			1735
Val Phe Lys Pro Ser Glu Pro Arg Pro Leu Tyr Ile Gln Lys Gly Ile			
387	392	397	402
tcc aga gag aaa gtc cag tgg gga gtg ttt gtt cca cga gat gtc cct			1783
Ser Arg Glu Lys Val Gln Trp Gly Val Phe Val Pro Arg Asp Val Pro			
403	408	413	418
gaa tcc ttc acc tca gaa gct tac cag tgg cta aat aga tcc cag ttt			1831
Glu Ser Phe Thr Ser Glu Ala Tyr Gln Trp Leu Asn Arg Ser Gln Phe			
419	424	429	434
tac ttc cta aca aaa tca cag agt tta ttg aca ttc agt aca aag tct			1879
Tyr Phe Leu Thr Lys Ser Gln Ser Leu Leu Thr Phe Ser Thr Lys Ser			
435	440	445	450
cca gaa gaa aaa ctc aca cca aca agc aaa cag ctg cta gca gaa gaa			1927
Pro Glu Glu Lys Leu Thr Pro Thr Ser Lys Gln Leu Leu Ala Glu Glu			
451	456	461	466
agt ctt ccc aca acc cca ttt tat ttc ata ttg gga aaa cac agg caa			1975
Ser Leu Pro Thr Thr Pro Phe Tyr Phe Ile Leu Gly Lys His Arg Gln			
467	472	477	482
cag cag gat gaa aaa cta aac gaa act tta gag aat gag ctg gta caa			2023
Gln Gln Asp Glu Lys Leu Asn Glu Thr Leu Glu Asn Glu Leu Val Gln			
483	488	493	498
cta ccc tta aca gaa aac ata ccc gca att agt gag ctt ctt cac act			2071
Leu Pro Leu Thr Glu Asn Ile Pro Ala Ile Ser Glu Leu Leu His Thr			

7	12	17	22	
agg aac ggc ctg cgg agc cag gta tac gct gtg aat ggc gac tac tat				329
Arg Asn Gly Leu Arg Ser Gln Val Tyr Ala Val Asn Gly Asp Tyr Tyr				
23	28	33	38	
gtg ggc gag tgg aag gac aac gtg aaa cac ggg aaa gga aca cag gtc				377
Val Gly Glu Trp Lys Asp Asn Val Lys His Gly Lys Gly Thr Gln Val				
39	44	49	54	
tgg aag aag aaa gga gcc atc tat gag ggg gac tgg aag ttt ggg aag				425
Trp Lys Lys Lys Gly Ala Ile Tyr Glu Gly Asp Trp Lys Phe Gly Lys				
55	60	65	70	
cga gac ggc tac ggc acc ctc agc ctt cct gac caa cag aca gga aag				473
Arg Asp Gly Tyr Gly Thr Leu Ser Leu Pro Asp Gln Gln Thr Gly Lys				
71	76	81	86	
tgc agg aga gtc tac tca ggc tgg tgg aaa ggt gat aag aaa tcg ggt				521
Cys Arg Arg Val Tyr Ser Gly Trp Trp Lys Gly Asp Lys Lys Ser Gly				
87	92	97	102	
tat ggg atc cag ttt ttc gga ccc aag gag tat tat gag ggt gac tgg				569
Tyr Gly Ile Gln Phe Phe Gly Pro Lys Glu Tyr Tyr Glu Gly Asp Trp				
103	108	113	118	
tgt ggc agc cag cgc agc ggg tgg ggc cgc atg tat tac agc aac ggc				617
Cys Gly Ser Gln Arg Ser Gly Trp Gly Arg Met Tyr Tyr Ser Asn Gly				
119	124	129	134	
gac atc tac gag gga cag tgg gag aac gac aag ccc aac ggg gag ggc				665
Asp Ile Tyr Glu Gly Gln Trp Glu Asn Asp Lys Pro Asn Gly Glu Gly				
135	140	145	150	
atg ctg cgc ctg agtcaa aat cct aga ccc tga tggtgtgc tggcgagcc				716
Met Leu Arg Leu Ser Gln Asn Pro Arg Pro *				
151	156	161		
ttggccatgt tcaggaagac agaggaagga gattgatgcc agagaacaca aacgcttcag				776
gagaaattca agcctgtgtc acccgatcgc tcagaccagt gcggtctgg ctggaggagt				836
cagcagcagc tccaggcatg acccccggcac cctcataggg cccctcacta cccccagcac				896
tgggtcattt cttgccaata ggaaggctgg tgcttctctc ccaggctgtc ctggggaccc				956
tcttcattct ctgatctcat cctggaatgc atgagaataa agaataacca agtggaaaaaa				1016
aaaaaaaaaa				1024

<210> 92
 <211> 2818
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (449)..(2818)

<400> 92 aaggatcctt aattaaatata atccccccccc ccccccctggc tcgtctgaac ttgaagacac cccacattcc aagatgccccg aggttcctgg gaatgcctgg gggttcttgcga tccggaaaat cctaccggca tcctccttagg gagggattat tattattatttttctttaat ctgaaagaga agagaacaag ttgtgctttt ccccccctct tcttgctaaa tgccatggat ataactgaat aagcggctca gggcttccc cgcggtggacg tccgaggcca ccattctgcct gcattcgccg gagccgcccgg agggtttagc tcgagtctgt ctcgggggggg gaaggatgctg tggccgagcc ggggagcccg ggcgcggccgc ggagccggcc tcggtgccac ccagccgggg gtagatgctg cctcgcccaag gcgctgagtg accagacc ---atg gag acc ctg ctt ggt ggc ctg ---472 Met Glu Thr Leu Leu Gly Gly Leu 1 5	
cta gcg ttt ggc atg gcg ttt gcc gtg gtc gac gcc tgc ccc aag tac Leu Ala Phe Gly Met Ala Phe Ala Val Val Asp Ala Cys Pro Lys Tyr 9 14 19 24	520
tgt gtc tgc cag aat ctg tct gag tca ctg ggg acc ctg tgc ccc tcc Cys Val Cys Gln Asn Leu Ser Glu Ser Leu Gly Thr Leu Cys Pro Ser 25 30 35 40	568
aag ggg ctg ctc ttt gta ccc cct gat att gac cgg cgg aca gtg gag Lys Gly Leu Leu Phe Val Pro Pro Asp Ile Asp Arg Arg Thr Val Glu 41 46 51 56	616
ctg cgc ctg ggc aac ttc atc atc cac atc agc cgc cag gac ttt Leu Arg Leu Gly Gly Asn Phe Ile Ile His Ile Ser Arg Gln Asp Phe 57 62 67 72	664
gcc aac atg acg ggg ctg gtg gac ctg acc ctg tcc agg aac acc atc Ala Asn Met Thr Gly Leu Val Asp Leu Thr Leu Ser Arg Asn Thr Ile 73 78 83 88	712
agc cac atc cag ccc ttt tcc ttt ctg gac ctc gag agc ctc cgc tcc Ser His Ile Gln Pro Phe Ser Phe Leu Asp Leu Glu Ser Leu Arg Ser 89 94 99 104	760
ctg cat ctt gac agc aat cgg ctg cca agc ctt ggg gag gac acc ctc Leu His Leu Asp Ser Asn Arg Leu Pro Ser Leu Gly Glu Asp Thr Leu 105 110 115 120	808
cgg ggc ctg gtc aac ctg cag cac ctt atc gtg aac aac aac cag ctg Arg Gly Leu Val Asn Leu Gln His Leu Ile Val Asn Asn Asn Gln Leu 121 126 131 136	856
ggc ggc atc gca gat gag gct ttt gag gac ttc ctg ctg aca ttg gag	904

Gly	Gly	Ile	Ala	Asp	Glu	Ala	Phe	Glu	Asp	Phe	Leu	Leu	Thr	Leu	Glu	
137				142				147					152			
gat ctg gac ctc tcc tac aac aac ctc cat ggc ctg ccg tgg gac tcc															952	
Asp	Leu	Asp	Leu	Ser	Tyr	Asn	Asn	Leu	His	Gly	Leu	Pro	Trp	Asp	Ser	
153				158				163				168				
gtg cga cgc atg gtc aac ctc cac cag ctg agc ctg gac cac aac ctg															1000	
Val	Arg	Arg	Met	Val	Asn	Leu	His	Gln	Leu	Ser	Leu	Asp	His	Asn	Leu	
169				174				179				184				
ctg gat cac atc gcc gag ggc acc ttt gca gac ctg cag aaa ctg gcc															1048	
Leu	Asp	His	Ile	Ala	Glu	Gly	Thr	Phe	Ala	Asp	Leu	Gln	Lys	Leu	Ala	
185				190				195				200				
cgc ctg gat ctc acc tcc aat cgg ctg cag aag ctg ccc cct gat ccc															1096	
Arg	Leu	Asp	Leu	Thr	Ser	Asn	Arg	Leu	Gln	Lys	Leu	Pro	Pro	Asp	Pro	
201				206				211				216				
atc ttt gcc cgc tcc cag gct tcg gct ttg aca gcc aca ccc ttt gcc															1144	
Ile	Phe	Ala	Arg	Ser	Gln	Ala	Ser	Ala	Leu	Thr	Ala	Thr	Pro	Phe	Ala	
217				222				227				232				
cca ccc ttg tcc ttt agt ttt ggg ggt aac cca ctt cac tgc aat tgt															1192	
Pro	Pro	Leu	Ser	Phe	Ser	Phe	Gly	Gly	Asn	Pro	Leu	His	Cys	Asn	Cys	
233				238				243				248				
gag ctt ctc tgg ctg cgg agg ctc gag cgg gac gat gac ctg gaa acc															1240	
Glu	Leu	Leu	Trp	Leu	Arg	Arg	Leu	Glu	Arg	Asp	Asp	Asp	Leu	Glu	Thr	
249				254				259				264				
tgt ggc tcc cca ggg ggc ctc aag ggt cgc tac ttc tgg cat gtg cgt															1288	
Cys	Gly	Ser	Pro	Gly	Gly	Leu	Lys	Gly	Arg	Tyr	Phe	Trp	His	Val	Arg	
265				270				275				280				
gag gag gag ttt gtg tgc gag ccg cct ctc atc acc cag cac aca cac															1336	
Glu	Glu	Glu	Phe	Val	Cys	Glu	Pro	Pro	Leu	Ile	Thr	Gln	His	Thr	His	
281				286				291				296				
aag ttg ctg gtt ctg gag ggc cag gcg gcc aca ctc aag tgc aaa gcc															1384	
Lys	Leu	Leu	Val	Leu	Glu	Gly	Gln	Ala	Ala	Thr	Leu	Lys	Cys	Lys	Ala	
297				302				307				312				
att ggg gac ccc agc ccc ctt atc cac tgg gta gcc ccc gat gac cgc															1432	
Ile	Gly	Asp	Pro	Ser	Pro	Leu	Ile	His	Trp	Val	Ala	Pro	Asp	Asp	Arg	
313				318				323				328				
ctg gta ggg aac tcc tca agg acc gct gtc tat gac aat ggc acc ccg															1480	
Leu	Val	Gly	Asn	Ser	Ser	Arg	Thr	Ala	Val	Tyr	Asp	Asn	Gly	Thr	Pro	
329				334				339				344				
gac atc ttc atc acc aca tct cag gac agt ggt gcc ttc acc tgc att															1528	
Asp	Ile	Phe	Ile	Thr	Thr	Ser	Gln	Asp	Ser	Gly	Ala	Phe	Thr	Cys	Ile	
345				350				355				360				
gct gcc aat gct gcc gga gag gcc acg gcc atg gtg gag gtc tcc atc															1576	
Ala	Ala	Asn	Ala	Ala	Gly	Glu	Ala	Thr	Ala	Met	Val	Glu	Val	Ser	Ile	

361	366	371	376	
gtc cag ctg cca cac ctc agc aac agc acc agc cgc act gca ccc ccc Val Gln Leu Pro His Leu Ser Asn Ser Thr Ser Arg Thr Ala Pro Pro				1624
377 382		387	392	
aag tcc cgc ctc tca gac atc act ggc tcc agc aag acc agc cgg gga Lys Ser Arg Leu Ser Asp Ile Thr Gly Ser Ser Lys Thr Ser Arg Gly				1672
393 398		403	408	
ggt gga ggc agt ggg ggc gga gag cct ccc aaa agc ccc ccg gaa cgg Gly Gly Gly Ser Gly Gly Glu Pro Pro Lys Ser Pro Pro Glu Arg				1720
409 414		419	424	
gct gtg ctt gtg tct gaa gtg acc acc acc tcg gcc ctg gtc aag tgg Ala Val Leu Val Ser Glu Val Thr Thr Ser Ala Leu Val Lys Trp				1768
425 430		435	440	
tct gtc agc aag tca gca ccc cgg gtg aag atg tac cag ctg cag tac Ser Val Ser Lys Ser Ala Pro Arg Val Lys Met Tyr Gln Leu Gln Tyr				1816
441 446		451	456	
aac tgc tct gac gat gag gta ctg att tac agg atg atc cca gcc tcc Asn Cys Ser Asp Asp Glu Val Leu Ile Tyr Arg Met Ile Pro Ala Ser				1864
457 462		467	472	
aac aag gcc ttc gtg gtc aac aac ctg gtg tca ggg act ggc tac gac Asn Lys Ala Phe Val Val Asn Asn Leu Val Ser Gly Thr Gly Tyr Asp				1912
473 478		483	488	
ttg tgt gtg ctg gcc atg tgg gat gac aca gcc acg aca ctc acg gcc Leu Cys Val Leu Ala Met Trp Asp Asp Thr Ala Thr Thr Leu Thr Ala				1960
489 494		499	504	
acc aac atc gtg ggc tgc gcc cag ttc acc aag gct gac tac ccg Thr Asn Ile Val Gly Cys Ala Gln Phe Phe Thr Lys Ala Asp Tyr Pro				2008
505 510		515	520	
cag tgc cag tcc atg cac agc cag att ctg ggc ggc acc atg atc ctg Gln Cys Gln Ser Met His Ser Gln Ile Leu Gly Gly Thr Met Ile Leu				2056
521 526		531	536	
gtc atc ggg ggc atc atc gtg gcc acg ctg ctg gtc ttc atc gtc atc Val Ile Gly Ile Ile Val Ala Thr Leu Leu Val Phe Ile Val Ile				2104
537 542		547	552	
ctc atg gtg cgc tac aag gtc tgc aac cac gag gcc ccc agc aag atg Leu Met Val Arg Tyr Lys Val Cys Asn His Glu Ala Pro Ser Lys Met				2152
553 558		563	568	
gca gcg gcc gtg agc aat gtg tac tcg cag acc aac ggc gcc cag cca Ala Ala Ala Val Ser Asn Val Tyr Ser Gln Thr Asn Gly Ala Gln Pro				2200
569 574		579	584	
ccg cct cca agc agc gca cca gcc ggg gcc ccg ccg cag ggc ccg ccg Pro Pro Pro Ser Ser Ala Pro Ala Gly Ala Pro Pro Gln Gly Pro Pro				2248
585 590		595	600	

aag gtg gtg gtg cgc aac gag ctc ctg gac ttc acc gcc agc ctg gcc		2296
Lys Val Val Val Arg Asn Glu Leu Leu Asp Phe Thr Ala Ser Leu Ala		
601 606 611 616		
cgc gcc agt gac tcc tct tcc tcc agc tcc ctg ggc agt ggg gag gct		2344
Arg Ala Ser Asp Ser Ser Ser Ser Ser Leu Gly Ser Gly Glu Ala		
617 622 627 632		
gcg ggg ctg gga cgg gcc ccc tgg agg atc cca ccc tcc gcc ccg cgc		2392
Ala Gly Leu Gly Arg Ala Pro Trp Arg Ile Pro Pro Ser Ala Pro Arg		
633 638 643 648		
ccc aag ccc agc ctt gac cgc ctg atg ggg gcc ttc gcc tcc ctg gac		2440
Pro Lys Pro Ser Leu Asp Arg Leu Met Gly Ala Phe Ala Ser Leu Asp		
649 654 659 664		
ctc aag agt cag aga aag gag gag ctg ctg gac tcc agg act cca gcc		2488
Leu Lys Ser Gln Arg Lys Glu Glu Leu Leu Asp Ser Arg Thr Pro Ala		
665 670 675 680		
ggg aga ggg gct ggg acg tcg gcc cgg ggc cac cac tcg gac cga gag		2536
Gly Arg Gly Ala Gly Thr Ser Ala Arg Gly His His Ser Asp Arg Glu		
681 686 691 696		
cca ctg ctg ggg ccc cct gcg gcc cgg gcc agg agc ctg ctc ccc ttg		2584
Pro Leu Leu Gly Pro Pro Ala Ala Arg Ala Arg Ser Leu Leu Pro Leu		
697 702 707 712		
ccg ttg gag ggc aag gcc aaa cgc agc cac tcc ttc gac atg ggg gac		2632
Pro Leu Glu Gly Lys Ala Lys Arg Ser His Ser Phe Asp Met Gly Asp		
713 718 723 728		
ttt gct gct gcg gcg gga ggg gtc gtg ccg ggc ggc tac agt cct		2680
Phe Ala Ala Ala Ala Gly Gly Val Val Pro Gly Gly Tyr Ser Pro		
729 734 739 744		
cct cggt aag gtc tcg aac atc tgg acg aag cgc agc ctc tct gtc aac		2728
Pro Arg Lys Val Ser Asn Ile Trp Thr Lys Arg Ser Leu Ser Val Asn		
745 750 755 760		
ggc atg ctc ttg ccc ttt gag gag agt gac ctg gtg ggg gcc cgg ggg		2776
Gly Met Leu Leu Pro Phe Glu Glu Ser Asp Leu Val Gly Ala Arg Gly		
761 766 771 776		
act ttt ggc agc tcc gaa tgg gtg atg gag agc acg gtc tag		2818
Thr Phe Gly Ser Ser Glu Trp Val Met Glu Ser Thr Val *		
777 782 787		

<210> 93
 <211> 3626
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (296) . . (3325)

cag gtc aag aaa ctc gag cag gct ttg aag gat ggg tcg gca ggg ctg Gln Val Lys Lys Leu Glu Gln Ala Leu Lys Asp Gly Ser Ala Gly Leu 162 167 172 177	826
gat ccc cag tta cca ggg act tgt tac tcc cca cac tgc cct cct gac Asp Pro Gln Leu Pro Gly Thr Cys Tyr Ser Pro His Cys Pro Pro Asp 178 183 188 193	874
aag gca gag gca ggg tcc acc ctt cct gag aac ctg gga ggc ggg agt Lys Ala Glu Ala Gly Ser Thr Leu Pro Glu Asn Leu Gly Gly Ser 194 199 204 209	922
ggc tca gaa gtc agc cag agg gtc cac ccc tcg gac ctg gaa ggc agg Gly Ser Glu Val Ser Gln Arg Val His Pro Ser Asp Leu Glu Gly Arg 210 215 220 225	970
gag ccc acc cct gag ctt gtg gag gac agg aaa ggt tca tgc aga agg Glu Pro Thr Pro Glu Leu Val Glu Asp Arg Lys Gly Ser Cys Arg Arg 226 231 236 241	1018
ccc tgg gac cg ^g agc ctt gag aac gtg tat agg ggc tcg gag ggt tcc Pro Trp Asp Arg Ser Leu Glu Asn Val Tyr Arg Gly Ser Glu Gly Ser 242 247 252 257	1066
ccc aca aag ccc ttc atc aac cct ctg cca aaa ccc cg ^g aga acg ttc Pro Thr Lys Pro Phe Ile Asn Pro Leu Pro Lys Pro Arg Arg Thr Phe 258 263 268 273	1114
aaa cat gcc gga gaa ggg gac aaa gat ggg aag cct ggc atc ggc ttc Lys His Ala Gly Glu Gly Asp Lys Asp Gly Lys Pro Gly Ile Gly Phe 274 279 284 289	1162
agg aaa gag aaa aga aat ctg cct ctt ccc tct cta cct ccc ccg Arg Lys Glu Lys Arg Asn Leu Pro Pro Leu Pro Ser Leu Pro Pro Pro 290 295 300 305	1210
cct ctg ccc tcc tct ccc cca cct tcc tct gtg aac aga aga ctg tgg Pro Leu Pro Ser Ser Pro Pro Pro Ser Ser Val Asn Arg Arg Leu Trp 306 311 316 321	1258
acc ggg aga cag aaa tcc agt gca gac cac aga aag tcc tat gag ttt Thr Gly Arg Gln Lys Ser Ser Ala Asp His Arg Lys Ser Tyr Glu Phe 322 327 332 337	1306
gaa gat tta ctg cag tct tcc tct gag agc agc agg gtg gac tgg tac Glu Asp Leu Leu Gln Ser Ser Ser Glu Ser Ser Arg Val Asp Trp Tyr 338 343 348 353	1354
gcg cag act aag ctg ggg ctg aca cgc act tta tcg gag gag aac gtc Ala Gln Thr Lys Leu Gly Leu Thr Arg Thr Leu Ser Glu Glu Asn Val 354 359 364 369	1402
tat gaa gac att cta gat ccg cca atg aag gag aac cct tat gag gac Tyr Glu Asp Ile Leu Asp Pro Pro Met Lys Glu Asn Pro Tyr Glu Asp 370 375 380 385	1450

atc gag tta cat ggt cgc tgc ctg gga aag aag tgt gtc ttg aat ttt Ile Glu Leu His Gly Arg Cys Leu Gly Lys Lys Cys Val Leu Asn Phe 386 391 396 401	1498
cct gct tct ccc acc tct tcc atc cct gac aca ctc acc aag cag tca Pro Ala Ser Pro Thr Ser Ser Ile Pro Asp Thr Leu Thr Lys Gln Ser 402 407 412 417	1546
ttg tcc aaa cct gct ttt ttc cga caa aat tca gag agg agg aac ttc Leu Ser Lys Pro Ala Phe Phe Arg Gln Asn Ser Glu Arg Arg Asn Phe 418 423 428 433	1594
aag ctg ctg gac act agg aag ctg agt cgg gat gga act ggg tcc cct Lys Leu Leu Asp Thr Arg Lys Leu Ser Arg Asp Gly Thr Gly Ser Pro 434 439 444 449	1642
tcc aaa atc agc cct ccc tcc act ccc agc agc cct gat gac att ttc Ser Lys Ile Ser Pro Pro Ser Thr Pro Ser Pro Asp Asp Ile Phe 450 455 460 465	1690
ttt=aac=ctt=gga=gac cca=cag aac=ggc=agg=aag=aag=aga=aag=ata=ccc Phe Asn Leu Gly Asp Pro Gln Asn Gly Arg Lys Lys Arg Lys Ile Pro 466 471 476 481	1738
aag ctg gtg ttg cga atc aac gcc att tat gag gtc cgg aga gga aag Lys Leu Val Leu Arg Ile Asn Ala Ile Tyr Glu Val Arg Arg Gly Lys 482 487 492 497	1786
aaa cgg gtg aag agg ctg tcc cag tca atg gag agc aac tca gga aaa Lys Arg Val Lys Arg Leu Ser Gln Ser Met Glu Ser Asn Ser Gly Lys 498 503 508 513	1834
gtg aca gat gag aac agt gag tct gac agt gac aca gag gag aag ctg Val Thr Asp Glu Asn Ser Glu Ser Asp Ser Asp Thr Glu Glu Lys Leu 514 519 524 529	1882
aaa gct cac agc cag cgc ctg gtc aac gtg aag tcc cgg ctg aag cag Lys Ala His Ser Gln Arg Leu Val Asn Val Lys Ser Arg Leu Lys Gln 530 535 540 545	1930
gcg cct cggt tac cca tca ctt gcc cggt gaa ctc atc gag tac cag gag Ala Pro Arg Tyr Pro Ser Leu Ala Arg Glu Leu Ile Glu Tyr Gln Glu 546 551 556 561	1978
agg cag ctc ttc gag tac ttt gtg gtt gtg tct ttg cac aag aag cag Arg Gln Leu Phe Glu Tyr Phe Val Val Val Ser Leu His Lys Lys Gln 562 567 572 577	2026
gcc ggg gct gcc tac gtg cca gaa ctc acc caa cag ttc cct ctg aag Ala Gly Ala Ala Tyr Val Pro Glu Leu Thr Gln Gln Phe Pro Leu Lys 578 583 588 593	2074
ttg gaa agg tct ttc aag ttc atg aga gaa gct gag gac caa ctg aag Leu Glu Arg Ser Phe Lys Phe Met Arg Glu Ala Glu Asp Gln Leu Lys 594 599 604 609	2122
gcc att ccc cag ttc tgt ttt ccc gat gcc aag gat tgg gtt cct gtc	2170

Ala Ile Pro Gln Phe Cys Phe Pro Asp Ala Lys Asp Trp Val Pro Val			
610	615	620	625
cag cag ttc acc agt gaa aca ttc tcg ttt gtc tta act gga gaa gat			2218
Gln Gln Phe Thr Ser Glu Thr Phe Ser Phe Val Leu Thr Gly Glu Asp			
626	631	636	641
ggg agc aga agg ttc ggt tac tgc cga aga ctg ctg cct gga ggc aaa			2266
Gly Ser Arg Arg Phe Gly Tyr Cys Arg Arg Leu Leu Pro Gly Gly Lys			
642	647	652	657
ggg aag cgc ctt cct gaa gtt tac tgc att gtg agc cgc ctg gga tgc			2314
Gly Lys Arg Leu Pro Glu Val Tyr Cys Ile Val Ser Arg Leu Gly Cys			
658	663	668	673
ttc agc ctc ttt tca agg atc ttg gat gag gtg gaa aaa aga cga ggc			2362
Phe Ser Leu Phe Ser Arg Ile Leu Asp Glu Val Glu Lys Arg Arg Gly			
674	679	684	689
atc tct cct gcc ctg gtt cag cca ctc atg aga agt gtc atg gaa gcc			2410
Ile Ser Pro Ala Leu Val Gln Pro Leu Met Arg Ser Val Met Glu Ala			
690	695	700	705
cct ttc cca gcc ctg ggc aaa acc atc ctt gtc aag aac ttc ctg cca			2458
Pro Phe Pro Ala Leu Gly Lys Thr Ile Leu Val Lys Asn Phe Leu Pro			
706	711	716	721
ggt tca gga act gag gtg atc gaa ctg tgc cgc ccg ctg gac tcc cg			2506
Gly Ser Gly Thr Glu Val Ile Glu Leu Cys Arg Pro Leu Asp Ser Arg			
722	727	732	737
gtc gag cac gtg gac ttt gag tct ctc ttc tcc ctc agc gtc cgc			2554
Val Glu His Val Asp Phe Glu Ser Leu Phe Ser Ser Leu Ser Val Arg			
738	743	748	753
cac ctg gtc tgt gtg ttt gcc tcc ctg ctt ctg gag agg agg gtc atc			2602
His Leu Val Cys Val Phe Ala Ser Leu Leu Glu Arg Arg Val Ile			
754	759	764	769
ttc att gca gac aag ctc agc atc ctg tcc aag tgc tgc cac gcg atg			2650
Phe Ile Ala Asp Lys Leu Ser Ile Leu Ser Lys Cys Cys His Ala Met			
770	775	780	785
gtg gcg ctg atc tac ccc ttc gcc tgg cag cac acc tac atc ccg gt			2698
Val Ala Leu Ile Tyr Pro Phe Ala Trp Gln His Thr Tyr Ile Pro Val			
786	791	796	801
ctg cca ccc gcc atg gtc gac atc gtg tgc tcg ccg acg ccc ttc ctc			2746
Leu Pro Pro Ala Met Val Asp Ile Val Cys Ser Pro Thr Pro Phe Leu			
802	807	812	817
atc ggg ctg ctc tcc agc tcg ctg cca ctg ctc agg gag ctg ccg ctg			2794
Ile Gly Leu Leu Ser Ser Leu Pro Leu Leu Arg Glu Leu Pro Leu			
818	823	828	833
gaa gag gtc ctt gtg gtt gac ctc gtc aac agc cgg ttc ctc aga cag			2842
Glu Glu Val Leu Val Val Asp Leu Val Asn Ser Arg Phe Leu Arg Gln			

834	839	844	849	
atg gac gat gag gac tcc atc ctg ccc cgg aag ctt cag gtg gcc ctg Met Asp Asp Glu Asp Ser Ile Leu Pro Arg Lys Leu Gln Val Ala Leu				2890
850	855	860	865	
gaa cac att ctg gaa cag agg aac gag ctg gct tgt gag cag gac gaa Glu His Ile Leu Glu Gln Arg Asn Glu Leu Ala Cys Glu Gln Asp Glu				2938
866	871	876	881	
ggg ccc cta gac ggc agg cac ggt cca gag tcc agc ccc ttg aac gag Gly Pro Leu Asp Gly Arg His Gly Pro Glu Ser Ser Pro Leu Asn Glu				2986
882	887	892	897	
gtg gtg tct gaa gcc ttt gtc cgc ttc gtg gag att gtg gga cac Val Val Ser Glu Ala Phe Val Arg Phe Val Glu Ile Val Gly His				3034
898	903	908	913	
tac tct ttg ttc ctg acg tcg ggc gag cgt gag gag aga acc ctg cag Tyr Ser Leu Phe Leu Thr Ser Gly Glu Arg Glu Arg Thr Leu Gln				3082
914	919	924	929	
cg ^g gag gcc ttc cgc aaa gct gtc tcc tcc aag agc ctc cgc cac ttc Arg Glu Ala Phe Arg Lys Ala Val Ser Ser Lys Ser Leu Arg His Phe				3130
930	935	940	945	
ctg gag gtc ttc atg gag act cag atg ttt cgg ggc ttc atc cag gag Leu Glu Val Phe Met Glu Thr Gln Met Phe Arg Gly Phe Ile Gln Glu				3178
946	951	956	961	
cg ^g gag ctg cgc cgg cag gat gcc aaa ggt ctg ttt gag gtc cga gcc Arg Glu Leu Arg Arg Gln Asp Ala Lys Gly Leu Phe Glu Val Arg Ala				3226
962	967	972	977	
caa gag tat ctg gaa aca ctc ccc agt gga gag cac agc ggt gtc aat Gln Glu Tyr Leu Glu Thr Leu Pro Ser Gly Glu His Ser Gly Val Asn				3274
978	983	988	993	
aag ttc ctg aag gga cta ggc aat aaa atg aaa ttt ctc cac aag aaa Lys Phe Leu Lys Gly Leu Gly Asn Lys Met Lys Phe Leu His Lys Lys				3322
994	999	1004	1009	
taa ctct cagcctcaag ggaaaacttc ctccatgtgc agccctatgc tttaaaaaaca				3379
*				
1010				
gttcctggtg gcctttctga aaggctgggt cccaggttgt cacgggtcg ^g aactggaggc				3439
cgcgggtggct tctggccgag gctgggctct tccctggatg aggacctggg agccgcctgg				3499
gaggacagcc ccagaaagg ^g agccc gagac caggcgtgtc gccgacatgc aaatgggttg				3559
ttttgggtggt tgggtttttt ttttatctt agatattaaa agtaagaaaa atgtgaaaaaa				3619
aaaaaaaa				3626

<210> 94
<211> 1897
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (527)..(1897)

<400> 94

cggaattccc	gggtcgaccc	acgcgtccgc	acagtccccca	ctgatgctaa	cctctgtgtt	60
tggaaaatact	ctttgtctgg	agacacttct	gtgggctact	tctttttca	ggcagaactc	120
aaccttggtg	tgttatctga	ccaacttccc	acatacgctg	aagagaagtg	cacatggcca	180
tcaaaggcac	gccccccccc	cttccttca	gctgccttgg	cagctgccga	acccaccctc	240
gcagtggctg	cccagaacct	ttacacatgt	atgtgtgcgc	gtgtgcagag	catgacaagg	300
caggtggctg	gggctccagc	ctggctaaag	agaacttgcc	cttagggca	agagagggag	360
gcactgcatt	tccagttcg	ttctggaagt	gcccacctga	catctgttgt	gcccactgat	420
ctttacagat	atcctgctgg	atgacattgt	ctttacccat	tctctttcc	tcccgacgga	480
gaaatttctg	caggagctac	accagtaatt	tgttcggca	ggaggc	atg gag ggc	535
					Met Glu Gly	
					1	
cct gaa ggg	ctg ggc	cgg aag	caa gcc	tgt cta	gcc atg	583
Pro	Glu	Gly	Leu	Gly	Arg	
4	9	14	19			
ttc ttg gac acc tac cag	ggg ctg ctt	caa gag	gaa gag	ggg gcc	ggc	631
Phe	Leu	Asp	Thr	Tyr	Gln	Gly
20	25	30			35	
cac atc atc aag gat	cta tac ctg	cta att	atg aag	gac gag	tcc ctt	679
His	Ile	Ile	Lys	Asp	Leu	Tyr
36	41			46		51
tac cag ggc ctc cga gag	gac act ctg	agg ctg	cac cag	ctg gtg	gag	727
Tyr	Gln	Gly	Leu	Arg	Glu	Asp
52	57			62		67
acg gtg gaa cta aag	att cca gag	gag aac	cag cca	ccc agc	aag cag	775
Thr	Val	Glu	Leu	Lys	Ile	Pro
68	73			78		83
gtg aag cca ctc ttc	cgc cac ttc	cgc cgg	ata gac	tcc tgt	ctg cag	823
Val	Lys	Pro	Leu	Phe	Arg	His
84	89			94		99
acc cgg gtg gcc	ttc cgg	ggc tct	gat gag	atc ttc	tgc cgt	871

Thr Arg Val Ala Phe Arg Gly Ser Asp Glu Ile Phe Cys Arg Val Tyr			
100	105	110	115
atg cct gac cac tct tat gtg acc ata cgc agc cgc ctt tca gca tct			919
Met Pro Asp His Ser Tyr Val Thr Ile Arg Ser Arg Leu Ser Ala Ser			
116	121	126	131
gtg cag gac att ctg ggc tct gtg acg gag aaa ctt caa tat tca gag			967
Val Gln Asp Ile Leu Gly Ser Val Thr Glu Lys Leu Gln Tyr Ser Glu			
132	137	142	147
gag ccc gcg ggg cgt gag gat tcc ctc atc ctg gta gct gtg tcc tcc			1015
Glu Pro Ala Gly Arg Glu Asp Ser Leu Ile Leu Val Ala Val Ser Ser			
148	153	158	163
tct gga gag aag gtc ctt ctc cag ccc act gag gac tgt gtt ttc acc			1063
Ser Gly Glu Lys Val Leu Leu Gln Pro Thr Glu Asp Cys Val Phe Thr			
164	169	174	179
<u>gca</u> <u>ctg</u> <u>ggc</u> <u>atc</u> <u>aac</u> <u>agc</u> <u>cac</u> <u>ctg</u> <u>ttt</u> <u>gcc</u> <u>tgt</u> <u>act</u> <u>cgg</u> <u>gac</u> <u>agc</u> <u>tat</u>			1111
Ala Leu Gly Ile Asn Ser His Leu Phe Ala Cys Thr Arg Asp Ser Tyr			
180	185	190	195
gag gct ctg gtg ccc ctc ccc gag gag atc cag gtc tcc cct gga gac			1159
Glu Ala Leu Val Pro Leu Pro Glu Glu Ile Gln Val Ser Pro Gly Asp			
196	201	206	211
aca gag atc cac cga gtg gag cct gag gac gtt gcc aac cac cta act			1207
Thr Glu Ile His Arg Val Glu Pro Glu Asp Val Ala Asn His Leu Thr			
212	217	222	227
gcc ttc cac tgg gag ctg ttc cga tgt gtg cat gag ctg gag ttc gtg			1255
Ala Phe His Trp Glu Leu Phe Arg Cys Val His Glu Leu Glu Phe Val			
228	233	238	243
gac tac gtg ttc cac ggg gag cgc ggc cgc cgg gag acg gcc aac ttg			1303
Asp Tyr Val Phe His Gly Glu Arg Gly Arg Glu Thr Ala Asn Leu			
244	249	254	259
gag ctg ctg ctg cag cgc tgc agc gag gtc acg cac tgg gtg gcc acc			1351
Glu Leu Leu Leu Gln Arg Cys Ser Glu Val Thr His Trp Val Ala Thr			
260	265	270	275
gaa gtg ctg ctc tgc gag gcc ccg ggc aag cgc gcg cag ctg ctc aag			1399
Glu Val Leu Leu Cys Glu Ala Pro Gly Lys Arg Ala Gln Leu Lys			
276	281	286	291
aag ttc atc aag atc gcg gcc ctc tgc aag cag aac cag gac ctg ctg			1447
Lys Phe Ile Lys Ile Ala Ala Leu Cys Lys Gln Asn Gln Asp Leu Leu			
292	297	302	307
tct ttc tac gcc gtg gtc atg ggg ctg gac aac gcc gct gtc agc cgc			1495
Ser Phe Tyr Ala Val Val Met Gly Leu Asp Asn Ala Ala Val Ser Arg			
308	313	318	323
ctt cga ctc acc tgg gag aag ctg cca ggg aaa ttc aag aac ttg ttt			1543
Leu Arg Leu Thr Trp Glu Lys Leu Pro Gly Lys Phe Lys Asn Leu Phe			

324	329	334	339	
cgc aaa ttt gag aac ctg acg gac ccc tgc agg aac cac aaa agc tac Arg Lys Phe Glu Asn Leu Thr Asp Pro Cys Arg Asn His Lys Ser Tyr				1591
340	345	350		355
cga gaa gtg atc tcc aaa atg aag ccc cct gtg att ccc ttc gtg cct Arg Glu Val Ile Ser Lys Met Lys Pro Pro Val Ile Pro Phe Val Pro				1639
356	361	366		371
ctg atc ctc aaa gac ctg act ttc ctg cac gaa ggg agt aag acc ctt Leu Ile Leu Lys Asp Leu Thr Phe Leu His Glu Gly Ser Lys Thr Leu				1687
372	377	382		387
gta gat ggt ttg gtg aac atc gag aag ctg cat tca gtg gcc gaa aaa Val Asp Gly Leu Val Asn Ile Glu Lys Leu His Ser Val Ala Glu Lys				1735
388	393	398		403
gtg agg aca atc cgc aaa tac cgg agc cgg ccc ctt tgc ctg gac atg Val Arg Thr Ile Arg Lys Tyr Arg Ser Arg Pro Leu Cys Leu Asp Met				1783
404	409	414		419
gag gca tcc ccc aat cac ctg cag acc aag gcc tat gtg cgc cag ttt Glu Ala Ser Pro Asn His Leu Gln Thr Lys Ala Tyr Val Arg Gln Phe				1831
420	425	430		435
cag gtc atc gac aac cag aac ctc ctc ttc gag ctc tcc tac aag ctg Gln Val Ile Asp Asn Gln Asn Leu Leu Phe Glu Leu Ser Tyr Lys Leu				1879
436	441	446		451
gag gca aac agt cag tga Glu Ala Asn Ser Gln *				1897
452	457			

<210> 95
 <211> 2894
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (372)..(2894)

<400> 95 atttggccct cgaggccaag aattcggcac gagctggctt gtctggagcc agcctgttagg gttggggagc ctttctctcc atagttccag ggtttggta agcatcttac accagtaagt	60
attgattgaa cgtctgtcag tgacctctgc aaactctgct tttgtttag gaagcagtac aggttttgat taagcactca gctgatgtca atgcaaggga caagaactgg cagacccctc	120
ttcatgtggc agcagccaac aaggctgtca aatgtgcaga agtgcatt cccctgctga	180
	240
	300

gcagtgtcaa tgtctccgac cgaggggggc gcacagcctt gcaccatgcg gctctgaacg	360
gccacgtgga g atg gtc aat tta ctc ttg gcc aaa ggg gca aat atc aat Met Val Asn Leu Leu Ala Lys Gly Ala Asn Ile Asn	410
1 5 10	
gca ttt gac aag aag gac cgg cgt gct ctg cac tgg gca gca tac atg Ala Phe Asp Lys Lys Asp Arg Arg Ala Leu His Trp Ala Ala Tyr Met	458
14 19 24 29	
ggc cac ttg gat gtt gta gca ttg ctc att aac cat ggc gca gaa gtg Gly His Leu Asp Val Val Ala Leu Leu Ile Asn His Gly Ala Glu Val	506
30 35 40 45	
acc tgt aag gat aag aag ggt tat acc cct ctg cat gct gca gcc tcc Thr Cys Lys Asp Lys Lys Gly Tyr Thr Pro Leu His Ala Ala Ser	554
46 51 56 61	
aat gga_cag_att aat_gtt_gtc aag_cat_ctc_ctg_aac_ctg_ggg_gtg_gag Asn Gly Gln Ile Asn Val Val Lys His Leu Leu Asn Leu Gly Val Glu	602
62 67 72 77	
att gat gaa atc aat gtc tat gga aat aca gcg ctt cac atc gcc tgc Ile Asp Glu Ile Asn Val Tyr Gly Asn Thr Ala Leu His Ile Ala Cys	650
78 83 88 93	
tac aat gga cag gat gct gtg gtt aac gag ttg att gac tac ggt gct Tyr Asn Gly Gln Asp Ala Val Val Asn Glu Leu Ile Asp Tyr Gly Ala	698
94 99 104 109	
aac gtg aac cag cca aac aat aat ggg ttc acc cct ttg cat ttt gct Asn Val Asn Gln Pro Asn Asn Asn Gly Phe Thr Pro Leu His Phe Ala	746
110 115 120 125	
gct gcc tcc act cat ggt gct ttg tgt ctt gaa ttg tta gta aac aac Ala Ala Ser Thr His Gly Ala Leu Cys Leu Glu Leu Leu Val Asn Asn	794
126 131 136 141	
ggg gca gat gtt aac att cag agt aaa gat ggc aaa agt cca ctg cac Gly Ala Asp Val Asn Ile Gln Ser Lys Asp Gly Lys Ser Pro Leu His	842
142 147 152 157	
atg aca gct gtc cat gga agg ttc aca cgg tca cag acc ctc att cag Met Thr Ala Val His Gly Arg Phe Thr Arg Ser Gln Thr Leu Ile Gln	890
158 163 168 173	
aat gga ggt gaa att gac tgt gtg gat aag gac ggc aac act cct ctc Asn Gly Gly Glu Ile Asp Cys Val Asp Lys Asp Gly Asn Thr Pro Leu	938
174 179 184 189	
cat gtg gct gca aga tac ggt cat gag ctt ttg att aac acc tta ata His Val Ala Ala Arg Tyr Gly His Glu Leu Leu Ile Asn Thr Leu Ile	986
190 195 200 205	
acc agc gga gct gac aca gcc aag tgt gga atc cat agc atg ttc cct Thr Ser Gly Ala Asp Thr Ala Lys Cys Gly Ile His Ser Met Phe Pro	1034

206	211	216	221	
tta cat tta gct gcc cta aat gct cac tct gac tgc tgc aga aag ttg Leu His Leu Ala Ala Leu Asn Ala His Ser Asp Cys Cys Arg Lys Leu				1082
222 227 232 237				
tta tca tcg gga caa aag tat agc ata gta tcc ttg ttt agt aat gag Leu Ser Ser Gly Gln Lys Tyr Ser Ile Val Ser Leu Phe Ser Asn Glu				1130
238 243 248 253				
cac gtg ctg tct gca ggc ttt gaa ata gac acc cca gat aaa ttt gga His Val Leu Ser Ala Gly Phe Glu Ile Asp Thr Pro Asp Lys Phe Gly				1178
254 259 264 269				
aga acg tgc ctt cat gct gct gca gga ggt aat gtg gaa tgt ata Arg Thr Cys Leu His Ala Ala Ala Gly Gly Asn Val Glu Cys Ile				1226
270 275 280 285				
aaa ctc ttg cag agc agc gga gca gat ttc cat aaa aag gac aag tgt Lys Leu Leu Gln Ser Ser Gly Ala Asp Phe His Lys Lys Asp Lys Cys				1274
286 291 296 301				
ggg agg acc cct ttg cac tat gca gct gcg aat tgt cat ttc cac tgt Gly Arg Thr Pro Leu His Tyr Ala Ala Ala Asn Cys His Phe His Cys				1322
302 307 312 317				
att gag aca tta gtg acc aca ggg gcc aac gtt aat gaa aca gat gac Ile Glu Thr Leu Val Thr Thr Gly Ala Asn Val Asn Glu Thr Asp Asp				1370
318 323 328 333				
tgg gga cgc aca gct ttg cat tac gcc gct gca tca gac atg gat aga Trp Gly Arg Thr Ala Leu His Tyr Ala Ala Ala Ser Asp Met Asp Arg				1418
334 339 344 349				
aat aag act atc tta gga aat gcc cat gat aat tca gaa gaa ctt gaa Asn Lys Thr Ile Leu Gly Asn Ala His Asp Asn Ser Glu Glu Leu Glu				1466
350 355 360 365				
aga gcc agg gag ctg aag gaa aag gaa gcc aca cta tgt cta gag ttt Arg Ala Arg Glu Leu Lys Glu Ala Thr Leu Cys Leu Glu Phe				1514
366 371 376 381				
ctg ctt caa aat gat gca aat cca tct atc cgg gac aag gaa ggt tac Leu Leu Gln Asn Asp Ala Asn Pro Ser Ile Arg Asp Lys Glu Gly Tyr				1562
382 387 392 397				
aat agc ata cat tat gct gcc tat ggg cac agg cag tgt ctg gaa Asn Ser Ile His Tyr Ala Ala Ala Tyr Gly His Arg Gln Cys Leu Glu				1610
398 403 408 413				
ttg ctt ttg gaa aga aca aac agt gga ttt gaa gaa tca gat tct ggt Leu Leu Leu Glu Arg Thr Asn Ser Gly Phe Glu Glu Ser Asp Ser Gly				1658
414 419 424 429				
gct act aag agt cca ctc cac tta gct gcc tac aat ggg cac cat caa Ala Thr Lys Ser Pro Leu His Leu Ala Ala Tyr Asn Gly His His Gln				1706
430 435 440 445				

,gcc ttg gaa gtc ctt ctg cag tcg ttg gtg gac ctg gac atc agg gat Ala Leu Glu Val Leu Leu Gln Ser Leu Val Asp Leu Asp Ile Arg Asp 446 451 456 461	1754
gag aaa ggc cgc act gct ctg gat ctg gct gcc ttt aaa gga cac aca Glu Lys Gly Arg Thr Ala Leu Asp Leu Ala Ala Phe Lys Gly His Thr 462 467 472 477	1802
gaa tgt gtg gaa gcg ctt atc aat cag ggc gca tcc atc ttt gtg aaa Glu Cys Val Glu Ala Leu Ile Asn Gln Gly Ala Ser Ile Phe Val Lys 478 483 488 493	1850
gac aat gta acc aaa aga acc cca ctt cat gcc tcg gta att aat ggt Asp Asn Val Thr Lys Arg Thr Pro Leu His Ala Ser Val Ile Asn Gly 494 499 504 509	1898
cac aca ctg tgt tta cgg ctg ttg cta gaa att gca gac aac ceg gag His Thr Leu Cys Leu Arg Leu Leu Glu Ile Ala Asp Asn Pro Glu 510 515 520 525	1946
gcg gtc gat gtg aaa gat gcc aaa gga caa aca cca ctg atg ctt gca Ala Val Asp Val Lys Asp Ala Lys Gly Gln Thr Pro Leu Met Leu Ala 526 531 536 541	1994
gta gca tat gga cat att gac gct gtt tca ttg tta ctt gaa aag gaa Val Ala Tyr Gly His Ile Asp Ala Val Ser Leu Leu Leu Glu Lys Glu 542 547 552 557	2042
gcc aac gta gac act gtt gac atc cta gga tgc aca gct tta cac aga Ala Asn Val Asp Thr Val Asp Ile Leu Gly Cys Thr Ala Leu His Arg 558 563 568 573	2090
ggg att atg aca gga cac gag gaa tgt gtg caa atg ctg ctg gaa caa Gly Ile Met Thr Gly His Glu Glu Cys Val Gln Met Leu Leu Glu Gln 574 579 584 589	2138
gaa gtg tca att ctc tgt aaa gat tcc aga ggg agg acg ccc ttg cac Glu Val Ser Ile Leu Cys Lys Asp Ser Arg Gly Arg Thr Pro Leu His 590 595 600 605	2186
tat gca gct gct cgt ggc cac gcc acg tgg ctg agc gag ctg ctc caa Tyr Ala Ala Ala Arg Gly His Ala Thr Trp Leu Ser Glu Leu Leu Gln 606 611 616 621	2234
atg gct ctt tct gag gag gac tgt tgt ttc aaa gat aac caa ggc tac Met Ala Leu Ser Glu Glu Asp Cys Cys Phe Lys Asp Asn Gln Gly Tyr 622 627 632 637	2282
acg ccg ctg cac tgg gct tgt tac aat ggt aat gaa aac tgt ata gag Thr Pro Leu His Trp Ala Cys Tyr Asn Gly Asn Glu Asn Cys Ile Glu 638 643 648 653	2330
gta ctt ttg gag caa aaa tgt ttt cgc aaa ttt atc ggt aat ccc ttt Val Leu Leu Glu Gln Lys Cys Phe Arg Lys Phe Ile Gly Asn Pro Phe 654 659 664 669	2378

act cca ctg cac tgt gca ata atc aat gat cat ggg aat tgt gca tca		2426
Thr Pro Leu His Cys Ala Ile Ile Asn Asp His Gly Asn Cys Ala Ser		
670 675 680 685		
ttg ctg ctt ggg gcc ata gat tcc agt atc gtc agt tgt aga gat gac		2474
Leu Leu Leu Gly Ala Ile Asp Ser Ser Ile Val Ser Cys Arg Asp Asp		
686 691 696 701		
aaa ggc agg aca ccc ctt cat gcg gca ttt gct gat cat gtg gag		2522
Lys Gly Arg Thr Pro Leu His Ala Ala Ala Phe Ala Asp His Val Glu		
702 707 712 717		
tgc ttg cag ctt ctg aga cac agt gct cca gtg aac gca gta gat		2570
Cys Leu Gln Leu Leu Leu Arg His Ser Ala Pro Val Asn Ala Val Asp		
718 723 728 733		
aat tca ggg aaa aca gca ctg atg atg gct gct gag aat ggg cag gca		2618
Asn Ser Gly Lys Thr Ala Leu Met Met Ala Ala Glu Asn Gly Gln Ala		
734 739 744 749		
gac gct gtg gat att ttg gtg aac agt gcc cag gct gat ctg act gta		2666
Gly Ala Val Asp Ile Leu Val Asn Ser Ala Gln Ala Asp Leu Thr Val		
750 755 760 765		
aag gat aag gac ttg aat aca ccc tta cat ttg gct tgt agt aaa ggt		2714
Lys Asp Lys Asp Leu Asn Thr Pro Leu His Leu Ala Cys Ser Lys Gly		
766 771 776 781		
cat gaa aaa tgt gcc ttg tta ata ctt gac aag ata caa gac gag agc		2762
His Glu Lys Cys Ala Leu Leu Ile Leu Asp Lys Ile Gln Asp Glu Ser		
782 787 792 797		
ctt att aat gaa aaa aat aat gca ctg cag aca ccc ctc cac gtc gct		2810
Leu Ile Asn Glu Lys Asn Asn Ala Leu Gln Thr Pro Leu His Val Ala		
798 803 808 813		
gcg cgc aat ggc tta aag gtg gta gtt gag gag ttg ctg gcc aaa ggg		2858
Ala Arg Asn Gly Leu Lys Val Val Val Glu Glu Leu Leu Ala Lys Gly		
814 819 824 829		
gcc tgt gta ctt gct gta gat gaa aat ggc tgt taa		2894
Ala Cys Val Leu Ala Val Asp Glu Asn Gly Cys *		
830 835 840		

<210> 96
<211> 1522
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (158)...(1303)

<400> 96
 atttggccct cgaggccaaa aattcgac gaggattat ttacaaaatg gactgcttag 60
 tacgtgtcga gaacttctc gagccactgc cgaattggaa cgagcatgga gagaatatga 120
 taagtttagaa tacgatgtaa ctgttaccag gaaccag atg caa gag cag ctg gat 175
 Met Gln Glu Gln Leu Asp
 1
 cac ctt ggt gaa gtt cag acg gaa tca gca gga att cag cgt gca cag 223
 His Leu Gly Glu Val Gln Thr Glu Ser Ala Gly Ile Gln Arg Ala Gln
 7 12 17 22
 att cag aaa gaa ctt tgg cga att cag gat gtc atg gaa ggg ctg agt 271
 Ile Gln Lys Glu Leu Trp Arg Ile Gln Asp Val Met Glu Gly Leu Ser
 23 28 33 38
 aaa cat aag cag caa aga ggt act aca gaa ata ggt atg ata gga tca 319
 Lys His Lys Gln Gln Arg Gly Thr Thr Glu Ile Gly Met Ile Gly Ser
 39 44 49 54
 aag cct ttc tca aca gtt aag tac aaa aat gag ggt cca gat tat aga 367
 Lys Pro Phe Ser Thr Val Lys Tyr Lys Asn Glu Gly Pro Asp Tyr Arg
 55 60 65 70
 ctc tac aag agt gaa cca gag tta aca aca gtg gca gaa gtt gat gaa 415
 Leu Tyr Lys Ser Glu Pro Glu Leu Thr Thr Val Ala Glu Val Asp Glu
 71 76 81 86
 tct aat gga gaa gaa aaa tca gaa cct gtt tca gag ata gaa act tca 463
 Ser Asn Gly Glu Glu Lys Ser Glu Pro Val Ser Glu Ile Glu Thr Ser
 87 92 97 102
 gtt gtt aaa ggt tcc cac ttt cct gtt gga gta gtc cct cca aga gca 511
 Val Val Lys Gly Ser His Phe Pro Val Gly Val Val Pro Pro Arg Ala
 103 108 113 118
 aaa tca cca aca ccc gaa tct tcg aca ata gct tcc tat gta acc ttg 559
 Lys Ser Pro Thr Pro Glu Ser Ser Thr Ile Ala Ser Tyr Val Thr Leu
 119 124 129 134
 agg aaa act aag aag atg atg gat cta aga acg gaa aga cca aga agt 607
 Arg Lys Thr Lys Lys Met Met Asp Leu Arg Thr Glu Arg Pro Arg Ser
 135 140 145 150
 gca gtg gaa cag ctc tgt ttg gct gaa agt act cga cca agg atg act 655
 Ala Val Glu Gln Leu Cys Leu Ala Glu Ser Thr Arg Pro Arg Met Thr
 151 156 161 166
 gtg gaa gag caa atg gaa aga ata aga aga cat caa caa gcg tgc ctg 703
 Val Glu Glu Gln Met Glu Arg Ile Arg Arg His Gln Gln Ala Cys Leu
 167 172 177 182
 agg gag aag aaa aaa ggg tta aat gtt atc ggt gct tca gac cag tca 751
 Arg Glu Lys Lys Lys Gly Leu Asn Val Ile Gly Ala Ser Asp Gln Ser
 183 188 193 198

ccc tta caa agc cct tca aat tta agg gat aat cca ttt agg act act		799
Pro Leu Gln Ser Pro Ser Asn Leu Arg Asp Asn Pro Phe Arg Thr Thr		
199	204	209
		214
cag act cga agg agg gat gat aag gaa ctg gac act gcc att aga gaa		847
Gln Thr Arg Arg Asp Asp Lys Glu Leu Asp Thr Ala Ile Arg Glu		
215	220	225
		230
aat gat gta aag cca gac cat gaa act cct gca aca gaa att gtt caa		895
Asn Asp Val Lys Pro Asp His Glu Thr Pro Ala Thr Glu Ile Val Gln		
231	236	241
		246
cta aaa gaa acc gaa ccc caa aat gtg gac ttc agc aaa gag tta aaa		943
Leu Lys Glu Thr Glu Pro Gln Asn Val Asp Phe Ser Lys Glu Leu Lys		
247	252	257
		262
aaa act gaa aac att tca tat gaa atg ctt ttt gaa cct gag cca aat		991
Lys Thr Glu Asn Ile Ser Tyr Glu Met Leu Phe Glu Pro Glu Pro Asn		
263	268	273
		278
gga gta aat tct gtg gaa atg atg gat aaa gaa aga aac aaa gac aaa		1039
Gly Val Asn Ser Val Glu Met Met Asp Lys Glu Arg Asn Lys Asp Lys		
279	284	289
		294
atg cct gag gat gtt aca ttc agc cct caa gat gaa aca cag acc gca		1087
Met Pro Glu Asp Val Thr Phe Ser Pro Gln Asp Glu Thr Gln Thr Ala		
295	300	305
		310
aat cat aaa cca gaa gag cat cct gaa gaa aat aca aag aac agt gtt		1135
Asn His Lys Pro Glu Glu His Pro Glu Glu Asn Thr Lys Asn Ser Val		
311	316	321
		326
gac gaa cag gaa gaa act gtt att tct tac gaa tca act cct gag gtt		1183
Asp Glu Gln Glu Glu Thr Val Ile Ser Tyr Glu Ser Thr Pro Glu Val		
327	332	337
		342
tct aga gga aat caa aca atg gca gtg aaa agt ctg tcc cca tct cct		1231
Ser Arg Gly Asn Gln Thr Met Ala Val Lys Ser Leu Ser Pro Ser Pro		
343	348	353
		358
gag tcc tcg gca tcg cca gtt cca tcc act cag ccg cag ctc aca gaa		1279
Glu Ser Ser Ala Ser Pro Val Pro Ser Thr Gln Pro Gln Leu Thr Glu		
359	364	369
		374
gga tca cat ttc atg tgt gtg tag tcttagaaga actatactga cttctgttga		1333
Gly Ser His Phe Met Cys Val *		
375	380	
aaccattcaa agctaaagac atggaccttc agcagtgtaa gaagatattg tacagtatat		1393
ttaaatcta tgaaattcat agttctgatg ctttggta cagagcatca ttttatcact		1453
tctggaaaaa tgtttattcc aaaacagctt taatggccca tatgtacacc ttctgtatct		1513
tcaaggta		1522

<210> 97
<211> 1202
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (155)..(976)

<400> 97
atttggccct cgaggccaag aattcggcac gagaactgga agagcaggtg aagaggctcc 60
ttgggtgggc acccctggcg tcctcccatg agggcagcct cacaggggtg tctgcctgtg 120
agttttgtta cagggcctca ccaagagagg gcct atg gag gcc gag gac cag 172
Met Glu Ala Glu Asp Gln
1
ggg gag ctt ttc ctg cac ctc cgg tca gtg gca cgt gcc ccc cag acc 220
Gly Glu Leu Phe Leu His Leu Arg Ser Val Ala Arg Ala Pro Gln Thr
7 12 17 22
tta tct atg cac cga ctc cag aga aag ctg aag gag gca gcc aga aaa 268
Leu Ser Met His Arg Leu Gln Arg Lys Leu Lys Glu Ala Ala Arg Lys
23 28 33 38
atc atc agc ctc cgc ctg gag aaa gag cag ctc atc gag atg ggg aac 316
Ile Ile Ser Leu Arg Leu Glu Lys Glu Gln Leu Ile Glu Met Gly Asn
39 44 49 54
agg ctc cgt gca gag ctg ggc cga ccc gaa agg tgg ctg ttg cac cac 364
Arg Leu Arg Ala Glu Leu Gly Arg Pro Glu Arg Trp Leu Leu His His
55 60 65 70
gcc ctc cct cct gcc cct gag gcc cgg aag cca ggc gag gag ccc agg 412
Ala Leu Pro Pro Ala Pro Glu Ala Arg Lys Pro Gly Glu Glu Pro Arg
71 76 81 86
agg cct ttg gat cgc agc cca cct ttg gga cag gtg cag ccc cat ttt 460
Arg Pro Leu Asp Arg Ser Pro Pro Leu Gly Gln Val Gln Pro His Phe
87 92 97 102
aca tct cag gac gcc aag agt gcc gag gat gag gct cct aga cac 508
Thr Ser Gln Asp Ala Lys Ser Ala Glu Asp Glu Ala Pro Ser Arg His
103 108 113 118
ttg gga aag cac cag ccc cgc tca gca cag gtg ggc agc aga ctt gac 556
Leu Gly Lys His Gln Pro Arg Ser Ala Gln Val Gly Ser Arg Leu Asp
119 124 129 134
gcc ctg caa ggc ccg aag aca caa cac agc atc cac acg gtg acc tgt 604
Ala Leu Gln Gly Pro Lys Thr Gln His Ser Ile His Thr Val Thr Cys
135 140 145 150
aaa tca cct cgg cag aaa gaa gac agg tcc cca aag cca ccc cag gct 652

Lys Ser Pro Arg Gln Lys Glu Asp Arg Ser Pro Lys Pro Pro Gln Ala			
151	156	161	166
ccc cag cac cct gag gag cat ggt cgc caa tcc cac agc tcc tcc tcc			700
Pro Gln His Pro Glu Glu His Gly Arg Gln Ser His Ser Ser Ser Ser			
167	172	177	182
ttt gcc agt ggc acc ctc cag gac atg tgg agg ttg cta gac ctg gga			748
Phe Ala Ser Gly Thr Leu Gln Asp Met Trp Arg Leu Leu Asp Leu Gly			
183	188	193	198
tcc agc cct tct ggt gtc acc tcc cag ggt gac tca act cca gag ctc			796
Ser Ser Pro Ser Gly Val Thr Ser Gln Gly Asp Ser Thr Pro Glu Leu			
199	204	209	214
cca gct cct cca gca gcc gac agg agg ccc gtc aag atg cag gca ggc			844
Pro Ala Pro Pro Ala Ala Asp Arg Arg Pro Val Lys Met Gln Ala Gly			
215	220	225	230
att gcc acc cca ggg atg aag aca gca gcc cag gca aag gcc aag acc			892
Ile Ala Thr Pro Gly Met Lys Thr Ala Ala Gln Ala Lys Ala Lys Thr			
231	236	241	246
aca gga gcc tcc cggtct cat cct gca aaa gct aaa ggc tgc cag agg			940
Thr Gly Ala Ser Arg Ser His Pro Ala Lys Ala Lys Gly Cys Gln Arg			
247	252	257	262
ccc ccc aag atc cgt aac tac aac att atg gac tga cttc ctcccccac			990
Pro Pro Lys Ile Arg Asn Tyr Asn Ile Met Asp *			
263	268	273	
cccgcccccac taagggtgc tcggggcctc cgcatggtgc ctgtgctttc acctacgtgt			1050
tgtggggggg tgtgggcaca gcgtgcaggg tggaggcagg gagctgcagg gcaggctccc			1110
aaatgctgct gaggcgaccc tgctgactga aggctccct gagcacaggg cccattaaaa			1170
ccaggttctt ccctggggaa aaaaaaaaaa aa			1202

<210> 98
<211> 6314
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(5379)

<400> 98
atg gcc cca gaa tcc cat ata tta gct tct aac acc atg gag acc cat
Met Ala Pro Glu Ser His Ile Leu Ala Ser Asn Thr Met Glu Thr His
1 5 10

ata tta gca tcc aac acc atg gac tcc caa atg cta gcg tcc aac acc 96

Ile Leu Ala Ser Asn Thr Met Asp Ser Gln Met Leu Ala Ser Asn Thr			
17	22	27	32
atg gac tcc cag atg cta gca tcc aac acc atg gac tcc cag atg tta			144
Met Asp Ser Gln Met Leu Ala Ser Asn Thr Met Asp Ser Gln Met Leu			
33	38	43	48
gcg tct agc acc atg gac tcc cag atg tta gca act agc tcc atg gac			192
Ala Ser Ser Thr Met Asp Ser Gln Met Leu Ala Thr Ser Ser Met Asp			
49	54	59	64
tcc caa atg cta gcg tcc aac acc atg gac tcc cag atg cta gca tcc			240
Ser Gln Met Leu Ala Ser Asn Thr Met Asp Ser Gln Met Leu Ala Ser			
65	70	75	80
aac acc atg gac tcc cag atg tta gcg tct agc acc atg gac tcc cag			288
Asn Thr Met Asp Ser Gln Met Leu Ala Ser Ser Thr Met Asp Ser Gln			
81	86	91	96
atg <u>tta</u> <u>gca</u> <u>act</u> <u>agc</u> <u>tcc</u> <u>atg</u> <u>gac</u> <u>tcc</u> <u>cag</u> <u>atg</u> <u>tta</u> <u>gca</u> <u>act</u> <u>agc</u> <u>tcc</u>			336
Met Leu Ala Thr Ser Ser Met Asp Ser Gln Met Leu Ala Thr Ser Ser			
97	102	107	112
atg gac tcc cag atg tta gca act agc act atg gac tcc cag atg tta			384
Met Asp Ser Gln Met Leu Ala Thr Ser Thr Met Asp Ser Gln Met Leu			
113	118	123	128
gca acc agt tcc atg gac tcc cag atg tta gca acc agc tcc atg gac			432
Ala Thr Ser Ser Met Asp Ser Gln Met Leu Ala Thr Ser Ser Met Asp			
129	134	139	144
tcc cag atg tta gca acc agc tcc atg gac tcc cag atg tta gca acc			480
Ser Gln Met Leu Ala Thr Ser Ser Met Asp Ser Gln Met Leu Ala Thr			
145	150	155	160
agc tcc atg gac tcc cag atg tta gca acc agc acc atg gat tct cag			528
Ser Ser Met Asp Ser Gln Met Leu Ala Thr Ser Thr Met Asp Ser Gln			
161	166	171	176
atg tta gca acc agc acc atg gac tcc cag atg tta gca act agc tca			576
Met Leu Ala Thr Ser Thr Met Asp Ser Gln Met Leu Ala Thr Ser Ser			
177	182	187	192
atg gat tcc cag atg tta gca tct ggc act atg gac tct caa atg tta			624
Met Asp Ser Gln Met Leu Ala Ser Gly Thr Met Asp Ser Gln Met Leu			
193	198	203	208
gct tct ggc acc atg gat gct cag atg tta gcg tct ggt acc atg gat			672
Ala Ser Gly Thr Met Asp Ala Gln Met Leu Ala Ser Gly Thr Met Asp			
209	214	219	224
gcc cag atg tta gcg tct agt acc caa gat tct gct atg ttg ggt tca			720
Ala Gln Met Leu Ala Ser Ser Thr Gln Asp Ser Ala Met Leu Gly Ser			
225	230	235	240
aaa tct cct gat ccc tat agg tta gct cag gat cct tac agg tta gct			768
Lys Ser Pro Asp Pro Tyr Arg Leu Ala Gln Asp Pro Tyr Arg Leu Ala			

241	246	251	256		
cag	gat	ccc	tat	agg ttg ggc cat gac ccc tat aga tta ggt cat gat	816
Gln	Asp	Pro	Tyr	Arg Leu Gly His Asp Pro Tyr Arg Leu Gly His Asp	
257	262		267	272	
gct	tac	agg	tta	gga caa gac cct tat aga tta ggc cat gat ccc tac	864
Ala	Tyr	Arg	Leu	Gly Gln Asp Pro Tyr Arg Leu Gly His Asp Pro Tyr	
273	278		283	288	
aga	cta	act	cct	gat ccc tat agg atg tca cct aga ccc tac agg ata	912
Arg	Leu	Thr	Pro	Asp Pro Tyr Arg Met Ser Pro Arg Pro Tyr Arg Ile	
289	294		299	304	
gca	ccc	agg	tcc	tat aga ata gca ccc agg cca tat agg tta gca cct	960
Ala	Pro	Arg	Ser	Tyr Arg Ile Ala Pro Arg Pro Tyr Arg Leu Ala Pro	
305	310		315	320	
aga	ccc	ctg	atg	tta gca tct aga cgt tct atg atg atg tcc tat gct	1008
Arg	Pro	Leu	Met	Leu Ala Ser Arg Arg Ser Met Met Ser Tyr Ala	
321	326		331	336	
gca	gaa	cgt	tcc	atg atg tca tct tac gaa cgc tct atg atg tct tat	1056
Ala	Glu	Arg	Ser	Met Met Ser Ser Tyr Glu Arg Ser Met Met Ser Tyr	
337	342		347	352	
gag	cgg	tct	atg	tcc cct atg gct gaa cgc tct atg atg tca gcc	1104
Glu	Arg	Ser	Met	Met Ser Pro Met Ala Glu Arg Ser Met Met Ser Ala	
353	358		363	368	
tac	gag	cgc	tct	atg atg tca gcc tac gag cgc tct atg atg tcc cct	1152
Tyr	Glu	Arg	Ser	Met Met Ser Ala Tyr Glu Arg Ser Met Met Ser Pro	
369	374		379	384	
atg	gct	gag	cgc	tct atg atg tca gct tat gaa cgc tcc atg atg tca	1200
Met	Ala	Glu	Arg	Ser Met Met Ser Ala Tyr Glu Arg Ser Met Met Ser	
385	390		395	400	
gct	tat	gaa	cgc	tcc atg atg tcc cca atg gct gat cga tct atg atg	1248
Ala	Tyr	Glu	Arg	Ser Met Met Ser Pro Met Ala Asp Arg Ser Met Met	
401	406		411	416	
tcc	atg	ggt	gct	gac cgg tct atg atg tcg tca tac tct gct gct gac	1296
Ser	Met	Gly	Ala	Asp Arg Ser Met Met Ser Tyr Ser Ala Ala Asp	
417	422		427	432	
cgg	tct	atg	atg	tca tcg tac tct gca gct gac cga tct atg atg tca	1344
Arg	Ser	Met	Met	Ser Ser Tyr Ser Ala Ala Asp Arg Ser Met Met Ser	
433	438		443	448	
tct	tat	act	gct	gat cgt tca atg atg tct atg gct gct gat tct tac	1392
Ser	Tyr	Thr	Ala	Asp Arg Ser Met Met Ser Met Ala Ala Asp Ser Tyr	
449	454		459	464	
acc	gat	tct	tac	act gac aca tat aca gag gca tat atg gtg cca cct	1440
Thr	Asp	Ser	Tyr	Thr Asp Thr Tyr Thr Tyr Glu Ala Tyr Met Val Pro Pro	
465	470		475	480	

ttg cct cct gaa gag ccc cca aca atg cca ccg ttg cca cct gag gag		1488
Leu Pro Pro Glu Glu Pro Pro Thr Met Pro Pro Leu Pro Pro Glu Glu		
481 486 491 496		
cca cca atg aca cca cca ttg cct cct gag gaa cca cca gag ggt cca		1536
Pro Pro Met Thr Pro Pro Leu Pro Pro Glu Glu Pro Pro Glu Gly Pro		
497 502 507 512		
gca ttg ccc act gag cag tca gca tta aca gct gaa aat act tgg cct		1584
Ala Leu Pro Thr Glu Gln Ser Ala Leu Thr Ala Glu Asn Thr Trp Pro		
513 518 523 528		
aca gag gtg cca tca tta cca tct gaa gag tct gta tcg cag cct gag		1632
Thr Glu Val Pro Ser Leu Pro Ser Glu Glu Ser Val Ser Gln Pro Glu		
529 534 539 544		
cct cct gtg agt caa agt gag att tcg gag cct tca gca gtg cct act		1680
Pro Pro Val Ser Gln Ser Glu Ile Ser Glu Pro Ser Ala Val Pro Thr		
545 550 555 560		
gat tat tca gtg tca gca tca gat ccc tca gtt tta gta tca gag gct		1728
Asp Tyr Ser Val Ser Ala Ser Asp Pro Ser Val Leu Val Ser Glu Ala		
561 566 571 576		
gct gtg act gtt cca gaa cca cca gag cca gaa tct tca att acg		1776
Ala Val Thr Val Pro Glu Pro Pro Glu Pro Glu Ser Ser Ile Thr		
577 582 587 592		
tta aca cct gta gag tct gca gta gca gaa gaa cat gaa gtt gtt		1824
Leu Thr Pro Val Glu Ser Ala Val Val Ala Glu Glu His Glu Val Val		
593 598 603 608		
cca gag aga cca gtg act tgt atg gta tct gaa act ccc gcc atg tca		1872
Pro Glu Arg Pro Val Thr Cys Met Val Ser Glu Thr Pro Ala Met Ser		
609 614 619 624		
gct gaa cca act gtg tta gca tca gag cct cct gtt atg tca gag aca		1920
Ala Glu Pro Thr Val Leu Ala Ser Glu Pro Pro Val Met Ser Glu Thr		
625 630 635 640		
gca gaa aca ttt gat tcc atg aga gcc tca gga cat gtt gcc tca gaa		1968
Ala Glu Thr Phe Asp Ser Met Arg Ala Ser Gly His Val Ala Ser Glu		
641 646 651 656		
gta tct aca tcc ttg ttg gtt cca gca gta act act cca gtg ctg gca		2016
Val Ser Thr Ser Leu Leu Val Pro Ala Val Thr Thr Pro Val Leu Ala		
657 662 667 672		
gag agc att ctg gag ccg cca gcc atg gct gcc cca gag tct tca gct		2064
Glu Ser Ile Leu Glu Pro Pro Ala Met Ala Ala Pro Glu Ser Ser Ala		
673 678 683 688		
atg gct gtc ctg gag tct tcg gct gtg acc gtc ctg gag tct tcg act		2112
Met Ala Val Leu Glu Ser Ser Ala Val Thr Val Leu Glu Ser Ser Thr		
689 694 699 704		

gtg act gtc ctg gag tct tcg act gta act gtc ctg gag cct tcg gtt		2160	
Val Thr Val Leu Glu Ser Ser Thr Val Thr Val Leu Glu Pro Ser Val			
705	710	715	720
gtg act gtc ccg gag cct cct gtt gtg gct gag cca gac tct gtt acc		2208	
Val Thr Val Pro Glu Pro Pro Val Val Ala Glu Pro Asp Ser Val Thr			
721	726	731	736
att cct gtg cca gtt gtt tct gcg ctg gag cct tct gtg cct gtt ctg		2256	
Ile Pro Val Pro Val Val Ser Ala Leu Glu Pro Ser Val Pro Val Leu			
737	742	747	752
gaa cca gcg gtg tca gtc ctt caa cct tct atg att gtt tca gaa cca		2304	
Glu Pro Ala Val Ser Val Leu Gln Pro Ser Met Ile Val Ser Glu Pro			
753	758	763	768
tct gtt tct gtc cag gaa tcg act gtg aca gtt tca gag cct gct gtc		2352	
Ser Val Ser Val Gln Glu Ser Thr Val Thr Val Ser Glu Pro Ala Val			
769	774	779	784
aca gtc tca gag cag act caa gta ata cca act gag gtg gct ata gag		2400	
Thr Val Ser Glu Gln Thr Gln Val Ile Pro Thr Glu Val Ala Ile Glu			
785	790	795	800
tcc aca cca atg ata ctg gaa tct agt atc atg tca tca cat gtt atg		2448	
Ser Thr Pro Met Ile Leu Glu Ser Ser Ile Met Ser Ser His Val Met			
801	806	811	816
aaa gga att aat cta tcc tct ggt gat caa att ctt gct cca gag att		2496	
Lys Gly Ile Asn Leu Ser Ser Gly Asp Gln Ile Leu Ala Pro Glu Ile			
817	822	827	832
ggc atg cag gag att gca ttg cat tca ggt gaa gaa cca cat gct gag		2544	
Gly Met Gln Glu Ile Ala Leu His Ser Gly Glu Glu Pro His Ala Glu			
833	838	843	848
gaa cac ctg aaa ggt gac ttt tac gaa agt gaa cat ggt ata aat ata		2592	
Glu His Leu Lys Gly Asp Phe Tyr Glu Ser Glu His Gly Ile Asn Ile			
849	854	859	864
gac ctt aat ata aat agt cat tta att gct aaa gag atg gaa cat aat		2640	
Asp Leu Asn Ile Asn Ser His Leu Ile Ala Lys Glu Met Glu His Asn			
865	870	875	880
aca gtg tgt gct ggt act agt cct gtt ggg gaa att ggt gaa gag		2688	
Thr Val Cys Ala Ala Gly Thr Ser Pro Val Gly Glu Ile Gly Glu Glu			
881	886	891	896
aaa att ttg ccc acc agt gag act aaa cag cgc aca gta ttg gat acc		2736	
Lys Ile Leu Pro Thr Ser Glu Thr Lys Gln Arg Thr Val Leu Asp Thr			
897	902	907	912
tac cct ggt gtt agt gaa gct gat gca gga gaa act cta tct tct act		2784	
Tyr Pro Gly Val Ser Glu Ala Asp Ala Gly Glu Thr Leu Ser Ser Thr			
913	918	923	928
ggt cct ttt gct ctg gaa cct gat gca aca gga act agt aag ggt att		2832	

Gly Pro Phe Ala Leu Glu Pro Asp Ala Thr Gly Thr Ser Lys Gly Ile				
929	934	939	944	
gaa ttt acc aca gca tct act ctc agt tta gtt aat aaa tat gat gtt				2880
Glu Phe Thr Thr Ala Ser Thr Leu Ser Leu Val Asn Lys Tyr Asp Val				
945	950	955	960	
gat tta tct tta act act caa gat act gaa cat gac atg gta ata att				2928
Asp Leu Ser Leu Thr Thr Gln Asp Thr Glu His Asp Met Val Ile Ile				
961	966	971	976	
tcc acc agt cct agt ggt ggt agt gaa gct gac att gaa ggg cct ttg				2976
Ser Thr Ser Pro Ser Gly Gly Ser Glu Ala Asp Ile Glu Gly Pro Leu				
977	982	987	992	
cct gct aaa gat att cat ctt gat tta cca tct aat aat aac ctt gtt				3024
Pro Ala Lys Asp Ile His Leu Asp Leu Pro Ser Asn Asn Asn Leu Val				
993	998	1003	1008	
agt aag gat aca gaa gaa cca tta cct gta aaa gag agt gac cag aca				3072
Ser Lys Asp Thr Glu Glu Pro Leu Pro Val Lys Glu Ser Asp Gln Thr				
1009	1014	1019	1024	
ata gca gcc ttg ctc agc cct aaa gaa agt agt gga gga gaa aaa gaa				3120
Ile Ala Ala Leu Leu Ser Pro Lys Glu Ser Ser Gly Gly Glu Lys Glu				
1025	1030	1035	1040	
gta cct ccc cct aaa gag aca ctg cct gat tca gga ttt tct gcc				3168
Val Pro Pro Pro Lys Glu Thr Leu Pro Asp Ser Gly Phe Ser Ala				
1041	1046	1051	1056	
aat att gag gat att aat gaa gca gat tta gtg aga ccg tta ctt cct				3216
Asn Ile Glu Asp Ile Asn Glu Ala Asp Leu Val Arg Pro Leu Leu Pro				
1057	1062	1067	1072	
aag gac atg gaa cgt ctt aca agc ctt aga gct ggc att gaa gga cct				3264
Lys Asp Met Glu Arg Leu Thr Ser Leu Arg Ala Gly Ile Glu Gly Pro				
1073	1078	1083	1088	
tta ctt gca agt gat gtt gga cgt gac aga tct gct gcc agc ccg gtt				3312
Leu Leu Ala Ser Asp Val Gly Arg Asp Arg Ser Ala Ala Ser Pro Val				
1089	1094	1099	1104	
gta agt agt atg cca gaa aga gct tca gag tct tct tca gag gaa aaa				3360
Val Ser Ser Met Pro Glu Arg Ala Ser Glu Ser Ser Glu Glu Lys				
1105	1110	1115	1120	
gat gat tat gaa att ttt gta aaa gtt aag gac act cac gaa aaa agc				3408
Asp Asp Tyr Glu Ile Phe Val Lys Val Lys Asp Thr His Glu Lys Ser				
1121	1126	1131	1136	
aag aaa aat aag aac cgt gat aag ggg gag aaa gag aag aaa aga gat				3456
Lys Lys Asn Lys Asn Arg Asp Lys Gly Glu Lys Glu Lys Lys Arg Asp				
1137	1142	1147	1152	
cct cat tta aga tct cga agt aag cgt tcc aaa tct tct gaa cac aaa				3504
Pro His Leu Arg Ser Arg Ser Lys Arg Ser Ser Glu His Lys				

1153	1158	1163	1168	
tca cgc aag cgt acc agt gaa tct cgt tct agg gca aga aag aga tca Ser Arg Lys Arg Thr Ser Glu Ser Arg Ser Arg Ala Arg Lys Arg Ser				3552
1169 1174 1179 1184				
tct aag tcc aag tct cat cgc tct cag aca cgt tca cgg tca cgt tca Ser Lys Ser Lys Ser His Arg Ser Gln Thr Arg Ser Arg Ser Arg Ser				3600
1185 1190 1195 1200				
aga cgc agg agg aga agc agc aga tca aga tca aag tct aga gga aga Arg Arg Arg Arg Ser Ser Arg Ser Lys Ser Arg Gly Arg				3648
1201 1206 1211 1216				
aga tct gta tca aaa gag aag cgc aaa aga tct cca aag cac aga tcc Arg Ser Val Ser Lys Glu Lys Arg Lys Arg Ser Pro Lys His Arg Ser				3696
1217 1222 1227 1232				
aag tct agg gaa aga aaa aga aaa aga tca agc tcc agg gat aac cga Lys Ser Arg Glu Arg Lys Arg Ser Ser Ser Arg Asp Asn Arg				3744
1233 1238 1243 1248				
aag aca gtt aga gct cga agt cga acc cca agt cgt cgg agt cgg agt Lys Thr Val Arg Ala Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg				3792
1249 1254 1259 1264				
cat act cca agt cgt cga agg tct aga tct gtg ggt aga aga agg His Thr Pro Ser Arg Arg Arg Ser Arg Val Gly Arg Arg Arg				3840
1265 1270 1275 1280				
agc ttt agc att tcc cca agc cgc cgc agc cgc acc ccc agc cgc cgc Ser Phe Ser Ile Ser Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg				3888
1281 1286 1291 1296				
agc cgc acc ccc agc cgc cgc agc cgc acc ccc agc cgc cgc agc cgc Ser Arg Thr Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg				3936
1297 1302 1307 1312				
acc ccc agc cgc cgg agc cgc acc cct agc cgt cgg agc cgc acc cca Thr Pro Ser Arg Arg Ser Arg Thr Pro Ser Arg Arg Ser Arg Thr Pro				3984
1313 1318 1323 1328				
agc cgc cgg aga aga tca agg tct gtg gta aga aga cga agc ttc agt Ser Arg Arg Arg Ser Arg Ser Val Val Arg Arg Arg Ser Phe Ser				4032
1329 1334 1339 1344				
atc tca cca gtc aga tta agg cga tca aga aca ccc tta aga aga agg Ile Ser Pro Val Arg Leu Arg Arg Ser Arg Thr Pro Leu Arg Arg Arg				4080
1345 1350 1355 1360				
ttt agc aga tct ccc atc cgt cgt aaa aga tcc agg tct tct gaa cga Phe Ser Arg Ser Pro Ile Arg Arg Lys Arg Ser Arg Ser Ser Glu Arg				4128
1361 1366 1371 1376				
ggc aga tca ccc aaa cgt ctg aca gat ttg gat aag gct caa tta ctt Gly Arg Ser Pro Lys Arg Leu Thr Asp Leu Asp Lys Ala Gln Leu Leu				4176
1377 1382 1387 1392				

gaa ata gcc aaa gct aat gca gct gcc atg tgt gct aag gct ggt gtc Glu Ile Ala Lys Ala Asn Ala Ala Ala Met Cys Ala Lys Ala Gly Val	1393	1398	1403	1408	4224
cct tta cca cca aac cta aag cct gca cct cca cct act ata gtt gag Pro Leu Pro Pro Asn Leu Lys Pro Ala Pro Pro Pro Thr Ile Val Glu	1409	1414	1419		4272
aaa gtt gct aaa aag tca gga gga gct act ata gaa gaa cta act gag Lys Val Ala Lys Lys Ser Gly Gly Ala Thr Ile Glu Glu Leu Thr Glu	1425	1430	1435	1440	4320
aaa tgt aaa cag atc gca cag agt aaa gaa gat gat gat gta ata gtg Lys Cys Lys Gln Ile Ala Gln Ser Lys Glu Asp Asp Asp Val Ile Val	1441	1446	1451	1456	4368
aat aaa cct cat gtt tcg gat gaa gag gaa gaa gaa cct cct ttt tat Asn Lys Pro His Val Ser Asp Glu Glu Glu Glu Pro Pro Phe Tyr	1457	1462	1467		4416
cat cat ccc ttt aaa ctc agt gaa ttt aaa cct att ttt ttc aat ctg His His Pro Phe Lys Leu Ser Glu Phe Lys Pro Ile Phe Phe Asn Leu	1473	1478	1483	1488	4464
aat att gct gca gca aaa cca act cca cca aaa agc cag gta aca tta Asn Ile Ala Ala Ala Lys Pro Thr Pro Pro Lys Ser Gln Val Thr Leu	1489	1494	1499	1504	4512
aca aaa gaa ttc cct gta tca tct gga tct caa cat cgg aaa aaa gaa Thr Lys Glu Phe Pro Val Ser Ser Gly Ser Gln His Arg Lys Lys Glu	1505	1510	1515	1520	4560
gcg gat agt gtt tat gga gaa tgg gtt cct gtg gag aaa aat ggt gaa Ala Asp Ser Val Tyr Gly Glu Trp Val Pro Val Glu Lys Asn Gly Glu	1521	1526	1531	1536	4608
gaa aac aaa gat gat gat aat gtt ttc agc agc aat ttg ccc tca gag Glu Asn Lys Asp Asp Asp Asn Val Phe Ser Ser Asn Leu Pro Ser Glu	1537	1542	1547	1552	4656
cct gtg gac atc tct aca gca atg agt gaa cgg gca ctt gct cag aaa Pro Val Asp Ile Ser Thr Ala Met Ser Glu Arg Ala Leu Ala Gln Lys	1553	1558	1563	1568	4704
aga ctc agt gag aat gca ttt gat ctt gaa gcc atg agc atg tta aat Arg Leu Ser Glu Asn Ala Phe Asp Leu Glu Ala Met Ser Met Leu Asn	1569	1574	1579	1584	4752
aga gct cag gaa agg att gat gcc tgg gct cag ctg aac tct att cct Arg Ala Gln Glu Arg Ile Asp Ala Trp Ala Gln Leu Asn Ser Ile Pro	1585	1590	1595	1600	4800
ggc cag ttc aca gga agt aca gga gta cag gtt ttg aca caa gaa cag Gly Gln Phe Thr Gly Ser Thr Gly Val Gln Val Leu Thr Gln Glu Gln	1601	1606	1611	1616	4848

ttg gcc aat act ggt gcc caa gcc tgg att aaa aag gat cag ttc tta Leu Ala Asn Thr Gly Ala Gln Ala Trp Ile Lys Lys Asp Gln Phe Leu	1617	1622	1627	1632	4896
aga gca gcc ccg gta act gga gga atg gga gcc gtt ttg atg aga aaa Arg Ala Ala Pro Val Thr Gly Met Gly Ala Val Leu Met Arg Lys	1633	1638	1643	1648	4944
atg ggc tgg aga gaa gga gaa gga tta gga aaa aac aaa gaa ggc aat Met Gly Trp Arg Glu Gly Glu Gly Leu Gly Lys Asn Lys Glu Gly Asn	1649	1654	1659	1664	4992
aag gaa ccc atc cta gtt gat ttt aag aca gac cga aaa ggt ctt gtt Lys Glu Pro Ile Leu Val Asp Phe Lys Thr Asp Arg Lys Gly Leu Val	1665	1670	1675	1680	5040
gca gta gga gaa aga gca caa aag agg tct ggg aac ttc tct gct gca Ala Val Gly Glu Arg Ala Gln Lys Arg Ser Gly Asn Phe Ser Ala Ala	1681	1686	1691	1696	5088
atg aaa gat ctg tca ggc aaa cat cct gtg tct gct ttg atg gag atc Met Lys Asp Leu Ser Gly Lys His Pro Val Ser Ala Leu Met Glu Ile	1697	1702	1707	1712	5136
tgt aat aaa aga agg tgg caa cca cct gaa ttt cta ttg gtc cat gat Cys Asn Lys Arg Arg Trp Gln Pro Pro Glu Phe Leu Leu Val His Asp	1713	1718	1723	1728	5184
agt ggc cct gat cat cgc aaa cat ttt ctc ttt agg gta ttg ata aat Ser Gly Pro Asp His Arg Lys His Phe Leu Phe Arg Val Leu Ile Asn	1729	1734	1739	1744	5232
gga agc gct tac cag ccc agc ttt gcc agc cct aat aag aag cat gct Gly Ser Ala Tyr Gln Pro Ser Phe Ala Ser Pro Asn Lys Lys His Ala	1745	1750	1755	1760	5280
aaa gcc aca gca gct act gtg gtt ctt caa gca atg ggc ctt gta cca Lys Ala Thr Ala Ala Thr Val Val Leu Gln Ala Met Gly Leu Val Pro	1761	1766	1771	1776	5328
aag gac ctc atg gct aat gcc act tgc ttc agg agt gcc tca cgt aga Lys Asp Leu Met Ala Asn Ala Thr Cys Phe Arg Ser Ala Ser Arg Arg	1777	1782	1787	1792	5376
tag attg aggtttata ataatcattt cagaatttta ctctgcata caatgtattt *	1793				5433
cctcttaat gttgtaaata tttggcaatt taagacattt tgtaaaaagc aatctgtaaa					5493
aacatctcca ggcttgatt tttgtaccat ggaaattgta tttaaccata cagggtttg					5553
gtatgttat attgttacc tttagtcatgt atttgtttaa gtggctaaca tccaaacgac					5613
tgtttgaagg catcagagta atcttcagtg tggaatgtta aataacgctt ttatactgtta					5673
ttttgtacta ttagttaact ccccttcattt atggcttaggc tactgttaaca cttgcctgtta					5733

atcagtgaag ggctgtgcac cttgtactat ttcacaatgg gttctgctgg acagataatg	5793
ggccagtgtt attgaggtga tcaagatctg ttccacaggg ctaatgccac catctcccct	5853
caaaattttg tagaggttct aaaaagaaag tggtatgttg tgtgatgatc agcactaagt	5913
cctgcattcc tgttaaagcc acttgggtca taagaaggga gtaaaaaaaaatg aagtctgact	5973
agaattctat tgcagaggcc aagtacattt agtatggcat tgagttgtga tatagttttta	6033
cttgatgtg catttgaat ttcagctaca cctagataga cgtaaaaaatga taattaaaaat	6093
gctgtAACCA acttatctaa taaaattggc aaccagccac tattttgttg actatgaaaaa	6153
agttaaaaagt ttatgttaat ttttagggtc tgatagaata tttcatgtgtt attacagtgg	6213
tattcatatg ctatgtctct aaactttatt ttcaaaagct taaggccccaa atacaaaactt	6273
ctctggataaacgtggtgtt ttatTTAAA aaaaaaaaaa a ..	6314

<210> 99
 <211> 1606
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (103)..(1071)

<400> 99

atttggccct cgaggccaag aattcggcac gagggcagct gcagggtctc gctgggggccc	60
gctcgggacc aattttgaag aggactgaga gtggcttca ca atg gaa ggg atc	114
Met Glu Gly Ile	
1	

agt aat ttc aag aca cca agc aaa tta tca gaa aaa aag aaa tct gta	162
Ser Asn Phe Lys Thr Pro Ser Lys Leu Ser Glu Lys Lys Ser Val	
5 10 15 20	

tta tgt tca act cca act ata aat atc ccg gcc tct ccg ttt atg cag	210
Leu Cys Ser Thr Pro Thr Ile Asn Ile Pro Ala Ser Pro Phe Met Gln	
21 26 31 36	

aag ctt ggc ttt ggt act ggg gta aat gtg tac cta atg aaa aga tct	258
Lys Leu Gly Phe Gly Thr Gly Val Asn Val Tyr Leu Met Lys Arg Ser	
37 42 47 52	

cca aga ggt ttg tct cat tct cct tgg gct gta aaa aag att aat cct	306
Pro Arg Gly Leu Ser His Ser Pro Trp Ala Val Lys Lys Ile Asn Pro	
53 58 63 68	

ata tgt aat gat cat tat cga agt gtg tat caa aag aga cta atg gat	354
---	-----

Ile Cys Asn Asp His Tyr Arg Ser Val Tyr Gln Lys Arg Leu Met Asp			
69	74	79	84
gaa gct aag att ttg aaa agc ctt cat cat cca aac att gtt ggt tat			402
Glu Ala Lys Ile Leu Lys Ser Leu His His Pro Asn Ile Val Gly Tyr			
85	90	95	100
cgt gct ttt act gaa gcc aat gat ggc agt ctg tgt ctt gct atg gaa			450
Arg Ala Phe Thr Glu Ala Asn Asp Gly Ser Leu Cys Leu Ala Met Glu			
101	106	111	116
tat gga ggt gaa aag tct cta aat gac tta ata gaa gaa cga tat aaa			498
Tyr Gly Gly Glu Lys Ser Leu Asn Asp Leu Ile Glu Glu Arg Tyr Lys			
117	122	127	132
gcc agc caa gat cct ttt cca gca gcc ata att tta aaa gtt gct ttg			546
Ala Ser Gln Asp Pro Phe Pro Ala Ala Ile Ile Leu Lys Val Ala Leu			
133	138	143	148
aat atg gca aga ggg tta aag tat ctg cac caa gaa aag aaa ctg ctt			594
Asn Met Ala Arg Gly Leu Lys Tyr Leu His Gln Glu Lys Lys Leu Leu			
149	154	159	164
cat gga gac ata aag tct tca aat gtt gta att aaa ggc gat ttt gaa			642
His Gly Asp Ile Lys Ser Ser Asn Val Val Ile Lys Gly Asp Phe Glu			
165	170	175	180
aca att aaa atc tgt gat gta gga gtc tct cta cca ctg gat gaa aat			690
Thr Ile Lys Ile Cys Asp Val Gly Val Ser Leu Pro Leu Asp Glu Asn			
181	186	191	196
atg act gtg act gac cct gag gct tgt tac att ggc aca gag cca tgg			738
Met Thr Val Thr Asp Pro Glu Ala Cys Tyr Ile Gly Thr Glu Pro Trp			
197	202	207	212
aaa ccc aaa gaa gct gtg gag gag aat ggt gtt att act gac aag gca			786
Lys Pro Lys Glu Ala Val Glu Glu Asn Gly Val Ile Thr Asp Lys Ala			
213	218	223	228
gac ata ttt gcc ttt ggc ctt act ttg tgg gaa atg atg act tta tcg			834
Asp Ile Phe Ala Phe Gly Leu Thr Leu Trp Glu Met Met Thr Leu Ser			
229	234	239	244
att cca cac att aat ctt tca aat gat gat gat gaa gat aaa act			882
Ile Pro His Ile Asn Leu Ser Asn Asp Asp Asp Glu Asp Lys Thr			
245	250	255	260
ttt gat gaa agt gat ttt gat gat gaa gca tac tat gca gcg ttg gga			930
Phe Asp Glu Ser Asp Phe Asp Asp Glu Ala Tyr Tyr Ala Ala Leu Gly			
261	266	271	276
act agg cca cct att aat atg gaa gaa ctg gat gaa tca tac cag aaa			978
Thr Arg Pro Pro Ile Asn Met Glu Glu Leu Asp Glu Ser Tyr Gln Lys			
277	282	287	292
gta att gaa ctc ttc tct gta tgc act aat gaa gac cct aaa gat cgt			1026
Val Ile Glu Leu Phe Ser Val Cys Thr Asn Glu Asp Pro Lys Asp Arg			

293	298	303	308	
cct tct gct gca cac att gtt gaa gct ctg gaa aca gat gtc tag tga				1074
Pro Ser Ala Ala His Ile Val Glu Ala Leu Glu Thr Asp Val *				
309	314	319		
tcatctcagc tgaagtgtgg cttgcataaaa taactgttta ttccaaaata tttacatagt				1134
tactatcagt agttattaga ctctaaaatt ggcataatttggaggaccataag tttcttggta				1194
acatatggat aactatttct aatatgaaat atgcttatat tggctataag cacttggaat				1254
tgtactgggt tttctgtaaa gtttttagaaa ctagctacat aagtactttg atactgctca				1314
tgctgactta aaacactagc agtaaaacgc tgtaaactgt aacattaaat tgaatgacca				1374
ttacttttat taatgatctt tcttaaatat tctatatttt aatggatcta ctgacattag				1434
cactttgtac agtacaaaat aaagtctaca tttgtttaaa acaaaaaaaaaaaaaaa				1494
ttgcggccgc tctagagtat ccctcaaaga ggcccaagct tacgcgtacc cagtttctt				1554
gtacaaaagtgtgcccgtat gtgagacgaa tcatggctat atcgacgatc gc				1606

<210> 100
 <211> 2275
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (770)..(2230)

<400> 100				
ccactttgtcaagaaagct gggtaacgcgt aagctgggc ccctcttaggg atactctaga				60
gcggccgccc ttttttttttttttttttaaacacatt ttttcctgg cttcgacat				120
cagactgctg cagccctaacc ttcccagggttcagcttttggagctgcc cattcctccg				180
gctgcgagaa aggacgcgcg ccctgcgtcg ggcgaagaaa agaagcaaaa cttgtcgaaa				240
gggtttcgatc atcaacactcc ttcccgcaaa cctaaacctc ctgccggggc catccctaga				300
cagaggaaag ttccctgcaga gccgaccagc cctagtggat ctggggcagg cagcggcgat				360
ggctgtggaa ttagatctgt tttgaaccca gtggagcgca tcgctgggc tcggaaatca				420
ccgtccgcgg gcacccgggtt ggcgtgccc gagtggaaacc gacagttgc gagcctcgcc				480
tgcaagtggc ctctccccc cgccgttgcgtt gttcagtgatc gggtgagggc tgccgtgtg				540
gcaagttgca aagagagcct cagaggtccg aagagcgctg cgctcctact cgccgttcgt				600

tcttcctctt	ctcggttccc	tactgtgaaa	tcgcagcgac	atttacaag	gcctccgggt	660
cctaccgaga	ccgatccgca	gcgtttggcc	cggtcgcgcc	tattgcatacg	ggagcccccg	720
agcaccggcg	aaggactggc	gggtggggta	gggaggtggc	ggcggcggc	atg gcg Met Ala 1	775
agg ttc ccg aag gcc gac ctg gcc gct gca gga gtt atg tta ctt tgc						823
Arg Phe Pro Lys Ala Asp Leu Ala Ala Gly Val Met Leu Leu Cys						
3	8	13	18			
cac ttc ttc acg gac cag ttt cag ttc gcc gat ggg aaa ccc gga gac						871
His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro Gly Asp						
19	24	29	34			
caa atc ctt gat tgg cag tat gga gtt act cag gcc ttc cct cac aca						919
Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro His Thr						
35	40	45	50			
gag gag gag gtg gaa gtt gat tca cac gcg tac agc cac agg tgg aaa						967
Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg Trp Lys						
51	56	61	66			
aga aac ttg gac ttt ctc aag gcg gta gac acg aac cga gca agc gtc						1015
Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala Ser Val						
67	72	77	82			
ggc caa gac tct gag ccc aga agc ttc aca gac ctg ctg ctg gat						1063
Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu Asp						
83	88	93	98			
gat ggg cag gac aat aac act cag atc gag gag gat aca gac cac aat						1111
Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp His Asn						
99	104	109	114			
tac tat ata tct cga ata tat ggt cca tct gat tct gcc agc cgg gat						1159
Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp						
115	120	125	130			
tta tgg gtg aac ata gac caa atg gaa aaa gat aaa gtg aag att cat						1207
Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys Ile His						
131	136	141	146			
gga ata ttg tcc aat act cat cgg caa gct gca aga gtg aat ctg tcc						1255
Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser						
147	152	157	162			
ttc gat ttt cca ttt tat ggc cac ttc cta cgt gaa atc act gtg gca						1303
Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala						
163	168	173	178			
acc ggg ggt ttc ata tac act gga gaa gtc gta cat cga atg cta aca						1351
Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr						
179	184	189	194			
gcc aca cag tac ata gca cct tta atg gca aat ttc gat ccc agt gta						1399

Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val			
195	200	205	210
tcc aga aat tca act gtc aga tat ttt gat aat ggc aca gca ctt gtg			1447
Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu Val			
211	216	221	226
gtc cag tgg gac cat gta cat ctc cag.gat aat tat aac ctg gga agc			1495
Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu Gly Ser			
227	232	237	242
ttc aca ttc cag gca acc ctg ctc atg gat gga cga atc atc ttt gga			1543
Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile Phe Gly			
243	248	253	258
tac aaa gaa att cct gtc ttg gtc aca cag ata agt tca acc aat cat			1591
Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr Asn His			
259	264	269	274
cca gtg aaa gtc gga ctg tcc gat gca ttt gtc gtt gtc cac agg atc			1639
Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His Arg Ile			
275	280	285	290
caa caa att ccc aat gtt cga aga aga aca att tat gaa tac cac cga			1687
Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr His Arg			
291	296	301	306
gtt gag cta caa atg tca aaa att acc aac att tcg gct gtg gag atg			1735
Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val Glu Met			
307	312	317	322
acc cca tta ccc aca tgc ctc cag ttt aac aga tgt ggc ccc tgt gta			1783
Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro Cys Val			
323	328	333	338
tct tct cag att ggc ttc aac tgc agt tgg tgt agt aaa ctt caa aga			1831
Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu Gln Arg			
339	344	349	354
tgt tcc agt gga ttt gat cgt cat cgg cag gac tgg gtg gac agt gga			1879
Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp Ser Gly			
355	360	365	370
tgc cct gaa gag tca aaa gag aag atg tgt gag aat aca gaa cca gtg			1927
Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val			
371	376	381	386
gaa act tct tct cga acc acc aca acc ata gga gcg aca acc acc cag			1975
Glu Thr Ser Ser Arg Thr Thr Thr Ile Gly Ala Thr Thr Gln			
387	392	397	402
ttc agg gtc cta act acc acc aga aga gca gtg act tct cag ttt ccc			2023
Phe Arg Val Leu Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro			
403	408	413	418
acc agc ctc cct aca gaa gat gat acc aag ata gca cta cat cta aaa			2071
Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys			

agcaccggcg aaggactggc ggggtgggta gggaggtggc ggccggcggc	atg gcg Met Ala 1	775
agg ttc ccg aag gcc gac ctg gcc gct gca gga gtt atg tta ctt tgc Arg Phe Pro Lys Ala Asp Leu Ala Ala Gly Val Met Leu Leu Cys 3 8 13 18		823
cac ttc ttc acg gac cag ttt cag ttc gcc gat ggg aaa ccc gga gac His Phe Phe Thr Asp Gln Phe Gln Phe Ala Asp Gly Lys Pro Gly Asp 19 24 29 34		871
caa atc ctt gat tgg cag tat gga gtt act cag gcc ttc cct cac aca Gln Ile Leu Asp Trp Gln Tyr Gly Val Thr Gln Ala Phe Pro His Thr 35 40 45 50		919
gag gag gag gtg gaa gtt gat tca cac gcg tac agc cac agg tgg aaa Glu Glu Glu Val Glu Val Asp Ser His Ala Tyr Ser His Arg Trp Lys 51 56 61 66		967
aga aac ttg gac ttt ctc aag gcg gta gac acg aac cga gca agc gtc Arg Asn Leu Asp Phe Leu Lys Ala Val Asp Thr Asn Arg Ala Ser Val 67 72 77 82		1015
ggc caa gac tct cct gag ccc aga agc ttc aca gac ctg ctg ctg gat Gly Gln Asp Ser Pro Glu Pro Arg Ser Phe Thr Asp Leu Leu Asp 83 88 93 98		1063
gat ggg cag gac aat aac act cag atc gag gag gat aca gac cac aat Asp Gly Gln Asp Asn Asn Thr Gln Ile Glu Glu Asp Thr Asp His Asn 99 104 109 114		1111
tac tat ata tct cga ata tat ggt cca tct gat tct gcc agc cgg gat Tyr Tyr Ile Ser Arg Ile Tyr Gly Pro Ser Asp Ser Ala Ser Arg Asp 115 120 125 130		1159
tta tgg gtg aac ata gac caa atg gaa aaa gat aaa gtg aag att cat Leu Trp Val Asn Ile Asp Gln Met Glu Lys Asp Lys Val Lys Ile His 131 136 141 146		1207
gga ata ttg tcc aat act cat cgg caa gct gca aga gtg aat ctg tcc Gly Ile Leu Ser Asn Thr His Arg Gln Ala Ala Arg Val Asn Leu Ser 147 152 157 162		1255
ttc gat ttt cca ttt tat ggc cac ttc cta cgt gaa atc act gtg gca Phe Asp Phe Pro Phe Tyr Gly His Phe Leu Arg Glu Ile Thr Val Ala 163 168 173 178		1303
acc ggg ggt ttc ata tac act gga gaa gtc gta cat cga atg cta aca Thr Gly Gly Phe Ile Tyr Thr Gly Glu Val Val His Arg Met Leu Thr 179 184 189 194		1351
gcc aca cag tac ata gca cct tta atg gca aat ttc gat ccc agt gta Ala Thr Gln Tyr Ile Ala Pro Leu Met Ala Asn Phe Asp Pro Ser Val 195 200 205 210		1399
tcc aga aat tca act gtc aga tat ttt gat aat ggc aca gca ctt gtg		1447

Ser Arg Asn Ser Thr Val Arg Tyr Phe Asp Asn Gly Thr Ala Leu Val			
211	216	221	226
gtc cag tgg gac cat gta cat ctc cag gat aat tat aac ctg gga agc			1495
Val Gln Trp Asp His Val His Leu Gln Asp Asn Tyr Asn Leu Gly Ser			
227	232	237	242
ttc aca ttc cag gca acc ctg ctc atg gat gga cga atc atc ttt gga			1543
Phe Thr Phe Gln Ala Thr Leu Leu Met Asp Gly Arg Ile Ile Phe Gly			
243	248	253	258
tac aaa gaa att cct gtc ttg gtc aca cag ata agt tca acc aat cat			1591
Tyr Lys Glu Ile Pro Val Leu Val Thr Gln Ile Ser Ser Thr Asn His			
259	264	269	274
cca gtg aaa gtc gga ctg tcc gat gca ttt gtc gtt gtc cac agg atc			1639
Pro Val Lys Val Gly Leu Ser Asp Ala Phe Val Val Val His Arg Ile			
275	280	285	290
caa caa att ccc aat gtt cga aga aga aca att tat gaa tac cac cga			1687
Gln Gln Ile Pro Asn Val Arg Arg Arg Thr Ile Tyr Glu Tyr His Arg			
291	296	301	306
gta gag cta caa atg tca aaa att acc aac att tcg gct gtg gag atg			1735
Val Glu Leu Gln Met Ser Lys Ile Thr Asn Ile Ser Ala Val Glu Met			
307	312	317	322
acc cca tta ccc aca tgc ctc cag ttt aac aga tgt ggc ccc tgt gta			1783
Thr Pro Leu Pro Thr Cys Leu Gln Phe Asn Arg Cys Gly Pro Cys Val			
323	328	333	338
tct tct cag att ggc ttc aac tgc agt tgg tgt agt aaa ctt caa aga			1831
Ser Ser Gln Ile Gly Phe Asn Cys Ser Trp Cys Ser Lys Leu Gln Arg			
339	344	349	354
tgt tcc agt gga ttt gat cgt cat cgg cag gac tgg gtg gac agt gga			1879
Cys Ser Ser Gly Phe Asp Arg His Arg Gln Asp Trp Val Asp Ser Gly			
355	360	365	370
tgc cct gaa gag tca aaa gag aag atg tgt gag aat aca gaa cca gtg			1927
Cys Pro Glu Glu Ser Lys Glu Lys Met Cys Glu Asn Thr Glu Pro Val			
371	376	381	386
gaa act tct tct cga acc acc aca acc ata gga gcg aca acc acc cag			1975
Glu Thr Ser Ser Arg Thr Thr Thr Ile Gly Ala Thr Thr Gln			
387	392	397	402
ttc agg gtc cta act acc acc aga aga gca gtg act tct cag ttt ccc			2023
Phe Arg Val Leu Thr Thr Arg Arg Ala Val Thr Ser Gln Phe Pro			
403	408	413	418
acc agc ctc cct aca gaa gat gat acc aag ata gca cta cat cta aaa			2071
Thr Ser Leu Pro Thr Glu Asp Asp Thr Lys Ile Ala Leu His Leu Lys			
419	424	429	434
gat aat gga gct tct aca gat gac agt gca gct gag aag aaa ggg gga			2119
Asp Asn Gly Ala Ser Thr Asp Asp Ser Ala Ala Glu Lys Lys Gly Gly			

435	440	445	450	
acc ctc cac gct ggc ctc atc att gga atc ctc atc ctg gtc ctc att				2167
Thr Leu His Ala Gly Leu Ile Ile Gly Ile Leu Ile Leu Val Leu Ile				
451	456	461	466	
gta gcc aca gcc att ctt gtg aca gtc tat atg tat cac cac cca aca				2215
Val Ala Thr Ala Ile Leu Val Thr Val Tyr Met Tyr His His Pro Thr				
467	472	477	482	
tca gca gcc agc atc ttc ttt att gag aga cgc cca agc aga tgg cct				2263
Ser Ala Ala Ser Ile Phe Phe Ile Glu Arg Arg Pro Ser Arg Trp Pro				
483	488	493	498	
gcg atg aag ttt aga aga ggc tct gga cat cct gcc tat gct gaa gtt				2311
Ala Met Lys Phe Arg Arg Gly Ser Gly His Pro Ala Tyr Ala Glu Val				
499	504	509	514	
gaa cca gtt gga gag aaa gaa ggc ttt att gta tca gag cag tgc taa				2359
Glu Pro Val Gly Glu Lys Glu Gly Phe Ile Val Ser Glu Gln Cys *				
515	520	525	530	
aatttctagg acagaacaac accagtactg gtttacaggt gtttaagacta aaattttgcc				2419
tataccctta agacaaacaa acaaacacac acacaaacaa gctctaagct gctgtagcct				
gaagaagaca agatttctgg acaagcttag cccaggaaac aaagggtaaa caaaaaacta				
aaacttatac aagataccat ttacactgaa catagaattc cctagtggaa tgtcatctat				
agttcactcg gaacatctcc cgtggactta tctgaagtat gacaagatta taatgcttt				
ggcttaggtg cagggttgca aaggatcag aaaaaaaaaa tcataataaa gcttttagttc				
atgagggatc gaaaaaaaaa aaaaaaaaaaagg gcggccgctc tagagtatcc ctcgaggggc				
ccaagcttac gcgtacccag ctttcttgta caaagtgg				2817

<210> 102
 <211> 1156
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (251)..(904)

<400> 102		
taatgctgta cgcctgcacg taccgggtccg gaattccccgg gtcgacgatt tcgtacaagt	60	
tgccggcagc tgagcgccgc gcctcctcct gctcgagcc ccctacgccc accccggcggc	120	
ggtgccagc gccaggacgc acatcccgcg gacaccgacc ccagatgtaa agcgggaccc	180	

cagccccctcg	ccccccggcg	cgatcgacag	tctcgccagc	gtctcctctg	ccaaaaccca	240
gggcttggaaag	atg tgg cag ccg gcc acg gag cgc ctg cag cac ttt cag					289
	Met Trp Gln Pro Ala Thr Glu Arg Leu Gln His Phe Gln					
1	5			10		
acc atg ctg aag tct aaa ttg aat gtc tta aca ctg aaa aag gaa cct						337
Thr Met Leu Lys Ser Lys Leu Asn Val Leu Thr Leu Lys Glu Pro						
14	19		24		29	
ctc cca gcg gtc atc ttc cat gag ccg gag gcc att gag ctg tgc acg						385
Leu Pro Ala Val Ile Phe His Glu Pro Glu Ala Ile Glu Leu Cys Thr						
30	35		40		45	
acc aca ccg ctg atg aag aca agg act cac agt ggc tgc aag gtt acc						433
Thr Thr Pro Leu Met Lys Thr Arg Thr His Ser Gly Cys Lys Val Thr						
46	51		56		61	
tac ctg ggc aaa gtc tcc acc act ggc atg cag ttt ttg tca ggc tgc						481
Tyr Leu Gly Lys Val Ser Thr Thr Gly Met Gln Phe Leu Ser Gly Cys						
62	67		72		77	
aca gaa aag cca gtc att gag ctc tgg aag aag cac acg cta gcc cga						529
Thr Glu Lys Pro Val Ile Glu Leu Trp Lys His Thr Leu Ala Arg						
78	83		88		93	
gag gat gtc ttt ccg gcc aat gcc ctc ctg gaa atc cgg cca ttc caa						577
Glu Asp Val Phe Pro Ala Asn Ala Leu Leu Glu Ile Arg Pro Phe Gln						
94	99		104		109	
gtt tgg ctc cat cat ctc gac cac aaa ggg gag gcc aca gtg cac atg						625
Val Trp Leu His His Leu Asp His Lys Gly Glu Ala Thr Val His Met						
110	115		120		125	
gat acc ttc cag gtg gcc cgc atc gcc tac tgc acc gcc gac cac aac						673
Asp Thr Phe Gln Val Ala Arg Ile Ala Tyr Cys Thr Ala Asp His Asn						
126	131		136		141	
gtg agc ccc aac atc ttc gcc tgg gtc tac agg gag atc aat gat gac						721
Val Ser Pro Asn Ile Phe Ala Trp Val Tyr Arg Glu Ile Asn Asp Asp						
142	147		152		157	
ctg tcc tac cag atg gac tgc cac gcc gtg gag tgc gag agc aag ctc						769
Leu Ser Tyr Gln Met Asp Cys His Ala Val Glu Cys Glu Ser Lys Leu						
158	163		168		173	
gag gcc aag aaa ctg gcc cac gcc atg atg gag gcc ttc agg aag act						817
Glu Ala Lys Lys Leu Ala His Ala Met Met Glu Ala Phe Arg Lys Thr						
174	179		184		189	
ttc cac agt atg aag agc gac ggg cgg atc cac agc aac agc tcc tcc						865
Phe His Ser Met Lys Ser Asp Gly Arg Ile His Ser Asn Ser Ser Ser						
190	195		200		205	
gaa gag gtt tcc cag gaa ttg gaa tcc gat gat ggc tga atgaacttga						914
Glu Glu Val Ser Gln Glu Leu Glu Ser Asp Asp Gly *						
206	211		216			

gacgcttcag caaaggcagc attggtcacg gagttcaagg gaatagatga gtaagcaacg	974
tttcaaattt gggataaaaa gactgccaaa ctattggctg accaaggaaa ttAAATTCAAG	1034
aagagcaatt ctaaatctaa agaaatgtat cattaaagta attacgttac attgaaaaaa	1094
aaaaaaaaaa aaacctatgc ggccgcaagc ttattccctt tagtgaggaa atactaaaac	1154
cg	1156

<210> 103
 <211> 3227
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (440)..(1747)

<400> 103	
atttggccct cgaggccaag aattcggcac gagatggcat ctccactctg tgacccagac	60
tgccacttgg ccccaaaaga a ^f atttcttc tgacagtgg aagctgacat atcaccactt	120
tccttctact gtgagtgct ctggatggc agaaaggaat ggccagcccc tggttatgg	180
catctaagg cacctctgaa atgctgtgag cccctttcc ttcctctcct ctgctatttc	240
ccatctctgc tggcagg agaatagaac cctggctgcc agagatgcaa gtgtgtgacg	300
atatgggtgc tggtgcatat ttagtatgtg cctgtgtcca gccatgtgca tgtgtgggtg	360
tgtgagtgta tgaccagcc cttcccccgt ggccaagcag agagagtggc cttgaggaag	420
ccatagcagc aggaccagc atg gcc tct gct gcc tct gtg acc agc ctg gca	472
Met Ala Ser Ala Ala Ser Val Thr Ser Leu Ala	
1 5	

gat gaa gtc aac tgc ccc atc tgt cag ggt acc ctg agg gag ccg gtc	520
Asp Glu Val Asn Cys Pro Ile Cys Gln Gly Thr Leu Arg Glu Pro Val	
12 17 22 27	

act atc gac tgc ggc cac aac ttc tgc cgg gcc tgc ctt acc cgc tac	568
Thr Ile Asp Cys Gly His Asn Phe Cys Arg Ala Cys Leu Thr Arg Tyr	
28 33 38 43	

tgt gag ata cca ggc cca gac ctg gag gag tcc cct act tgc cca ctc	616
Cys Glu Ile Pro Gly Pro Asp Leu Glu Ser Pro Thr Cys Pro Leu	
44 49 54 59	

tgc aaa gaa ccc ttc cgt cct ggg agc ttc cgg ccc aac tgg cag ctg	664
Cys Lys Glu Pro Phe Arg Pro Gly Ser Phe Arg Pro Asn Trp Gln Leu	
60 65 70 75	

gct aac gtg gtg gag aac att gag cgc ctc cag ctg gtg tcc aca ctg Ala Asn Val Val Glu Asn Ile Glu Arg Leu Gln Leu Val Ser Thr Leu	712
76 81 86 91	
ggt ttg gga gag gag gat gtc tgc caa gag cac gga gag aag atc tac Gly Leu Gly Glu Glu Asp Val Cys Gln Glu His Gly Glu Lys Ile Tyr	760
92 97 102 107	
ttc ttc tgt gag gat gag atg cag ttg tgc gtg gtg tgc cgg gag Phe Phe Cys Glu Asp Asp Glu Met Gln Leu Cys Val Val Cys Arg Glu	808
108 113 118 123	
gct ggg gag cac gct acc cac acc atg cgc ttc ctg gag gat gca gcg Ala Gly Glu His Ala Thr His Thr Met Arg Phe Leu Glu Asp Ala Ala	856
124 129 134 139	
gct ccc tat agg gaa caa atc cat aag tgt ctt aaa tgt cta aga aaa Ala Pro Tyr Arg Glu Gln Ile His Lys Cys Leu Lys Cys Leu Arg Lys	904
140 145 150 155	
gag aga gag gag att caa gaa atc cag tca aga gaa aat aaa agg atg Glu Arg Glu Glu Ile Gln Glu Ile Gln Ser Arg Glu Asn Lys Arg Met	952
156 161 166 171	
caa gtc ctc ctg act cag gtg tcc acc aag aga caa cag gtg att tct Gln Val Leu Leu Thr Gln Val Ser Thr Lys Arg Gln Gln Val Ile Ser	1000
172 177 182 187	
gag ttc gca cac ctg agg aag ttt cta gag gaa cag cag agc atc ctc Glu Phe Ala His Leu Arg Lys Phe Leu Glu Glu Gln Gln Ser Ile Leu	1048
188 193 198 203	
tta gca caa ttg gag agc cag gat ggg gac atc ttg agg caa cgg gat Leu Ala Gln Leu Glu Ser Gln Asp Gly Asp Ile Leu Arg Gln Arg Asp	1096
204 209 214 219	
gaa ttt gat ttg ctg gtt gct ggg gag atc tgc cgg ttt agt gct ctt Glu Phe Asp Leu Leu Val Ala Gly Glu Ile Cys Arg Phe Ser Ala Leu	1144
220 225 230 235	
att gaa gaa ctg gag gag aag aat gag agg cca gca agg gag ctc ctg Ile Glu Glu Leu Glu Glu Lys Asn Glu Arg Pro Ala Arg Glu Leu Leu	1192
236 241 246 251	
acg gac atc aga agc act cta ata aga tgt gaa acc aga aag tgc cgg Thr Asp Ile Arg Ser Thr Leu Ile Arg Cys Glu Thr Arg Lys Cys Arg	1240
252 257 262 267	
aaa ccg gtg gct gtg tcg cca gag ctg ggc cag agg att cgg gac ttt Lys Pro Val Ala Val Ser Pro Glu Leu Gly Gln Arg Ile Arg Asp Phe	1288
268 273 278 283	
ccc cag cag gcc ctc ccg ctg cag agg gag atg aag atg ttt ctg gaa Pro Gln Gln Ala Leu Pro Leu Gln Arg Glu Met Lys Met Phe Leu Glu	1336
284 289 294 299	

aaa cta tgc ttt gag ttg gac tat gag cca gct cac att tct cta gac		1384	
Lys Leu Cys Phe Glu Leu Asp Tyr Glu Pro Ala His Ile Ser Leu Asp			
300	305	310	315
cct cag act tcc cac ccc aag ctc ctc ttg tcc gag gac cac cag cga		1432	
Pro Gln Thr Ser His Pro Lys Leu Leu Ser Glu Asp His Gln Arg			
316	321	326	331
gct cag ttc tcc tac aaa tgg cag aac tca cca gac aac ccc cag cgt		1480	
Ala Gln Phe Ser Tyr Lys Trp Gln Asn Ser Pro Asp Asn Pro Gln Arg			
332	337	342	347
ttt gac cgg gcc acc tgt gtt ctg gcc cac act ggc atc aca ggg ggg		1528	
Phe Asp Arg Ala Thr Cys Val Leu Ala His Thr Gly Ile Thr Gly Gly			
348	353	358	363
aga cac acg tgg gtg gtg agt ata gac ctg gcc cat ggg ggc agc tgc		1576	
Arg His Thr Trp Val Val Ser Ile Asp Leu Ala His Gly Gly Ser Cys			
364	369	374	379
acc gtg ggc gtg gtg agc gag gat gtg cag cgg aag ggg gag ctt cgg		1624	
Thr Val Gly Val Val Ser Glu Asp Val Gln Arg Lys Gly Glu Leu Arg			
380	385	390	395
ctg cgg cca gag gag ggg gtg tgg gct gtg agg ctg gct tgg ggc ttc		1672	
Leu Arg Pro Glu Glu Gly Val Trp Ala Val Arg Ile Ala Trp Gly Phe			
396	401	406	411
gtc tcg gct ctg ggc tcc ttc ccc cac acg gct gac cct gaa gga gca		1720	
Val Ser Ala Leu Gly Ser Phe Pro His Thr Ala Asp Pro Glu Gly Ala			
412	417	422	427
gcc ccg gca ggt gag ggt gtc tct tga ctatg aggtggctg ggtgaccc		1772	
Ala Pro Ala Gly Glu Gly Val Ser *			
428	433		
accaacgctg tcacccgaga gccccatctac accttcactg ctccttcac taggaagg		1832	
ttcccttct ttgggctctg gggccgaggg tccagttct ccctgagctc ctgagaagga		1892	
gcagttacct actctccct aagtacagga ctcatatcaa cccaagtacc atgtggactt		1952	
gatccctggc tgaatcacct ggatgacttg gaatagaaat gactgcttta gaagatggga		2012	
tggggccggg tggtaaggga tagaagagag gactctcaat ctactgatca agtccttcc		2072	
ccaatgcccgtt gatggatggcc agggtaacctg gggactcagg ctgctgccag ttctgctcac		2132	
caccatccgt gcttggcaca gaagtagctg catagaaagg gcactggatt tgaagtcaga		2192	
agacctgggt tcttgaacca gcctgtcaac cagttgtatg actttaaaca aggcatctca		2252	
cctctttca tcttgttttc ttccaataat gtttagagttc atgtaatcac attctctaga		2312	
accattttagt ttgtgttaac tatgaaccaa gcagtgtggt ggccactggt gacttgaaaa		2372	
tatagagaaa aaaaaaaaaactt gctctatatc tgaaagagct cttggaaaga cagagaaaca		2432	

taaagaggaa attacagcac agtgtggtgg gtgttacggg aagtccaacc ccagcattat	2492
gggagttcag gggaaaggggc atagcccagc ctggaaggag agggtgagtg ggggatggct	2552
ttctgaaaag ggtggtctaa aggatgccta tggtaatag ggaaaagagg ggaagaagca	2612
tcttaagaag aggaaacagc agagaactgg ctggatgacc tgtgactctg gagcactggg	2672
ttgtctccat tgcattatg ggcagatgtg tgccatcccc agccgacgcc actcaactgcc	2732
tccttcctcc tgggtggcc acttctgggt gagattaagg tgcagggcct gggggcagga	2792
ggacataagg tatagccata aatcataacc cagggaccac actcaaccct agggaaattg	2852
tcttcctgtat cagttgatta ccatctgagg tcaagaaatg agatagtggg agcaaattggg	2912
tcacaaatag ctcagctgtg ggctcagaaa ctgctaggta aaagaattcc agaaggaggc	2972
cagggcataa gttggatgac ctatgaactt tagtctaaag aattgagact accgtaattg	3032
agactactgt agtgcacatct gagaaatggg atggaagagt gaccatgtt tattttcttg	3092
ttcttgcac tattggattt tattttgcatt aatcatgccc ttcactgaca gtctccttaa	3152
catcatctgt ttactctgct cagtgaaac tacaatgctc tgtcatctcc ctactgggtc	3212
tcctgggagg aggggg	3227

<210> 104
 <211> 7827
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (121)..(7497)

<400> 104	
ccattcccaa gctggctagc gtatagattt ccgttggta ccgagctcggttccactagt	60
ccagtgtggt ggaattcgag acatgtgact ttaccctctt cccctcgaag caacactccaa	120
atg gga gac aag gat gat gat gac gat gat gca gat gag aaa atg	168
Met Gly Asp Lys Asp Asp Asp Asp Asp Asp Ala Asp Glu Lys Met	
1 5 10 15	
cag tca tca ggg atc ccg aat ggt ggt cac atc cgt cag gaa agc cag	216
Gln Ser Ser Gly Ile Pro Asn Gly Gly His Ile Arg Gln Glu Ser Gln	
17 22 27 32	
gaa cag agt gag gtg gac cat gga gat ttt gag atg gtg tct gag tcg	264
Glu Gln Ser Glu Val Asp His Gly Asp Phe Glu Met Val Ser Glu Ser	
33 38 43 48	

atg gtc ctg gag aca gct gaa aat gtc aac aat ggc aac ccc tct ccc Met Val Leu Glu Thr Ala Glu Asn Val Asn Asn Gly Asn Pro Ser Pro	312
49 54 59 64	
ctg gag gcc ctg ctg gca ggc gca gag ggc ttc ccc ccc atg ctg gac Leu Glu Ala Leu Leu Ala Gly Ala Glu Gly Phe Pro Pro Met Leu Asp	360
65 70 75 80	
atc cca cct gat gca gat gac gag acc atg gtt gaa cta gcc att gcc Ile Pro Pro Asp Ala Asp Asp Glu Thr Met Val Glu Leu Ala Ile Ala	408
81 86 91 96	
ctg agc ctg cag cag gac caa caa ggc agc agc agc agt gcc ctg ggc Leu Ser Leu Gln Gln Asp Gln Gln Gly Ser Ser Ser Ala Leu Gly	456
97 102 107 112	
ctg cag agc ctg gga ctg tcc ggc cag gca ccc agc tct tcc tct ctg Leu Gln Ser Leu Gly Leu Ser Gly Gln Ala Pro Ser Ser Ser Leu	504
113 118 123 128	
gac gca gga acc ctc tct gac acc aca gca tca gct cca gcc tca gac Asp Ala Gly Thr Leu Ser Asp Thr Thr Ala Ser Ala Pro Ala Ser Asp	552
129 134 139 144	
gac gag ggc agt aca gca gcg aca gat ggt tct acc ctt cgg acc tct Asp Glu Gly Ser Thr Ala Ala Thr Asp Gly Ser Thr Leu Arg Thr Ser	600
145 150 155 160	
cct gct gac cac ggt ggt agt gtg ggc tcg gag agc ggg ggc agt gca Pro Ala Asp His Gly Gly Ser Val Gly Ser Glu Ser Gly Gly Ser Ala	648
161 166 171 176	
gtg gac tca gtg gct ggc gag cac agt gta tct ggc cgg agc agt gct Val Asp Ser Val Ala Gly Glu His Ser Val Ser Gly Arg Ser Ser Ala	696
177 182 187 192	
tat ggc gat gct aca gct gag ggg cat ccg gct gga cca gga agt gtc Tyr Gly Asp Ala Thr Ala Glu Gly His Pro Ala Gly Pro Gly Ser Val	744
193 198 203 208	
agc tca agc act gga gcc atc agc acc acc act ggg cac cag gag gga Ser Ser Thr Gly Ala Ile Ser Thr Thr Gly His Gln Glu Gly	792
209 214 219 224	
gat ggc tcc gag gga gaa gga gaa gga act gaa gga gat gtc cac Asp Gly Ser Glu Gly Glu Gly Glu Gly Thr Glu Gly Asp Val His	840
225 230 235 240	
act agc aac agg ctg cac atg gtc cgt cta atg ctg ttg gag aga tta Thr Ser Asn Arg Leu His Met Val Arg Leu Met Leu Leu Glu Arg Leu	888
241 246 251 256	
ctg cag acc ctg cct caa tta cga aac gtt ggc ggt gtc cgg gcc atc Leu Gln Thr Leu Pro Gln Leu Arg Asn Val Gly Gly Val Arg Ala Ile	936
257 262 267 272	

cca tac atg cag gtc att cta atg ctc act aca gat ctg gat gga gaa Pro Tyr Met Gln Val Ile Leu Met Leu Thr Thr Asp Leu Asp Gly Glu 273 278 283 288	984
gat gag aaa gac aag ggg gcc cta gac aac ctg ctc tcc cag ctt att Asp Glu Lys Asp Lys Gly Ala Leu Asp Asn Leu Leu Ser Gln Leu Ile 289 294 299 304	1032
gct gag ttg ggt atg gat aaa aag gat gtc tcc aag aag aat gag cgc Ala Glu Leu Gly Met Asp Lys Asp Val Ser Lys Lys Asn Glu Arg 305 310 315 320	1080
agc gcc ctg aat gaa gtc cat ctg gta gta atg aga ctc ctg agt gtc Ser Ala Leu Asn Glu Val His Leu Val Val Met Arg Leu Leu Ser Val 321 326 331 336	1128
tcc atg tcc cgc acc aaa tct gga tcc aag tct tcc ata tgt gag tca Phe Met Ser Arg Thr Lys Ser Gly Ser Lys Ser Ile Cys Glu Ser 337 342 347 352	1176
tct tcc ctc atc tcc agt gcc aca gca gca gct cta ctg agc tct ggg Ser Ser Leu Ile Ser Ser Ala Thr Ala Ala Leu Leu Ser Ser Gly 353 358 363 368	1224
gct gtg gac tac tgc ctg cac gtg ctc aaa tca ctg ctg gaa tat tgg Ala Val Asp Tyr Cys Leu His Val Leu Lys Ser Leu Leu Glu Tyr Trp 369 374 379 384	1272
aag agc caa cag aat gac gag gag cct gtg gct acc agc cag ttg ctg Lys Ser Gln Gln Asn Asp Glu Glu Pro Val Ala Thr Ser Gln Leu Leu 385 390 395 400	1320
aaa cca cat act acc tcc tcc cca cct gac atg agc cca ttc ttt ctc Lys Pro His Thr Thr Ser Ser Pro Pro Asp Met Ser Pro Phe Phe Leu 401 406 411 416	1368
cgc cag tat gtg aag ggt cat gct gct gat gtg ttt gag gcc tat act Arg Gln Tyr Val Lys Gly His Ala Ala Asp Val Phe Glu Ala Tyr Thr 417 422 427 432	1416
cag ctt cta aca gaa atg gta ctg agg ctt cct tac caa atc aaa aag Gln Leu Leu Thr Glu Met Val Leu Arg Leu Pro Tyr Gln Ile Lys Lys 433 438 443 448	1464
att act gac acc aat tct cga atc cca cct cct gtc ttt gac cac tcg Ile Thr Asp Thr Asn Ser Arg Ile Pro Pro Val Phe Asp His Ser 449 454 459 464	1512
tgg ttt tac ttt ctc tcc gag tac ctc atg atc cag cag act cca ttt Trp Phe Tyr Phe Leu Ser Glu Tyr Leu Met Ile Gln Gln Thr Pro Phe 465 470 475 480	1560
gtg cgc cgt caa gtc cgc aaa ctt ctg ctc ttc atc tgt gga tcc aaa Val Arg Arg Gln Val Arg Lys Leu Leu Leu Phe Ile Cys Gly Ser Lys 481 486 491 496	1608
gag aag tac cgc cag ctc cgg gat ttg cac acc ctg gac tct cac gtg	1656

Glu Lys Tyr Arg Gln Leu Arg Asp Leu His Thr Leu Asp Ser His Val			
497	502	507	512
cgt ggg atc aag aag ctg cta gaa gag cag ggg ata ttc ctc cgg gca			1704
Arg Gly Ile Lys Lys Leu Leu Glu Glu Gln Gly Ile Phe Leu Arg Ala			
513	518	523	528
agt gtg gtt aca gcc agc tca ggc tcc gcc ttg caa tat gac aca ctc			1752
Ser Val Val Thr Ala Ser Ser Gly Ser Ala Leu Gln Tyr Asp Thr Leu			
529	534	539	544
atc agc ctg atg gag cac ctg aaa gcc tgt gca gag att gcc gcc cag			1800
Ile Ser Leu Met Glu His Leu Lys Ala Cys Ala Glu Ile Ala Ala Gln			
545	550	555	560
cga acc atc aac tgg cag aaa ttc tgc atc aaa gat gac tcc gtc ctg			1848
Arg Thr Ile Asn Trp Gln Lys Phe Cys Ile Lys Asp Asp Ser Val Leu			
561	566	571	576
tac ttc ctc ctc caa gtc agt ttc ctt gtg gat gag ggc gtg tcc cca			1896
Tyr Phe Leu Leu Gln Val Ser Phe Leu Val Asp Glu Gly Val Ser Pro			
577	582	587	592
gtg ctg ctg caa ctg ctc tcc tgt gct ctg tgc ggc agc aag gtg ctc			1944
Val Leu Leu Gln Leu Leu Ser Cys Ala Leu Cys Gly Ser Lys Val Leu			
593	598	603	608
gct gca ctg gca gcc tct tcg gga tcc tcc agt gct tct tcc tcc tca			1992
Ala Ala Leu Ala Ala Ser Ser Gly Ser Ser Ala Ser Ser Ser Ser			
609	614	619	624
gcc cct gtg gct gcc agt tct gga caa gcc aca aca cag tcc aag tct			2040
Ala Pro Val Ala Ala Ser Ser Gly Gln Ala Thr Thr Gln Ser Lys Ser			
625	630	635	640
tcc act aaa aag agc aag aaa gaa gaa aaa aaa aag gag aaa gat ggt			2088
Ser Thr Lys Lys Ser Lys Glu Glu Lys Lys Lys Glu Lys Asp Gly			
641	646	651	656
gag acc tct ggc agc cag gag gac cag ctg tgc aca gct ctg gtg aac			2136
Glu Thr Ser Gly Ser Gln Glu Asp Gln Leu Cys Thr Ala Leu Val Asn			
657	662	667	672
cag ctg aac aaa ttt gcc gat aag gaa acc ctg atc cag ttc ctg cgt			2184
Gln Leu Asn Lys Phe Ala Asp Lys Glu Thr Leu Ile Gln Phe Leu Arg			
673	678	683	688
tgt ttc ctg tta gag tcc aat tct tcc tcg gtg cgc tgg cag gcc cac			2232
Cys Phe Leu Leu Glu Ser Asn Ser Ser Val Arg Trp Gln Ala His			
689	694	699	704
tgt ctg aca ctg cac atc tac aga aat tcc agc aaa tct caa cag gag			2280
Cys Leu Thr Leu His Ile Tyr Arg Asn Ser Ser Lys Ser Gln Gln Glu			
705	710	715	720
ctc ctg cta gat ctg atg tgg tcc atc tgg cca gaa ctc cca gcc tat			2328
Leu Leu Leu Asp Leu Met Trp Ser Ile Trp Pro Glu Leu Pro Ala Tyr			

721	726	731	736	
ggt cgt aag gct gcc cag ttt gtg gac cta cta gga tat ttc tcc ctg Gly Arg Lys Ala Ala Gln Phe Val Asp Leu Leu Gly Tyr Phe Ser Leu	737	742	747	2376
aaa act cca caa aca gag aag aag ttg aag gag tat tca cag aag gct Lys Thr Pro Gln Thr Glu Lys Lys Leu Lys Glu Tyr Ser Gln Lys Ala	753	758	763	2424
gtg gag att ctg cgg act caa aac cat att ctt acc aac cac ccc aac Val Glu Ile Leu Arg Thr Gln Asn His Ile Leu Thr Asn His Pro Asn	769	774	779	2472
tgc aac att tat aac act ttg tct ggc tta gtg gag ttt gat ggc tat Ser Asn Ile Tyr Asn Thr Leu Ser Gly Leu Val Glu Phe Asp Gly Tyr	785	790	795	2520
tac ctg gag agc gat ccc tgc ctg gtg tgt aat aac ccg gaa gta ccg Tyr Leu Glu Ser Asp Pro Cys Leu Val Cys Asn Asn Pro Glu Val Pro	801	806	811	2568
ttc tgt tat atc aag ctg tct tcc att aaa gtg gac acg cgg tac acc Phe Cys Tyr Ile Lys Leu Ser Ser Ile Lys Val Asp Thr Arg Tyr Thr	817	822	827	2616
acc acc cag cag gtt gtg aag ctc att ggc agt cac acc atc agc aaa Thr Thr Gln Gln Val Val Lys Leu Ile Gly Ser His Thr Ile Ser Lys	833	838	843	2664
gtg aca gtg aaa atc ggg gat ctg aaa cgg acc aag atg gtg cgg acc Val Thr Val Lys Ile Gly Asp Leu Lys Arg Thr Lys Met Val Arg Thr	849	854	859	2712
atc aac ctg tat tat aac aac cga acc gtg cag gcc atc gtg gag ttg Ile Asn Leu Tyr Tyr Asn Asn Arg Thr Val Gln Ala Ile Val Glu Leu	865	870	875	2760
aaa aac aag cca gct cgc tgg cac aaa gcc aag aag gtt cag ctg acc Lys Asn Lys Pro Ala Arg Trp His Ala Lys Lys Val Gln Leu Thr	881	886	891	2808
cct gga cag aca gag gtg aag att gac ctg ccg ttg ccc att gtg gcc Pro Gly Gln Thr Glu Val Lys Ile Asp Leu Pro Leu Pro Ile Val Ala	897	902	907	2856
tcc aat ctg atg att gag ttt gca gac ttc tat gaa aac tac cag gcc Ser Asn Leu Met Ile Glu Phe Ala Asp Phe Tyr Glu Asn Tyr Gln Ala	913	918	923	2904
tcc aca gag acc ctg cag tgc cct cgc tgt agt gcc tcg gtc cct gcc Ser Thr Glu Thr Leu Gln Cys Pro Arg Cys Ser Ala Ser Val Pro Ala	929	934	939	2952
aac cca gga gtc tgt ggc aac tgt gga gag aat gtg tac cag tgt cac Asn Pro Gly Val Cys Gly Asn Cys Gly Glu Asn Val Tyr Gln Cys His	945	950	955	3000
				960

aaa tgc aga tcc atc aac tac gat gaa aag gat ccc ttc ctc tgc aat Lys Cys Arg Ser Ile Asn Tyr Asp Glu Lys Asp Pro Phe Leu Cys Asn 961 966 971 976	3048
gcc tgt ggc ttc tgt aaa tat gcc cgc ttc gac ttc atg ctc tat gcc Ala Cys Gly Phe Cys Lys Tyr Ala Arg Phe Asp Phe Met Leu Tyr Ala 977 982 987 992	3096
aag cct tgc tgt gca gtg gat ccc att gag aat gaa gaa gac cgg aag Lys Pro Cys Cys Ala Val Asp Pro Ile Glu Asn Glu Glu Asp Arg Lys 993 998 1003 1008	3144
aag gct gta tcc aac atc aat aca ctt ttg gac aaa gct gat cga gtg Lys Ala Val Ser Asn Ile Asn Thr Leu Leu Asp Lys Ala Asp Arg Val 1009 1014 1019 1024	3192
tat cat cag ctg atg gga cac cgg cca cag ctg gag aac ctg ctc tgc Tyr His Gln Leu Met Gly His Arg Pro Gln Leu Glu Asn Leu Leu Cys 1025 1030 1035 1040	3240
aaa gtg aat gag gca gct cca gaa aag cca cag gat gac tca gga aca Lys Val Asn Glu Ala Ala Pro Glu Lys Pro Gln Asp Asp Ser Gly Thr 1041 1046 1051 1056	3288
gca ggg ggc atc agc tcc act tct gcc agt gtg aat cgt tac atc ctg Ala Gly Ile Ser Ser Thr Ser Ala Ser Val Asn Arg Tyr Ile Leu 1057 1062 1067 1072	3336
cag ttg gct cag gag tat tgt gga gac tgc aag aac tct ttt gat gaa Gln Leu Ala Gln Glu Tyr Cys Gly Asp Cys Lys Asn Ser Phe Asp Glu 1073 1078 1083 1088	3384
ctc tcc aaa atc atc cag aaa gtc ttt gct tcg cgc aaa gag ttg ttg Leu Ser Lys Ile Ile Gln Lys Val Phe Ala Ser Arg Lys Glu Leu Leu 1089 1094 1099 1104	3432
gaa tat gac cta cag cag agg gaa gca gcc act aaa tca tcc cgg acc Glu Tyr Asp Leu Gln Gln Arg Glu Ala Ala Thr Lys Ser Ser Arg Thr 1105 1110 1115 1120	3480
tcc gtg cag ccc aca ttc act gcc agc cag tac cgt gcc tta tcc gtc Ser Val Gln Pro Thr Phe Thr Ala Ser Gln Tyr Arg Ala Leu Ser Val 1121 1126 1131 1136	3528
ctg ggc tgt ggc cac aca tcc acc aag tgc tat ggc tgc gcc tcg Leu Gly Cys Gly His Thr Ser Ser Thr Lys Cys Tyr Gly Cys Ala Ser 1137 1142 1147 1152	3576
gct gtc aca gaa cat tgt atc aca cta ctt cgg gcc ctg gcc acc aac Ala Val Thr Glu His Cys Ile Thr Leu Leu Arg Ala Leu Ala Thr Asn 1153 1158 1163 1168	3624
cca gcc ttg agg cac atc ctt gtc tcc cag ggc ctt atc cgg gag ctc Pro Ala Leu Arg His Ile Leu Val Ser Gln Gly Leu Ile Arg Glu Leu 1169 1174 1179 1184	3672

ttt gat tat aat ctt cgc cga ggg gct gcg gcc atg cgg gag gag gtc Phe Asp Tyr Asn Leu Arg Arg Gly Ala Ala Met Arg Glu Glu Val	3720
1185 1190 1195 1200	
 cgc cag ctc atg tgc ctc cta act cga gac aac cca gaa gcc acc caa Arg Gln Leu Met Cys Leu Leu Thr Arg Asp Asn Pro Glu Ala Thr Gln	3768
1201 1206 1211 1216	
 cag atg aat gac ctg att att ggc aag gtc tcc aca gcc ctg aag ggc Gln Met Asn Asp Leu Ile Ile Gly Lys Val Ser Thr Ala Leu Lys Gly	3816
1217 1222 1227 1232	
 cac tgg gcc aac ccc gat ctg gca agt agc ctg cag tat gaa atg ctg His Trp Ala Asn Pro Asp Leu Ala Ser Ser Leu Gln Tyr Glu Met Leu	3864
1233 1238 1243 1248	
 ctg ctg acg gat tct atc tcc aag gag gac agc tgc tgg gag ctc cgg Leu Leu Thr Asp Ser Ile Ser Lys Glu Asp Ser Cys Trp Glu Leu Arg	3912
1249 1254 1259 1264	
 tta cgc tgt gct ctc agc ctt ttc ctc atg gct gtg aac att aag act Leu Arg Cys Ala Leu Ser Leu Phe Leu Met Ala Val Asn Ile Lys Thr	3960
1265 1270 1275 1280	
 cct gtg gtg gtt gaa aac att acc ctc atg tgc ctg agg atc ttg cag Pro Val Val Val Glu Asn Ile Thr Leu Met Cys Leu Arg Ile Leu Gln	4008
1281 1286 1291 1296	
 aag ctg ata aaa cca cct gct ccc act agc aag aac aag gat gtc Lys Leu Ile Lys Pro Pro Ala Pro Thr Ser Lys Lys Asn Lys Asp Val	4056
1297 1302 1307 1312	
 ccc gtt gag gcc ctc acc acg gtg aag cca tac tgc aat gag atc cat Pro Val Glu Ala Leu Thr Thr Val Lys Pro Tyr Cys Asn Glu Ile His	4104
1313 1318 1323 1328	
 gcc cag gct caa ctg tgg ctc aag aga gac ccc aag gca tcc tat gat Ala Gln Ala Gln Leu Trp Leu Lys Arg Asp Pro Lys Ala Ser Tyr Asp	4152
1329 1334 1339 1344	
 gcc tgg aag aag tgt ctt cct atc aga ggg ata gat ggc aat ggg aaa Ala Trp Lys Lys Cys Leu Pro Ile Arg Gly Ile Asp Gly Asn Gly Lys	4200
1345 1350 1355 1360	
 gcc ccc agc aaa tca gag ctc cgc cat ctc tat ttg act gag aag tat Ala Pro Ser Lys Ser Glu Leu Arg His Leu Tyr Leu Thr Glu Lys Tyr	4248
1361 1366 1371 1376	
 gtg tgg agg tgg aaa cag ttc ctg agt cgt cggt ggg aag agg acc tcc Val Trp Arg Trp Lys Gln Phe Leu Ser Arg Arg Gly Lys Arg Thr Ser	4296
1377 1382 1387 1392	
 ccc ttg gat ctc aaa ctg ggg cat aac aac tgg ctg cga caa gtg ctt Pro Leu Asp Leu Lys Leu Gly His Asn Asn Trp Leu Arg Gln Val Leu	4344
1393 1398 1403 1408	
 ttc act cca gca acg cag gcc gca cgg cag gca gcc tgt acc att gtg	4392

Phe	Thr	Pro	Ala	Thr	Gln	Ala	Ala	Arg	Gln	Ala	Ala	Cys	Thr	Ile	Val	
1409				1414				1419				1424				
gaa gct cta gcc acc att ccc agc cgc aag cag cag gtc ctg gac ctg															4440	
Glu Ala Leu Ala Thr Ile Pro Ser Arg Lys Gln Gln Val Leu Asp Leu																
1425		1430		1435		1440										
ctt acc agt tac ctg gat gag ctg agc ata gct ggg gag tgt gca gct															4488	
Leu Thr Ser Tyr Leu Asp Glu Leu Ser Ile Ala Gly Glu Cys Ala Ala																
1441		1446		1451		1456										
gag tac ctg gct ctc tac cag aag ctc atc act tct gcg cac tgg aaa															4536	
Glu Tyr Leu Ala Leu Tyr Gln Lys Leu Ile Thr Ser Ala His Trp Lys																
1457		1462		1467		1472										
gtc tac ttg gca gct cgg gga gtc cta ccc tat gtg ggc aac ctc atc															4584	
Val Tyr Leu Ala Ala Arg Gly Val Leu Pro Tyr Val Gly Asn Leu Ile																
1473		1478		1483		1488										
acc aag gaa ata gct cgt ctg ctg gcc ctg gag gag gct acc ctg agt															4632	
Thr Lys Glu Ile Ala Arg Leu Leu Ala Leu Glu Glu Ala Thr Leu Ser																
1489		1494		1499		1504										
acc gat ctg cag cag ggt tat gcc ctt aaa agt ctc aca ggc ctt ctc															4680	
Thr Asp Leu Gln Gln Gly Tyr Ala Leu Lys Ser Leu Thr Gly Leu Leu																
1505		1510		1515		1520										
tcc tcc ttt gtt gag gtg gaa tcc atc aaa aga cat ttt aaa agt cgc															4728	
Ser Ser Phe Val Glu Val Glu Ser Ile Lys Arg His Phe Lys Ser Arg																
1521		1526		1531		1536										
ttg gtg ggt act gtg ctg aat gga tac ctg tgc ttg cgg aag ctg gtg															4776	
Leu Val Gly Thr Val Leu Asn Gly Tyr Leu Cys Leu Arg Lys Leu Val																
1537		1542		1547		1552										
gtg cag agg acc aag ctg atc gat gag acg cag gac atg ctg ctg gag															4824	
Val Gln Arg Thr Lys Leu Ile Asp Glu Thr Gln Asp Met Leu Leu Glu																
1553		1558		1563		1568										
atg ctg gag gac atg acc aca ggt aca gaa tca gaa acc aag gcc ttc															4872	
Met Leu Glu Asp Met Thr Thr Gly Thr Glu Ser Glu Thr Lys Ala Phe																
1569		1574		1579		1584										
atg gct gtg tgc att gag aca gcc aag cgc tac aat ctg gat gac tac															4920	
Met Ala Val Cys Ile Glu Thr Ala Lys Arg Tyr Asn Leu Asp Asp Tyr																
1585		1590		1595		1600										
cg ^g acc ccg gtg ttc atc ttc gag agg ctc tgc agc atc att tat cct															4968	
Arg Thr Pro Val Phe Ile Phe Glu Arg Leu Cys Ser Ile Ile Tyr Pro																
1601		1606		1611		1616										
gag gag aat gaa gtc act gag ttc ttt gtg acc ctg gag aag gat ccc															5016	
Glu Glu Asn Glu Val Thr Glu Phe Phe Val Thr Leu Glu Lys Asp Pro																
1617		1622		1627		1632										
caa caa gaa gac ttc tta cag ggc agg atg cct ggg aac ccg tat agc															5064	
Gln Gln Glu Asp Phe Leu Gln Gly Arg Met Pro Gly Asn Pro Tyr Ser																

1633	1638	1643	1648	
agc aat gag cca ggc atc ggg ccg ctg atg agg gat ata aag aac aag Ser Asn Glu Pro Gly Ile Gly Pro Leu Met Arg Asp Ile Lys Asn Lys				5112
1649 1654 1659 1664				
att tgc cag gac tgt gac tta gtg gcc ctc ctg gaa gat gac agt ggc Ile Cys Gln Asp Cys Asp Leu Val Ala Leu Leu Glu Asp Asp Ser Gly				5160
1665 1670 1675 1680				
atg gag ctt cta gtg aac aat aaa atc att agt ttg gac ctt cct gtg Met Glu Leu Leu Val Asn Asn Lys Ile Ile Ser Leu Asp Leu Pro Val				5208
1681 1686 1691 1696				
gct gaa gtt tac aag aaa gtc tgg tgt acc acg aat gag gga gag ccc Ala Glu Val Tyr Lys Lys Val Trp Cys Thr Thr Asn Glu Gly Glu Pro				5256
1697 1702 1707 1712				
atg agg att gtt tat cgt atg cgg ggg ctg ctg ggc gat gcc aca gag Met Arg Ile Val Tyr Arg Met Arg Gly Leu Leu Gly Asp Ala Thr Glu				5304
1713 1718 1723 1728				
gag ttc att gag tcc ctg gac tct act aca gat gaa gaa gaa gat gaa Glu Phe Ile Glu Ser Leu Asp Ser Thr Thr Asp Glu Glu Glu Asp Glu				5352
1729 1734 1739 1744				
gaa gaa gtg tat aaa atg gct ggt gtg atg gcc cag tgt ggg ggc ctg Glu Glu Val Tyr Lys Met Ala Gly Val Met Ala Gln Cys Gly Gly Leu				5400
1745 1750 1755 1760				
gaa tgc atg ctt aac aga ctc gca ggg atc aga gat ttc aag cag gga Glu Cys Met Leu Asn Arg Leu Ala Gly Ile Arg Asp Phe Lys Gln Gly				5448
1761 1766 1771 1776				
cgc cac ctt cta aca gtg cta ctg aaa ttg ttc agt tac tgc gtg aag Arg His Leu Leu Thr Val Leu Leu Lys Leu Phe Ser Tyr Cys Val Lys				5496
1777 1782 1787 1792				
gtg aaa gtc aac cgg cag caa ctg gtc aaa ctg gaa atg aac acc ttg Val Lys Val Asn Arg Gln Gln Leu Val Lys Leu Glu Met Asn Thr Leu				5544
1793 1798 1803 1808				
aac gtc atg ctg ggg acc cta aac ctg gcc ctt gta gct gaa caa gaa Asn Val Met Leu Gly Thr Leu Asn Leu Ala Leu Val Ala Glu Gln Glu				5592
1809 1814 1819 1824				
agc aag gac agt ggg ggt gca gct gtg gct gag cag gtg ctt agc atc Ser Lys Asp Ser Gly Gly Ala Ala Val Ala Glu Gln Val Leu Ser Ile				5640
1825 1830 1835 1840				
atg gag atc att cta gat gag tcc aat gct gag ccc ctg agt gag gac Met Glu Ile Ile Leu Asp Glu Ser Asn Ala Glu Pro Leu Ser Glu Asp				5688
1841 1846 1851 1856				
aag ggc aac ctc ctc aca ggt gac aag gat caa ctg gtg atg ctc Lys Gly Asn Leu Leu Leu Thr Gly Asp Lys Asp Gln Leu Val Met Leu				5736
1857 1862 1867 1872				

ttg gac cag atc aac agc acc ttt gtt cgc tcc aac ccc agt gtg ctc Leu Asp Gln Ile Asn Ser Thr Phe Val Arg Ser Asn Pro Ser Val Leu	1873	1878	1883	1888	5784
cag ggc ctg ctt cgc atc atc ccg tac ctt tcc ttt gga gag gtg gag Gln Gly Leu Leu Arg Ile Ile Pro Tyr Leu Ser Phe Gly Glu Val Glu	1889	1894	1899	1904	5832
aaa atg cag atc ttg gtg gag cga ttc aaa cca tac tgc aac ttt gat Lys Met Gln Ile Leu Val Glu Arg Phe Lys Pro Tyr Cys Asn Phe Asp	1905	1910	1915	1920	5880
aaa tat gat gaa gat cac agt ggt gat gat aaa gtc ttc ctg gac tgc Lys Tyr Asp Glu Asp His Ser Gly Asp Asp Lys Val Phe Leu Asp Cys	1921	1926	1931	1936	5928
ttc tgt aaa ata gct gct ggc atc aag aac aac agc aat ggg cac cag Phe Cys Lys Ile Ala Ala Gly Ile Lys Asn Asn Ser Asn Gly His Gln	1937	1942	1947	1952	5976
ctg aag gat ctg att ctc cag aag ggg atc acc cag aat gca ctt gac Leu Lys Asp Leu Ile Leu Gln Lys Gly Ile Thr Gln Asn Ala Leu Asp	1953	1958	1963	1968	6024
tac atg aaa aag cac atc cct agc gcc aag aat ttg gat gcc gac atc Tyr Met Lys Lys His Ile Pro Ser Ala Lys Asn Leu Asp Ala Asp Ile	1969	1974	1979	1984	6072
tgg aaa aag ttt ttg tct cgc cca gcc ttg cca ttt atc cta agg ctg Trp Lys Phe Leu Ser Arg Pro Ala Leu Pro Phe Ile Leu Arg Leu	1985	1990	1995	2000	6120
ctt cgg ggc ctg gcc atc cag cac cct ggc acc cag gtt ctg att gga Leu Arg Gly Leu Ala Ile Gln His Pro Gly Thr Gln Val Leu Ile Gly	2001	2006	2011	2016	6168
act gat tcc atc ccg aac ctg cat aag ctg gag cag gtg tcc agt gat Thr Asp Ser Ile Pro Asn Leu His Lys Leu Glu Gln Val Ser Ser Asp	2017	2022	2027	2032	6216
gag ggc att ggg acc ttg gca gag aac ctg ctg gaa gcc ctg cgg gaa Glu Gly Ile Gly Thr Leu Ala Glu Asn Leu Leu Glu Ala Leu Arg Glu	2033	2038	2043	2048	6264
cac cct gac gta aac aag aag att gac gca gcc cgc agg gag acc cgg His Pro Asp Val Asn Lys Lys Ile Asp Ala Ala Arg Arg Glu Thr Arg	2049	2054	2059	2064	6312
gca gag aag aaa cgc atg gcc atg gca atg agg cag aag gcc ctg ggc Ala Glu Lys Lys Arg Met Ala Met Ala Met Arg Gln Lys Ala Leu Gly	2065	2070	2075	2080	6360
acc ctg ggc atg acg aca aat gaa aag ggc cag gtc gtg acc aag aca Thr Leu Gly Met Thr Thr Asn Glu Lys Gly Gln Val Val Thr Lys Thr	2081	2086	2091	2096	6408

gca ctc ctg aag cag atg gaa gag ctg atc gag gag cct ggc ctc acg Ala Leu Leu Lys Gln Met Glu Glu Leu Ile Glu Glu Pro Gly Leu Thr 2097 2102 2107 2112	6456
tgc tgc atc tgc agg gag gga tac aag ttc cag ccc aca aag gtc ctg Cys Cys Ile Cys Arg Glu Gly Tyr Lys Phe Gln Pro Thr Lys Val Leu 2113 2118 2123 2128	6504
ggc att tat acc ttc acg aag cgg gta gcc ttg gag gag ttg gag aat Gly Ile Tyr Thr Phe Thr Lys Arg Val Ala Leu Glu Glu Leu Glu Asn 2129 2134 2139 2144	6552
aag ccc cgg aaa cag cag ggc tac agc acc gtg tcc cac ttc aac att Lys Pro Arg Lys Gln Gln Gly Tyr Ser Thr Val Ser His Phe Asn Ile 2145 2150 2155 2160	6600
gtg cac tac gac tgc cat ctg gct gcc gtc agg ttg gct cga ggc cgg Val His Tyr Asp Cys His Leu Ala Ala Val Arg Leu Ala Arg Gly Arg 2161 2166 2171 2176	6648
gaa gag tgg gag agt gcc gcc ctg cag aat gcc aac acc aag tgc aac Glu Glu Trp Glu Ser Ala Ala Leu Gln Asn Ala Asn Thr Lys Cys Asn 2177 2182 2187 2192	6696
ggg ctc ctt ccg gtc tgg gga cct cat gtc cct gaa tca gct ttt gcc Gly Leu Leu Pro Val Trp Gly Pro His Val Pro Glu Ser Ala Phe Ala 2193 2198 2203 2208	6744
act tgc ttg gca aga cac aac act tac ctc cag gaa tgt aca ggc cag Thr Cys Leu Ala Arg His Asn Thr Tyr Leu Gln Glu Cys Thr Gly Gln 2209 2214 2219 2224	6792
cgg gag ccc acg tat cag ctc aac atc cat gac atc aaa ctg ctc ttc Arg Glu Pro Thr Tyr Gln Leu Asn Ile His Asp Ile Lys Leu Leu Phe 2225 2230 2235 2240	6840
ctg cgc ttc gcc atg gag cag tcg ttc agc gca gac act ggc ggg ggc Leu Arg Phe Ala Met Glu Gln Ser Phe Ser Ala Asp Thr Gly Gly 2241 2246 2251 2256	6888
ggc cgg gag agc aac atc cac ctg atc ccg tac atc att cac act gtg Gly Arg Glu Ser Asn Ile His Leu Ile Pro Tyr Ile Ile His Thr Val 2257 2262 2267 2272	6936
ctt tac gtc ctg aac aca acc cga gca act tcc cga gaa gag aag aac Leu Tyr Val Leu Asn Thr Thr Arg Ala Thr Ser Arg Glu Glu Lys Asn 2273 2278 2283 2288	6984
ctc caa ggc ttt ctg gaa cag ccc aag gag aag tgg gtg gag agt gcc Leu Gln Gly Phe Leu Glu Gln Pro Lys Glu Lys Trp Val Glu Ser Ala 2289 2294 2299 2304	7032
ttt gaa gtg gac ggg ccc tac tat ttc aca gtc ttg gcc ctt cac atc Phe Glu Val Asp Gly Pro Tyr Tyr Phe Thr Val Leu Ala Leu His Ile 2305 2310 2315 2320	7080
ctg ccc cct gag cag tgg aga gcc aca cgt gtg gaa atc ttg cgg agg	7128

Leu	Pro	Pro	Glu	Gln	Trp	Arg	Ala	Thr	Arg	Val	Glu	Ile	Leu	Arg	Arg
2321			2326			2331			2336						
ctg	ttg	gtg	acc	tcg	cag	gct	cgg	gca	gtg	gct	cca	ggg	gga	gcc	acc
Leu	Leu	Val	Thr	Ser	Gln	Ala	Arg	Ala	Val	Ala	Pro	Gly	Gly	Ala	Thr
2337			2342			2347			2352						7176
agg	ctg	aca	gat	aag	gca	gtg	aag	gac	tat	tcc	gct	tac	cgt	tct	tcc
Arg	Leu	Thr	Asp	Lys	Ala	Val	Lys	Asp	Tyr	Ser	Ala	Tyr	Arg	Ser	Ser
2353			2358			2363			2368						7224
ctt	ctc	ttt	tgg	gcc	ctc	gtc	gat	ctc	att	tac	aac	atg	ttt	aag	aag
Leu	Leu	Phe	Trp	Ala	Leu	Val	Asp	Leu	Ile	Tyr	Asn	Met	Phe	Lys	Lys
2369			2374			2379			2384						7272
gtg	cct	acc	agt	aac	aca	gag	gga	ggc	tgg	tcc	tgc	tct	ctc	gct	gag
Val	Pro	Thr	Ser	Asn	Thr	Glu	Gly	Gly	Trp	Ser	Cys	Ser	Leu	Ala	Glu
2385			2390			2395			2400						7320
tac	atc	cgc	cac	aac	gac	atg	ccc	atc	tac	gaa	gct	gcc	gac	aaa	gcc
Tyr	Ile	Arg	His	Asn	Asp	Met	Pro	Ile	Tyr	Glu	Ala	Alá	Asp	Lys	Ala
2401			2406			2411			2416						7368
ctg	aaa	acc	ttc	cag	gag	gag	ttc	atg	cca	gtg	gag	acc	ttc	tca	gag
Leu	Lys	Thr	Phe	Gln	Glu	Glu	Phe	Met	Pro	Val	Glu	Thr	Phe	Ser	Glu
2417			2422			2427			2432						7416
ttc	ctc	gat	gtg	gcc	ggt	ctt	tta	tca	gaa	atc	acc	gat	cca	gag	agc
Phe	Leu	Asp	Val	Ala	Gly	Leu	Leu	Ser	Glu	Ile	Thr	Asp	Pro	Glu	Ser
2433			2438			2443			2448						7464
ttc	ctg	aag	gac	ctg	ttg	aac	tca	gtc	ccc	tga	ccaccaca	cagcagctgc			
Phe	Leu	Lys	Asp	Leu	Leu	Asn	Ser	Val	Pro	*					7515
2449			2454			2459									
ggcggcgaag	acgaagctgg	cttgccttcc	accctctgtt	ctccctccctt	gtgcattaaag										7575
ttccctccgc	gggatgctgc	attgttaccc	cgcgcctcccc	tctctcattt	ttcttggtgt										7635
ggcttgggt	ttttaggctt	cctgttttat	ctcggtgtgt	tggtgacca	gctatgaggt										7695
tgtctgtAAC	ccaagccatc	aaaggccctg	tacataccta	ggagccatga	gttgtcccg										7755
ccagcttcat	acttgagtgt	gcacatctt	agaaataaac	aagtgactta	acacacattt										7815
aaaaaaaaaa	aa														7827

<210> 105
 <211> 3304
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (55) .. (2406)

<400> 105
cttcctctcc acgcgggtga gaagaccggt cggcctggc aacctgcgct gaag atg 57
.. Met
1

ccg gga aaa ctc cgt agt gac gct ggt ttg gaa tca gac acc gca atg 105
Pro Gly Lys Leu Arg Ser Asp Ala Gly Leu Glu Ser Asp Thr Ala Met
2 7 12 17

aaa aaa ggg gag aca ctg cga aag caa acc gag gag aaa gag aaa aaa 153
Lys Lys Gly Glu Thr Leu Arg Lys Gln Thr Glu Glu Lys Glu Lys Lys
18 23 28 33

gag aag cca aaa tct gat aag act gaa gag ata gca gaa gag gaa gaa 201
Glu Lys Pro Lys Ser Asp Lys Thr Glu Glu Ile Ala Glu Glu Glu
34 39 44 49

act gtt ttc ccc aaa gct aaa caa gtt aaa aag aaa gca gag cct tct 249
Thr Val Phe Pro Lys Ala Lys Gln Val Lys Lys Ala Glu Pro Ser
50 55 60 65

gaa gtt gac atg aat tct cct aaa tcc aaa aag gca aaa aag aaa gag 297
Glu Val Asp Met Asn Ser Pro Lys Ser Lys Lys Ala Lys Lys Glu
66 71 76 81

gag cca tct caa aat gac att tct cct aaa acc aaa agt ttg aga aag 345
Glu Pro Ser Gln Asn Asp Ile Ser Pro Lys Thr Lys Ser Leu Arg Lys
82 87 92 97

aaa aag gag ccc att gaa aag aaa gtg gtt tct tct aaa acc aaa aaa 393
Lys Lys Glu Pro Ile Glu Lys Lys Val Val Ser Ser Lys Thr Lys Lys
98 103 108 113

gtg aca aaa aat gag gag cct tct gag gaa gaa ata gat gct cct aag 441
Val Thr Lys Asn Glu Glu Pro Ser Glu Glu Ile Asp Ala Pro Lys
114 119 124 129

ccc aag aag atg aag aaa gaa aag gaa atg aat gga gaa act aga gag 489
Pro Lys Lys Met Lys Lys Glu Lys Glu Met Asn Gly Glu Thr Arg Glu
130 135 140 145

aaa agc ccc aaa ctg aag aat gga ttt cct cat cct gaa ccg gac tgt 537
Lys Ser Pro Lys Leu Lys Asn Gly Phe Pro His Pro Glu Pro Asp Cys
146 151 156 161

aac ccc agt gaa gct gcc agt gaa gaa agt aac agt gag ata gag cag 585
Asn Pro Ser Glu Ala Ala Ser Glu Glu Ser Asn Ser Glu Ile Glu Gln
162 167 172 177

gaa ata cct gtg gaa caa aaa gaa ggc gct ttc tct aat ttt ccc ata 633
Glu Ile Pro Val Glu Gln Lys Glu Gly Ala Phe Ser Asn Phe Pro Ile
178 183 188 193

tct gaa gaa act att aaa ctt ctc aaa ggc cga gga gtg acc ttc cta 681
Ser Glu Glu Thr Ile Lys Leu Leu Lys Gly Arg Gly Val Thr Phe Leu

194	199	204	209	
ttt cct ata caa gca aag aca ttc cat cat gtt tac agc ggg aag gac Phe Pro Ile Gln Ala Lys Thr Phe His His Val Tyr Ser Gly Lys Asp				729
210	215	220	225	
tta att gca cag gca cg ^g aca gga act ggg aag aca ttc tcc ttt gcc Leu Ile Ala Gln Ala Arg Thr Gly Thr Gly Lys Thr Phe Ser Phe Ala				777
226	231	236	241	
atc cct ttg att gag aaa ctt cat ggg gaa ctg caa gac agg aag aga Ile Pro Leu Ile Glu Lys Leu His Gly Glu Leu Gln Asp Arg Lys Arg				825
242	247	252	257	
ggc cgt gcc cct cag gta ctg gtt ctt gca cct aca aga gag ttg gca Gly Arg Ala Pro Gln Val Leu Val Leu Ala Pro Thr Arg Glu Leu Ala				873
258	263	268	273	
aat caa gta agc aaa gac ttc agt gac atc aca aaa aag ctg tca gtg <u>Asn Gln Val Ser Lys Asp Phe Ser Asp Ile Thr Lys Lys Leu Ser Val</u>				921
274	279	284	289	
gct tgt ttt tat ggt gga act ccc tat gga ggt caa ttt gaa cgc atg Ala Cys Phe Tyr Gly Gly Thr Pro Tyr Gly Gly Gln Phe Glu Arg Met				969
290	295	300	305	
agg aat ggg att gat atc ctg gtt gga aca cca ggt cgt atc aaa gac Arg Asn Gly Ile Asp Ile Leu Val Gly Thr Pro Gly Arg Ile Lys Asp				1017
306	311	316	321	
cac ata cag aat ggc aaa cta gat ctc acc aaa ctt aag cat gtt gtc His Ile Gln Asn Gly Lys Leu Asp Leu Thr Lys Leu Lys His Val Val				1065
322	327	332	337	
ctg gat gaa gtg gac cag atg ttg gat atg gga ttt gct gat caa gtg Leu Asp Glu Val Asp Gln Met Leu Asp Met Gly Phe Ala Asp Gln Val				1113
338	343	348	353	
gaa gag att tta agt gtg gca tac aag aaa gat tct gaa gac aat ccc Glu Glu Ile Leu Ser Val Ala Tyr Lys Lys Asp Ser Glu Asp Asn Pro				1161
354	359	364	369	
caa aca ttg ctt ttt tct gca act tgc cct cat tgg gta ttt aat gtt Gln Thr Leu Leu Phe Ser Ala Thr Cys Pro His Trp Val Phe Asn Val				1209
370	375	380	385	
gcc aag aaa tac atg aaa tct aca tat gaa cag gtg gac ctg att ggt Ala Lys Lys Tyr Met Lys Ser Thr Tyr Glu Gln Val Asp Leu Ile Gly				1257
386	391	396	401	
aaa aag act cag aaa acg gca ata act gtg gag cat ctg gct att aag Lys Lys Thr Gln Lys Thr Ala Ile Thr Val Glu His Leu Ala Ile Lys				1305
402	407	412	417	
tgc cac tgg act cag agg gca gca gtt att ggg gat gtc atc cga gta Cys His Trp Thr Gln Arg Ala Ala Val Ile Gly Asp Val Ile Arg Val				1353
418	423	428	433	

tat agt ggt cat caa gga cgc act atc atc ttt tgt gaa acc aag aaa		1401
Tyr Ser Gly His Gln Gly Arg Thr Ile Ile Phe Cys Glu Thr Lys Lys		
434	439	444
449		
gaa gcc cag gag ctg tcc cag aat tca gct ata aag cag gat gct cag		1449
Glu Ala Gln Glu Leu Ser Gln Asn Ser Ala Ile Lys Gln Asp Ala Gln		
450	455	460
465		
tcc ttg cat gga gac att cca cag aag caa agg gaa atc acc ctg aaa		1497
Ser Leu His Gly Asp Ile Pro Gln Lys Gln Arg Glu Ile Thr Leu Lys		
466	471	476
481		
ggg ttt aga aat ggt agt ttt gga gtt ttg gtg gca acc aat gtt gct		1545
Gly Phe Arg Asn Gly Ser Phe Gly Val Leu Val Ala Thr Asn Val Ala		
482	487	492
497		
gca cgt ggg tta gac atc cct gag gtt gat ttg gtt ata caa agc tct		1593
Ala Arg Gly Leu Asp Ile Pro Glu Val Asp Leu Val Ile Gln Ser Ser		
498	503	508
513		
cca cca aag gat gta gag tcc tac att cat cga tcc ggg cg aca ggc		1641
Pro Pro Lys Asp Val Glu Ser Tyr Ile His Arg Ser Gly Arg Thr Gly		
514	519	524
529		
aga gct gga agg acg ggg gtg tgc atc tgc ttt tat cag cac aag gaa		1689
Arg Ala Gly Arg Thr Gly Val Cys Ile Cys Phe Tyr Gln His Lys Glu		
530	535	540
545		
gaa tat cag tta gta caa gtg gag caa aaa gcg gga att aag ttc aaa		1737
Glu Tyr Gln Leu Val Gln Val Glu Gln Lys Ala Gly Ile Lys Phe Lys		
546	551	556
561		
cga ata ggt gtt cct tct gca aca gaa ata ata aaa gct tcc agc aaa		1785
Arg Ile Gly Val Pro Ser Ala Thr Glu Ile Ile Lys Ala Ser Ser Lys		
562	567	572
577		
gat gcc atc agg ctt ttg gat tcc gtg cct ccc act gcc att agt cac		1833
Asp Ala Ile Arg Leu Leu Asp Ser Val Pro Pro Thr Ala Ile Ser His		
578	583	588
593		
ttc aaa caa tca gct gag aag ctg ata gag gag aag gga gct gtg gaa		1881
Phe Lys Gln Ser Ala Glu Lys Leu Ile Glu Glu Lys Gly Ala Val Glu		
594	599	604
609		
gct ctg gca gca gca ctg gcc cat att tca ggt gcc acg tcc gta gac		1929
Ala Leu Ala Ala Ala Leu Ala His Ile Ser Gly Ala Thr Ser Val Asp		
610	615	620
625		
cag cgc tcc ttg atc aac tca aat gtg ggt ttt gtg acc atg atc ttg		1977
Gln Arg Ser Leu Ile Asn Ser Asn Val Gly Phe Val Thr Met Ile Leu		
626	631	636
641		
cag tgc tca att gaa atg cca aat att agt tat gct tgg aaa gaa ctt		2025
Gln Cys Ser Ile Glu Met Pro Asn Ile Ser Tyr Ala Trp Lys Glu Leu		
642	647	652
657		

aaa gag cag ctg ggc gag gag att gat tcc aaa gtg aag gga atg gtt Lys Glu Gln Leu Gly Glu Glu Ile Asp Ser Lys Val Lys Gly Met Val 658 663 668 673	2073
ttt ctc aaa gga aag ctg ggt gtt tgc ttt gat gta cct acc gca tca Phe Leu Lys Gly Lys Leu Gly Val Cys Phe Asp Val Pro Thr Ala Ser 674 679 684 689	2121
gta aca gaa ata cag gag aaa tgg cat gat tca cga cgc tgg cag ctc Val Thr Glu Ile Gln Glu Lys Trp His Asp Ser Arg Arg Trp Gln Leu 690 695 700 705	2169
tct gtg gcc aca gag caa cca gaa ctg gaa gga cca cg ^g gaa gga tat Ser Val Ala Thr Glu Gln Pro Glu Leu Glu Gly Pro Arg Glu Gly Tyr 706 711 716 721	2217
gga ggc ttc agg gga cag cg ^g gaa ggc agt cga ggc ttc agg gga cag Gly Gly Phe Arg Gly Gln Arg Glu Gly Ser Arg Gly Phe Arg Gly Gln 722 727 732 737	2265
cg ^g gac gga aac aga aga ttc aga gga cag cg ^g gaa ggc agt aga ggc Arg Asp Gly Asn Arg Arg Phe Arg Gly Gln Arg Glu Gly Ser Arg Gly 738 743 748 753	2313
ccg aga gga cag cga tca gga ggt ggc aac aaa agt aac aga tcc caa Pro Arg Gly Gln Arg Ser Gly Gly Asn Lys Ser Asn Arg Ser Gln 754 759 764 769	2361
aac aaa ggc cag aag cg ^g agt ttc agt aaa gca ttt ggt caa taa tta Asn Lys Gly Gln Lys Arg Ser Phe Ser Lys Ala Phe Gly Gln *770 775 780	2409
gaaatagaag attttatatac caaaaaagaga atgatgtttg gcaatatacactgaacatt	2469
attttcatg caaaataaa agcacattgt gcctcctttt gaccacttgc caagtccctg	2529
tctcttcag acacagacaa gcttcattta aattatttca tctgatcatt atcattata	2589
actttattgt tacttcttca tcagttttc ctttgaaag gtgtatgaat tcattacatt	2649
tttattctaa tgtattatct gtagattaga agataaaatc aagcatgtat ctgcctatac	2709
tttgtgagtt cacctgtctt tatactcaaa agtgtccctt aatagtgtcc ttccctgaaa	2769
taaataccta agggagtgtac acagtctctg gaggaccact ttgagccttt ggaagttaag	2829
gtttcctcag ccacctgccg aacagtttct catgtggtcc tattatttgt ctactgagac	2889
ttaatactga gcaatgtttt gaaacaagat ttcaaactaa tctgggttgt aatacagttt	2949
ataccagtgt atgctctaga cttggaagat gtagtatgtt tgatgtggat tacctatact	3009
tatgttcgtt ttgatcacatt tttagcttct cattataagg tgattcatgc ttttagtgaat	3069
tcttcataga tagtatatat aaaagtacat tttaatagaa agccagggtt ttaaggaatt	3129
tcacatgtat aaggtggctc catagcttta tttgtaagta ggctggataa atggtgctta	3189

aatggtaatg tactccactt cttcctattg gaagattaac attatttacc aagaaggact 3249
 taagggagta aggggcgcag attagcattg ctcaagagta tgaaaaaaaaaaaa 3304

<210> 106
 <211> 3757
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (83)..(2284)

<400> 106
 ttgaatcgta cgcctgcacg accgggccgg aattccccggg tcgacccacg cgtccggcaa 60
 tcagagcacc gcagccagg ag atg ctg gcg aga cga cag cga gat cct ctc 112
 Met Leu Ala Arg Arg Gln Arg Asp Pro Leu
 1 5

cag gcc ctg cgg cgc aat cag gag ctg aag caa cag gtt gat agt 160
 Gln Ala Leu Arg Arg Asn Gln Glu Leu Lys Gln Gln Val Asp Ser
 11 16 21 26

ttg ctt tct gag agc caa ctg aaa gaa gct cta gaa ccc aat aaa aga 208
 Leu Leu Ser Glu Ser Gln Leu Lys Glu Ala Leu Glu Pro Asn Lys Arg
 27 32 37 42

caa cat att tat caa aga tgt atc cag tta aag cag gca ata gat gaa 256
 Gln His Ile Tyr Gln Arg Cys Ile Gln Leu Lys Gln Ala Ile Asp Glu
 43 48 53 58

aat aaa aat gct ctt caa aaa tta agc aaa gct gat gaa tct gca cct 304
 Asn Lys Asn Ala Leu Gln Lys Leu Ser Lys Ala Asp Glu Ser Ala Pro
 59 64 69 74

gtt gca aac tat aat cag aga aaa gaa gag gag cat act ctt ttg gac 352
 Val Ala Asn Tyr Asn Gln Arg Lys Glu Glu His Thr Leu Leu Asp
 75 80 85 90

aag ctt acc caa caa ctg cag ggc ctt gct gtg aca ata agc aga gaa 400
 Lys Leu Thr Gln Gln Leu Gln Gly Leu Ala Val Thr Ile Ser Arg Glu
 91 96 101 106

aat ata act gaa gtt ggg gca cct act gaa gaa gag gaa agt gaa 448
 Asn Ile Thr Glu Val Gly Ala Pro Thr Glu Glu Glu Glu Ser Glu
 107 112 117 122

agt gaa gat agt gaa gac agt ggt ggg gag gaa gaa gat gca gag gag 496
 Ser Glu Asp Ser Glu Asp Ser Gly Gly Glu Glu Asp Ala Glu Glu
 123 128 133 138

gaa gag gaa gag aaa gag gaa aat gaa tct cac aaa tgg tca acc ggt 544

Glu	Glu	Glu	Glu	Lys	Glu	Glu	Asn	Glu	Ser	His	Lys	Trp	Ser	Thr	Gly		
139					144				149				154				
gaa gaa tac atc gct gtt gga gat ttt act gct cag caa gtt gga gat															592		
Glu	Glu	Tyr	Ile	Ala	Val	Gly	Asp	Phe	Thr	Ala	Gln	Gln	Val	Gly	Asp		
155					160				165				170				
ctt aca ttt aag aaa ggg gaa att ctc ctt gta att gaa aaa aaa cct															640		
Leu	Thr	Phe	Lys	Gly	Ile	Leu	Leu	Val	Ile	Glu	Lys	Lys	Pro				
171					176				181				186				
gat ggt tgg tgg ata gct aag gat gcc aaa gga aat gaa ggt ctt gtt															688		
Asp	Gly	Trp	Trp	Ile	Ala	Lys	Asp	Ala	Lys	Gly	Asn	Glu	Gly	Leu	Val		
187					192				197				202				
ccc aga acc tac cta gag cct tat agt gaa gaa gaa ggc caa gaa															736		
Pro	Arg	Thr	Tyr	Leu	Glu	Pro	Tyr	Ser	Glu	Glu	Glu	Gly	Gln	Glu			
203					208				213				218				
<u>tca</u> agt gaa gag <u>ggc</u> agt <u>gaa</u> <u>gaa</u> <u>gat</u> gta gag <u>gcg</u> <u>gtg</u> <u>gat</u> gaa aca															784		
Ser	Ser	Glu	Glu	Gly	Ser	Glu	Glu	Asp	Val	Glu	Ala	Val	Asp	Glu	Thr		
219					224				229				234				
gca gat gga gca gaa gtt aag caa aga act gat ccc cac tgg agt gct															832		
Ala	Asp	Gly	Ala	Glu	Val	Lys	Gln	Arg	Thr	Asp	Pro	His	Trp	Ser	Ala		
235					240				245				250				
gtt cag aaa gcg att tca gag gcg ggc atc ttc tgt ctt gtt aat cat															880		
Val	Gln	Lys	Ala	Ile	Ser	Glu	Ala	Gly	Ile	Phe	Cys	Leu	Val	Asn	His		
251					256				261				266				
gtc tcg ttt tgc tac cta ata gtt ctg atg cga aat agg atg gag act															928		
Val	Ser	Phe	Cys	Tyr	Leu	Ile	Val	Leu	Met	Arg	Asn	Arg	Met	Glu	Thr		
267					272				277				282				
gtg gaa gac acc aat gga tct gaa aca ggg ttc agg gca tgg aat gta															976		
Val	Glu	Asp	Thr	Asn	Gly	Ser	Glu	Thr	Gly	Phe	Arg	Ala	Trp	Asn	Val		
283					288				293				298				
cag agc aga gga cgt ata ttt ctg gtt tct aag cct gtg ctc cag cag															1024		
Gln	Ser	Arg	Gly	Arg	Ile	Phe	Leu	Val	Ser	Lys	Pro	Val	Leu	Gln	Gln		
299					304				309				314				
ata aac act gtt gat gtg tta act acg atg gga gct att cct gca ggg															1072		
Ile	Asn	Thr	Val	Asp	Val	Leu	Thr	Met	Gly	Ala	Ile	Pro	Ala	Gly			
315					320				325				330				
ttc agg cct tcc acg ctc tca cag ctt ctg gag gaa ggg aat caa ttt															1120		
Phe	Arg	Pro	Ser	Thr	Leu	Ser	Gln	Leu	Leu	Glu	Glu	Gly	Asn	Gln	Phe		
331					336				341				346				
cga gca aat tac ttc tta caa cca gag ctc atg cct tca caa ctg gcc															1168		
Arg	Ala	Asn	Tyr	Phe	Leu	Gln	Pro	Glu	Leu	Met	Pro	Ser	Gln	Leu	Ala		
347					352				357				362				
ttc aga gat ctg atg tgg gat gct aca gaa ggc act att agg tcg aga															1216		
Phe	Arg	Asp	Leu	Met	Trp	Asp	Ala	Thr	Glu	Gly	Thr	Ile	Arg	Ser	Arg		

363	368	373	378	
cca agt cgt att tca ttg att ctg aca tta tgg agc tgt aaa atg att				1264
Pro Ser Arg Ile Ser Leu Ile Leu Thr Leu Trp Ser Cys Lys Met Ile				
379	384	389	394	
cct ctt cca gga atg agc ata cag gtt ctc agc aga cat gta cgc ctc				1312
Pro Leu Pro Gly Met Ser Ile Gln Val Leu Ser Arg His Val Arg Leu				
395	400	405	410	
tgt cta ttt gat ggt aat aag gtt ctg agc aac att cat aca gtc aga				1360
Cys Leu Phe Asp Gly Asn Lys Val Leu Ser Asn Ile His Thr Val Arg				
411	416	421	426	
gcc aca tgg caa cct aaa aag ccc aaa aca tgg acc ttt tct ccc cag				1408
Ala Thr Trp Gln Pro Lys Lys Pro Lys Thr Trp Thr Phe Ser Pro Gln				
427	432	437	442	
gtt act cgc atc tta cca tgt ttg ctt gat ggt gat tgc ttt atc agg				1456
Val Thr Arg Ile Leu Pro Cys Leu Leu Asp Gly Asp Cys Phe Ile Arg				
443	448	453	458	
tct aat tct gca tct cca gat ctt gga ata tta ttt gaa ctt gga att				1504
Ser Asn Ser Ala Ser Pro Asp Leu Gly Ile Leu Phe Glu Leu Gly Ile				
459	464	469	474	
tct tat att cgc aat tca act ggt gaa aga gga gag tta agc tgt ggc				1552
Ser Tyr Ile Arg Asn Ser Thr Gly Glu Arg Gly Glu Leu Ser Cys Gly				
475	480	485	490	
tgg gtg ttt ctt aaa ctt ttt gat gcc agt gga gtt cct att cca gca				1600
Trp Val Phe Leu Lys Leu Phe Asp Ala Ser Gly Val Pro Ile Pro Ala				
491	496	501	506	
aaa act tat gag ctt ttc ttg aat ggt act cct tat gaa aaa ggt				1648
Lys Thr Tyr Glu Leu Phe Leu Asn Gly Gly Thr Pro Tyr Glu Lys Gly				
507	512	517	522	
att gaa gtg gac cct tca ata tcc aga aga gca cac ggc agt gtt ttc				1696
Ile Glu Val Asp Pro Ser Ile Ser Arg Arg Ala His Gly Ser Val Phe				
523	528	533	538	
tac cag att atg aca atg aga agg cag cct caa ctt cta gtg aaa ctg				1744
Tyr Gln Ile Met Thr Met Arg Arg Gln Pro Gln Leu Leu Val Lys Leu				
539	544	549	554	
aga tcc ttg aac aga aga tca aga aat gta cta agt cta ctg cca gaa				1792
Arg Ser Leu Asn Arg Arg Ser Arg Asn Val Leu Ser Leu Leu Pro Glu				
555	560	565	570	
aca tta att gga aat atg tgt tct att cac ttg ttg ata ttt tat cga				1840
Thr Leu Ile Gly Asn Met Cys Ser Ile His Leu Leu Ile Phe Tyr Arg				
571	576	581	586	
caa att ctt gga gat gtg ctc ctg aaa gac agg atg agc ttg caa agt				1888
Gln Ile Leu Gly Asp Val Leu Leu Lys Asp Arg Met Ser Leu Gln Ser				
587	592	597	602	

act gat tta att agc cat ccc atg ctg gcc acc ttc ccc atg ctc ttg		1936
Thr Asp Leu Ile Ser His Pro Met Leu Ala Thr Phe Pro Met Leu Leu		
603	608	613
618		
gag cag cct gat gtg atg gat gct ctc agg agt tcg tgg gct gga aaa		1984
Glu Gln Pro Asp Val Met Asp Ala Leu Arg Ser Ser Trp Ala Gly Lys		
619	624	629
634		
gaa agc aca tta aaa aga tca gag aag aga gac aaa gag ttc ctg aag		2032
Glu Ser Thr Leu Lys Arg Ser Glu Lys Arg Asp Lys Glu Phe Leu Lys		
635	640	645
650		
tcc acg ttt ctc ctg gtt tac cat gac tgc gtg ctc cca ctt ctc cac		2080
Ser Thr Phe Leu Leu Val Tyr His Asp Cys Val Leu Pro Leu Leu His		
651	656	661
666		
tcc aca cgc cta ccc cca ttc agg tgg gca gaa gaa gag act gag act		2128
Ser Thr Arg Leu Pro Pro Phe Arg Trp Ala Glu Glu Glu Thr Glu Thr		
667	672	677
682		
gca cg ^g tgg aaa gtt atc act gac ttc ctt aag caa aac caa gaa aac		2176
Ala Arg Trp Lys Val Ile Thr Asp Phe Leu Lys Gln Asn Gln Glu Asn		
683	688	693
698		
cag ggc gcc ctc caa gct ctg tca cca gac gga gtt cat gaa cct		2224
Gln Gly Ala Leu Gln Ala Leu Leu Ser Pro Asp Gly Val His Glu Pro		
699	704	709
714		
ttt gac ctt tca gag cag acc tat gac ttc ttg ggt gaa atg aga aag		2272
Phe Asp Leu Ser Glu Gln Thr Tyr Asp Phe Leu Gly Glu Met Arg Lys		
715	720	725
730		
aat gca gtg tga cag tggcagcctc tagccctcag cttcccacgg aatcagatgg		2327
Asn Ala Val *		
731		
atcctccacg attacgtgaa taaaatgatg gaacaaaaaa tcactgtcac tttacaactt		2387
aggttttact cttttctttc tacagaccat atttttaaag aaatgtttat acaataattt		2447
aaatattttt taaaaccata aaataaaattt ttataaggaa tactgttata tctaaattta		2507
aacagtattt atttttcaa aaacagctac ttaagttaat ggtatagatt tctataaaag		2567
caagattttg taaaaacta aatttatgat tattcaagaa agtggaaaaaa acaacctaca		2627
gaatggaaaa acatatttgc aaatcatcta actgataaag gtcttagtac caaaatattt		2687
aaatttatga gtgttaataa aatttatctt gttcaatgaa gaggaagtta aagtgatcca		2747
tttgagaaaag ttgtatcact taattcagtc tgatacttga atgtgatttta cccctaatta		2807
agtacaaaaaa cagagtgcgt tttgcctttt caaatcaaga aaataagtgc tctgtcaaaa		2867
gcacaaaaag aaactttcag gcactggaga gtggagtcga ctcacccttt caggcattgt		2927

tgcatctcag ataaacctgt gactgctggt aaaataatgt cccaaaggcctt tccttttagt	2987
gataaacagt agcagcctgc gttaatttag cacctactgt gtgtctgagc atttctcatt	3047
agcccagttt atcctcacac ctactgttagg agataggtac tttttttt tattaccgcc	3107
gaagaaaacag gccagataag tgaagtaatt tgcctaaggt cacagctaat aagtggcaca	3167
gctaatattc ccagtaaaga taccatgtat aattttctac aacctaagat gttctgcctt	3227
atcgccccgca accttttagg attccatgtg aaaataaaat atgagaaaaa gtttaaccta	3287
aataattaga atcccattag aggtactttt ttttgatggc atgctgcctt aaaagagcca	3347
tttattttta gagatctgtc atattatgaa agttctgggc tatcttagct aacttacct	3407
aaacccttaa cctaaattta acttgagccc cagtcctcaga aattaacatg gtatgaaagt	3467
gtttccaggc caggcgccgt ggctcacgcc tgtaatccca acactttggg aggccgaggt	3527
gggtggatca cctgaggtca ggagttttag accagcctgg ccaacactat ctgtactaaa	3587
aacacaaaat tagctgggtg tggtagtgcg tgcctgtat cccagctact tgggaggctg	3647
aggtagaaga attgtttgaa cctgggaggt ggaggttgca gtgagccaaat atcgtgccat	3707
tgcactccag cctaggcaac aagagtgaaa ctccatctca aaaaaaaaaaa	3757

<210> 107
 <211> 2783
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (84)..(1448)

<400> 107	
atctcagagt ggccggattc gccgggacca gcccgtcggtt gcccggctga tacagccgct	60
tcaccgtgcc cctgccccgca acc atg gcc tcc tcc gag gtg gcg cgg cac	110
Met Ala Ser Ser Glu Val Ala Arg His	
1 5	
ctg ctc ttt cag tct cac atg gca acg aaa aca act tgt atg tct tca	158
Leu Leu Phe Gln Ser His Met Ala Thr Lys Thr Thr Cys Met Ser Ser	
10 15 20 25	
caa gga tca gat gat gaa cag ata aaa aga gaa aac att cgt tcg ttg	206
Gln Gly Ser Asp Asp Glu Gln Ile Lys Arg Glu Asn Ile Arg Ser Leu	
26 31 36 41	
act atg tct ggc cat gtt ggt ttt gag agt ttg cct gat cag ctg gtg	254
Thr Met Ser Gly His Val Gly Phe Glu Ser Leu Pro Asp Gln Leu Val	

42	47	52	57	
aac aga tcc att cag caa ggg ttc tgc ttt aat att ctc tgt gtg ggg Asn Arg Ser Ile Gln Gln Gly Phe Cys Phe Asn Ile Leu Cys Val Gly	58	63	68	73
gaa act gga att gga aaa tca aca ctg att gac aca ttg ttt aat act Glu Thr Gly Ile Gly Lys Ser Thr Leu Ile Asp Thr Leu Phe Asn Thr	74	79	84	89
aat ttt gaa gac tat gaa tcc tca cat ttt tgc cca aat gtt aaa ctt Asn Phe Glu Asp Tyr Glu Ser Ser His Phe Cys Pro Asn Val Lys Leu	90	95	100	105
aaa gct cag aca tat gaa ctc cag gaa agt aat gtt caa ttg aaa ttg Lys Ala Gln Thr Tyr Glu Leu Gln Glu Ser Asn Val Gln Leu Lys Leu	106	111	116	121
acc att gtg aat aca gtg gga ttt ggt gac caa ata aat aaa gaa gag Thr Ile Val Asn Thr Val Gly Phe Gly Asp Gln Ile Asn Lys Glu Glu	122	127	132	137
agc tac caa cca ata gtt gac tac ata gat gct cag ttt gag gcc tat Ser Tyr Gln Pro Ile Val Asp Tyr Ile Asp Ala Gln Phe Glu Ala Tyr	138	143	148	153
ctc caa gaa gaa ctg aag att aag cgt tct ctc ttt acc tac cat gat Leu Gln Glu Glu Leu Lys Ile Lys Arg Ser Leu Phe Thr Tyr His Asp	154	159	164	169
tct cgc atc cat gtg tgt ctc tac ttc att tca ccg aca ggc cac tct Ser Arg Ile His Val Cys Leu Tyr Phe Ile Ser Pro Thr Gly His Ser	170	175	180	185
ctg aag aca ctt gat ctc tta acc atg aag aac ctt gac agc aag gta Leu Lys Thr Leu Asp Leu Leu Thr Met Lys Asn Leu Asp Ser Lys Val	186	191	196	201
aac att ata cca gtg att gcc aaa gca gat acg gtt tct aaa act gaa Asn Ile Ile Pro Val Ile Ala Lys Ala Asp Thr Val Ser Lys Thr Glu	202	207	212	217
tta cag aag ttt aag atc aag ctc atg agt gaa ttg gtc agc aat ggc Leu Gln Lys Phe Lys Ile Lys Leu Met Ser Glu Leu Val Ser Asn Gly	218	223	228	233
gtc cag ata tac cag ttc cca acg gat gat gac act att gct aag gtc Val Gln Ile Tyr Gln Phe Pro Thr Asp Asp Asp Thr Ile Ala Lys Val	234	239	244	249
aac gct gca atg aat gga cag ttg ccg ttt gct gtt gtg gga agt atg Asn Ala Ala Met Asn Gly Gln Leu Pro Phe Ala Val Val Gly Ser Met	250	255	260	265
gat gag gta aaa gtc gga aac aag atg gtc aaa gct cgc cag tac cct Asp Glu Val Lys Val Gly Asn Lys Met Val Lys Ala Arg Gln Tyr Pro	266	271	276	281

tgg ggt gtt gta caa gtg gaa aat gaa aac cac tgt gac ttt gta aag Trp Gly Val Val Gln Val Glu Asn Glu Asn His Cys Asp Phe Val Lys 282 287 292 297	974
ctg cgg gaa atg ctc att tgt aca aat atg gag gac ctg cga gag cag Leu Arg Glu Met Leu Ile Cys Thr Asn Met Glu Asp Leu Arg Glu Gln 298 303 308 313	1022
acc cat acc agg cac tat gag ctt tac agg cgc tgc aaa ctg gag gaa Thr His Thr Arg His Tyr Glu Leu Tyr Arg Arg Cys Lys Leu Glu Glu 314 319 324 329	1070
atg ggc ttt aca gat gtg ggc cca gaa aac aag cca gtc agt gtt caa Met Gly Phe Thr Asp Val Gly Pro Glu Asn Lys Pro Val Ser Val Gln 330 335 340 345	1118
gag acc tat gaa gcc aaa aga cat gag ttc cat ggt gaa cgt cag agg Glu Thr Tyr Glu Ala Lys Arg His Glu Phe His Gly Glu Arg Gln Arg 346 351 356 361	1166
aag gaa gaa gaa atg aaa cag atg ttt gtg cag cga gta aag gag aaa Lys Glu Glu Glu Met Lys Gln Met Phe Val Gln Arg Val Lys Glu Lys 362 367 372 377	1214
gaa gcc ata ttg aaa gaa gct gag aga gag cta cag gcc aaa ttt gag Glu Ala Ile Leu Lys Glu Ala Glu Arg Glu Leu Gln Ala Lys Phe Glu 378 383 388 393	1262
cac ctt aag aga ctt cac caa gaa gag aga atg aag ctt gaa gaa aag His Leu Lys Arg Leu His Gln Glu Glu Arg Met Lys Leu Glu Glu Lys 394 399 404 409	1310
aga aga ctt ttg gaa gaa ata att gct ttc tct aaa aag aaa gct Arg Arg Leu Leu Glu Glu Ile Ile Ala Phe Ser Lys Lys Lys Ala 410 415 420 425	1358
acc tcc gag ata ttt cac agc cag tcc ttt ctg gca aca ggc agc aac Thr Ser Glu Ile Phe His Ser Gln Ser Phe Leu Ala Thr Gly Ser Asn 426 431 436 441	1406
ctg agg aag gac aag gac cgt aag aac tcc aat ttt ttg taa aacagaa Leu Arg Lys Asp Lys Asp Arg Lys Asn Ser Asn Phe Leu * 442 447 452	1455
gttccagagc acagaaggc atcatcacaa gcaaacttta taaaaaaaaa actagaagtgc tgctttgatt ttgctgttat ttgtttatc acttctatat ttggtaaca gccacagtta ctgatattta tggaaaagta ctttcaagta caaggtcaat acataagccca gagtgaatga tactacaagt tgagcatctc taattcaaaa atctgaaatc cagaagcttc aaaatctgaa tctttttgag cactgacttg acccccacaag tggaaaattc cccacccgac acctttgctt tctgatgggt cagttaaac agattttgtt tcttgcacaa aatttttgta taaattactt	1515 1575 1635 1695 1755 1815

tcaggctata	tgtataaggt	ggatgtgaaa	catgaattat	gtaatttagag	tcgggtcccg	1875
ttgtgtatat	gcagatattc	caaacctgaa	atccaaaaca	cttctggtcc	ctagcatttt	1935
ggataaggga	tactcagctt	gtacctata	attcatata	attcactgtt	gttagaaatg	1995
tttaagttgc	tgttctgtga	tgaatctaaa	tctttctct	tgctaccaag	ctattgtcac	2055
tgcagtgc	tataccaaag	agcgaagtca	gtgccactga	aaatacagaa	cccattaata	2115
tcgtggctat	ctgattacat	ttatattcca	agatgaacct	tttttatata	tgctaaaaat	2175
tttgggaat	atgtttggg	atgtattatg	gagctaaaac	tctaaccctct	taatagttt	2235
atagaactta	aaaattttt	atacaattac	ccaattggtg	atatgatctt	aagcttttgt	2295
gtcagattat	ttaatatgat	gacttcatgc	tttattatgc	cttattatgg	ctgacgtatt	2355
actgtggtga	aacaaaat	ctttaaaagt	taaaacatcc	agatataaa	gctattttt	2415
cctaaggata	aagtacctt	gagcatgagt	gtatcacagc	tttcatttagg	aaaacttttc	2475
attacatact	tgtttaact	ctgtcttcca	gggtaaaaat	aataagggtt	aatcattttt	2535
ttaaaaatac	tttttaagaa	aataactatg	aacatctgaa	tattaaagat	ataaaaatgc	2595
acataattca	tatccaggt	ggtatccat	ttcagtgcc	tactggtatt	ctcagaacat	2655
tttaatgatt	tctaacattt	cttaacagtc	atagatata	acattttcat	ttttgtact	2715
tgaatattct	aaataaaact	gacatttact	cttgacaaat	aaaacatata	tttactaaaa	2775
aaaaaaaaa						2783

<210> 108
 <211> 2265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (79) .. (1614)

<400> 108

taagttcg	accgcagctc	tttcaccagc	ttgggtgggg	gcgtgttcgt	ggtctacgtg	60
gtgcacac	ct	atg tac ggc atc gtc tac acc cgc ccg tgc tcc				111
		Met Tyr Gly Ile Val Tyr Thr Arg Pro Cys Ser				
		1	5			
ggc	gac	gcc	aac	tgc	atc	159
Gly	Asp	Ala	Asn	Cys	Ile	Gln
12	17	22	27			
Pro	Tyr	Leu	Ala	Arg	Arg	Lys
						Leu

cag ctg agc gtg tac acc acg acg agg tcc cac ctg ggt gct gag aac Gln Leu Ser Val Tyr Thr Thr Arg Ser His Leu Gly Ala Glu Asn	207
28 33 38 43	
aac atc gac ctg gtc ttg aat gtg gaa gac ttt gat gtg gag tcc aaa Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe Asp Val Glu Ser Lys	255
44 49 54 59	
ttt gaa agg aca gtt aat gtt tct gta cca aag aaa acg aga aac aat Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys Lys Thr Arg Asn Asn	303
60 65 70 75	
ggg acg ctg tat gcc tac atc ttc ctc cat cac gct ggg gtc ctg ccg Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His Ala Gly Val Leu Pro	351
76 81 86 91	
tgg cac gac ggg aag cag gtg cac ctg gtc agt cct ctg acc acc tac Trp His Asp Gly Lys Gln Val His Leu Val Ser Pro Leu Thr Thr Tyr	399
92 97 102 107	
atg gtc ccc aag cca gaa gaa atc aac ctg ctc acc ggg gag tct gat Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu Thr Gly Glu Ser Asp	447
108 113 118 123	
aca cag atc gag gcg gag aag aag ccg acg agt gcc ctg gat gag cca Thr Gln Ile Glu Ala Glu Lys Lys Pro Thr Ser Ala Leu Asp Glu Pro	495
124 129 134 139	
gtg tcc cac tgg cga ccg cggt ctg gcg ctg aac gtg atg gcg gac aac Val Ser His Trp Arg Pro Arg Leu Ala Leu Asn Val Met Ala Asp Asn	543
140 145 150 155	
ttt gtc ttt gac ggg tcc tcc ctg cct gcc gat gtg cat cgg tac atg Phe Val Phe Asp Gly Ser Ser Leu Pro Ala Asp Val His Arg Tyr Met	591
156 161 166 171	
aag atg atc cag ctg ggg aaa acc gtg cat tac ctg ccc atc ctg ttc Lys Met Ile Gln Leu Gly Lys Thr Val His Tyr Leu Pro Ile Leu Phe	639
172 177 182 187	
atc gac cag ctc agc aac cgc gtg aag gac ctg atg gtc ata aac cgc Ile Asp Gln Leu Ser Asn Arg Val Lys Asp Leu Met Val Ile Asn Arg	687
188 193 198 203	
tcc acc acc gag ctg ccc ctc acc gtg tcc tac gac aag gtc tca ctg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser Tyr Asp Lys Val Ser Leu	735
204 209 214 219	
ggg cgg ctg cgc ttc tgg atc cac atg cag gac gcc gtg tac tcc ctg Gly Arg Leu Arg Phe Trp Ile His Met Gln Asp Ala Val Tyr Ser Leu	783
220 225 230 235	
cag cag ttc ggg ttt tca gag aaa gat gct gat gag gtg aaa gga att Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala Asp Glu Val Lys Gly Ile	831
236 241 246 251	
ttt gta gat acc aac tta tac ttc ctg gcg ctg acc ttc ttt gtc gca	879

Phe	Val	Asp	Thr	Asn	Leu	Tyr	Phe	Leu	Ala	Leu	Thr	Phe	Phe	Val	Ala
252					257				262			267			
gcg	tcc	cat	ctt	ctc	ttt	gat	tcc	ctg	gcc	ttt	aaa	aat	gac	atc	agt
Ala	Phe	His	Leu	Leu	Phe	Asp	Phe	Leu	Ala	Phe	Lys	Asn	Asp	Ile	Ser
268					273				278			283			
ttc	tgg	aag	aag	aag	aag	agc	atg	atc	ggc	atg	tcc	acc	aag	gca	gtg
Phe	Trp	Lys	Lys	Lys	Lys	Ser	Met	Ile	Gly	Met	Ser	Thr	Lys	Ala	Val
284						289			294			299			
ctc	tgg	cgc	tgc	ttc	agc	acc	gtg	gtc	atc	ttt	ctg	ttc	ctg	ctg	gac
Leu	Trp	Arg	Cys	Phe	Ser	Thr	Val	Val	Ile	Phe	Leu	Phe	Leu	Leu	Asp
300						305			310			315			
gag	cag	acg	agc	ctg	ctg	gtg	ctg	gtc	ccg	gcg	ggt	gtt	gga	gcc	gcc
Glu	Gln	Thr	Ser	Leu	Leu	Val	Leu	Val	Pro	Ala	Gly	Val	Gly	Ala	Ala
316						321			326			331			
att	gag	ctg	tgg	aaa	gtg	aag	aag	gca	ttg	aag	atg	act	att	ttt	tgg
Ile	Glu	Leu	Trp	Lys	Val	Lys	Lys	Ala	Leu	Lys	Met	Thr	Ile	Phe	Trp
332						337			342			347			
aga	ggc	ctg	atg	ccc	gaa	ttt	cag	ttt	ggc	act	tac	agc	gaa	tct	gag
Arg	Gly	Leu	Met	Pro	Glu	Phe	Gln	Phe	Gly	Thr	Tyr	Ser	Glu	Ser	Glu
348						353			358			363			
agg	aaa	acc	gag	gag	tac	gat	act	cag	gcc	atg	aag	tac	ttg	tca	tac
Arg	Lys	Thr	Glu	Glu	Tyr	Asp	Thr	Gln	Ala	Met	Lys	Tyr	Leu	Ser	Tyr
364						369			374			379			
ctg	ctg	tac	cct	ctc	tgt	gtc	ggg	ggt	gct	gtc	tat	tca	ctc	ctg	aat
Leu	Leu	Tyr	Pro	Leu	Cys	Val	Gly	Gly	Ala	Val	Tyr	Ser	Leu	Leu	Asn
380						385			390			395			
atc	aaa	tat	aag	agc	tgg	tac	tcc	tgg	tta	atc	aac	agc	ttc	gtc	aac
Ile	Lys	Tyr	Lys	Ser	Trp	Tyr	Ser	Trp	Leu	Ile	Asn	Ser	Phe	Val	Asn
396						401			406			411			
ggg	gtc	tat	gcc	ttt	ggt	ttc	ctc	ttc	atg	ctg	ccc	cag	ctc	ttt	gtg
Gly	Val	Tyr	Ala	Phe	Gly	Phe	Leu	Phe	Met	Leu	Pro	Gln	Leu	Phe	Val
412						417			422			427			
aac	tac	aag	ttg	aag	tca	gtg	gca	cat	ctg	ccc	tgg	aag	gcc	ttc	acc
Asn	Tyr	Lys	Leu	Lys	Ser	Val	Ala	His	Leu	Pro	Trp	Lys	Ala	Phe	Thr
428						433			438			443			
tac	aag	gct	ttc	aac	acc	ttc	att	gat	gac	gtc	ttt	gcc	ttc	atc	atc
Tyr	Lys	Ala	Phe	Asn	Thr	Phe	Ile	Asp	Asp	Val	Phe	Ala	Phe	Ile	Ile
444						449			454			459			
acc	atg	ccc	acg	tct	cac	cg	ctg	gcc	tgc	ttc	cg	gac	gac	gtg	gtg
Thr	Met	Pro	Thr	Ser	His	Arg	Leu	Ala	Cys	Phe	Arg	Asp	Asp	Val	Val
460						465			470			475			
ttt	ctg	gtc	tac	ctg	tac	cag	cg	tgg	ctt	tat	cct	gtg	gat	aaa	cgc
Phe	Leu	Val	Tyr	Leu	Tyr	Gln	Arg	Trp	Leu	Tyr	Pro	Val	Asp	Lys	Arg
															1551

476	481	486	491	
aga gtg aac gag ttt ggg gag tcc tac gag gag aag gcc acg cgg gcg Arg Val Asn Glu Phe Gly Glu Ser Tyr Glu Glu Lys Ala Thr Arg Ala				1599
492	497	502	507	
ccc cac acg gac tga aggccgccccg ggctgccgcc agccaagtgc aacttgaatt Pro His Thr Asp *				1654
508				
gtcaatgagt atttttggaa gcatttggag gaattcctag acattgcgtt ttctgtgttg				1714
ccaaaatccc ttccggacatt ttcagacat ctcccaagtt cccatcacgt cagatttggaa				1774
gctggtagcg cttacgatgc ccccacgtgt gaacatctgt cttggtcaca gagctgggtg				1834
ctgccggtca cttttagctg tggtggctcc cgccacacga gtgtccgggg ttccggccatg				1894
tcctcacgcg ggcaggggtg ggagccctca caggcaaggg ggctgttggaa ttccatttc				1954
aggtggtttt ctaagtgtctc cttatgtgaa tttcaaacac gtatggaaatt cattccgcatt				2014
ggactctggg atcaaaggct ctttcctt ttgtttgaga gttggttgtt ttaaagctta				2074
atgtatgttt ctattttaaa ataaaattttt ctggctgtgg caaaaaaaaaaaaaaaaag				2134
ggcggccgct ctagagtatc cttcgagggg cccaaagctta cgcttaccca gctttcttgt				2194
acaaagtggt ccctatagtg agtcgtatat aagctaggca gtttcatcca gcagtcaacc				2254
ctcatccttg g				2265
<210> 109 <211> 2349 <212> DNA <213> Homo sapiens				
<220> <221> CDS <222> (79)..(1698)				
<400> 109 taagcttgcg accgcagctc cttcaccagc ttgggtggtgg gcgtgttcgt ggtctacgtg 60				
gtgcacacct gctgggtc atg tac ggc atc gtc tac acc cgc ccc tgc tcc 111 Met Tyr Gly Ile Val Tyr Thr Arg Pro Cys Ser 1 5				
ggc gac gcc aac tgc atc cag ccc tac ctg gcg cgg cgg ccc aag ctg 159 Gly Asp Ala Asn Cys Ile Gln Pro Tyr Leu Ala Arg Arg Pro Lys Leu 12 17 22 27				
cag ctg agc gtg tac acc acg acg agg tcc cac ctg ggt gct gag aac 207 Gln Leu Ser Val Tyr Thr Thr Arg Ser His Leu Gly Ala Glu Asn				

28	33	38	43	
aac atc gac ctg gtc ttg aat gtg gaa gac ttt gat gtg gag tcc aaa Asn Ile Asp Leu Val Leu Asn Val Glu Asp Phe Asp Val Glu Ser Lys 44 49 54 59				255
ttt gaa agg aca gtt aat gtt tct gta cca aag aaa acg aga aac aat Phe Glu Arg Thr Val Asn Val Ser Val Pro Lys Lys Thr Arg Asn Asn 60 65 70 75				303
ggg acg ctg tat gcc tac atc ttc ctc cat cac gct ggg gtc ctg ccg Gly Thr Leu Tyr Ala Tyr Ile Phe Leu His His Ala Gly Val Leu Pro 76 81 86 91				351
tgg cac gac ggg aag cag gtg cac ctg gtc agt cct ctg acc acc tac Trp His Asp Gly Lys Gln Val His Leu Val Ser Pro Leu Thr Thr Tyr 92 97 102 107				399
atg gtc ccc aag cca gaa gaa atc aac ctg ctc acc ggg gag tct gat Met Val Pro Lys Pro Glu Glu Ile Asn Leu Leu Thr Gly Glu Ser Asp 108 113 118 123				447
aca cag atc gag gcg gag aag aag ccg acg agt gcc ctg gat gag cca Thr Gln Ile Glu Ala Glu Lys Lys Pro Thr Ser Ala Leu Asp Glu Pro 124 129 134 139				495
gtg tcc cac tgg cga ccg cgg ctg gcg ctg aac gtg atg gcg gac aac Val Ser His Trp Arg Pro Arg Leu Ala Leu Asn Val Met Ala Asp Asn 140 145 150 155				543
ttt gtc ttt gac ggg tcc tcc cct gcc gat gtg cat cgg tac atg Phe Val Phe Asp Gly Ser Ser Leu Pro Ala Asp Val His Arg Tyr Met 156 161 166 171				591
aag atg atc cag ctg ggg aaa acc gtg cat tac ctg ccc atc ctg ttc Lys Met Ile Gln Leu Gly Lys Thr Val His Tyr Leu Pro Ile Leu Phe 172 177 182 187				639
atc gac cag ctc agc aac cgc gtg aag gac ctg atg gtc ata aac cgc Ile Asp Gln Leu Ser Asn Arg Val Lys Asp Leu Met Val Ile Asn Arg 188 193 198 203				687
tcc acc acc gag ctg ccc ctc acc gtg tcc tac gac aag gtc tca ctg Ser Thr Thr Glu Leu Pro Leu Thr Val Ser Tyr Asp Lys Val Ser Leu 204 209 214 219				735
ggg cgg ctg cgc ttc tgg atc cac atg cag gac gcc gtg tac tcc ctg Gly Arg Leu Arg Phe Trp Ile His Met Gln Asp Ala Val Tyr Ser Leu 220 225 230 235				783
cag cag ttc ggg ttt tca gag aaa gat gct gat gag gtg aaa gga att Gln Gln Phe Gly Phe Ser Glu Lys Asp Ala Asp Glu Val Lys Gly Ile 236 241 246 251				831
ttt gta gat acc aac tta tac ttc ctg gcg ctg acc ttc ttt gtc gca Phe Val Asp Thr Asn Leu Tyr Phe Leu Ala Leu Thr Phe Phe Val Ala 252 257 262 267				879

gcg ttc cat ctt ctc ttt gat ttc ctg gcc ttt aaa aat gac atc agt Ala Phe His Leu Leu Phe Asp Phe Leu Ala Phe Lys Asn Asp Ile Ser 268 273 278 283	927
ttc tgg aag aag aag aag agc atg atc ggc atg tcc acc aag gca gtg Phe Trp Lys Lys Lys Ser Met Ile Gly Met Ser Thr Lys Ala Val 284 289 294 299	975
ctc tgg cgc tgc ttc agc acc gtg gtc atc ttt ctg ttc ctg ctg gac Leu Trp Arg Cys Phe Ser Thr Val Val Ile Phe Leu Phe Leu Leu Asp 300 305 310 315	1023
gag cag acg agc ctg ctg gtg ctg gtc ccg gcg ggt gtt gga gcc gac Glu Gln Thr Ser Leu Leu Val Leu Val Pro Ala Gly Val Gly Ala Ala 316 321 326 331	1071
att gag ctg tgg aaa gtg aag aag gca ttg aag atg act att ttt tgg Ile Glu Leu Trp Lys Val Lys Lys Ala Leu Lys Met Thr Ile Phe Trp 332 337 342 347	1119
aga ggc ctg atg ccc gaa ttt cag ttt ggc act tac agc gaa tct gag Arg Gly Leu Met Pro Glu Phe Gln Phe Gly Thr Tyr Ser Glu Ser Glu 348 353 358 363	1167
agg aaa acc gag gag tac act cag gcc atg aag tac ttg tca tac Arg Lys Thr Glu Glu Tyr Asp Thr Gln Ala Met Lys Tyr Leu Ser Tyr 364 369 374 379	1215
ctg ctg tac cct ctc tgt gtc ggg ggt gct gtc tat tca ctc ctg aat Leu Leu Tyr Pro Leu Cys Val Gly Gly Ala Val Tyr Ser Leu Leu Asn 380 385 390 395	1263
atc aaa tat aag agc tgg tac tcc tgg tta atc aac agc ttc gtc aac Ile Lys Tyr Lys Ser Trp Tyr Ser Trp Leu Ile Asn Ser Phe Val Asn 396 401 406 411	1311
ggg gtc tat gcc ttt ggt ttc ctc ttc atg ctg ccc cag ctc ttt gtg Gly Val Tyr Ala Phe Gly Phe Leu Phe Met Leu Pro Gln Leu Phe Val 412 417 422 427	1359
aac tac aag gta aga cgg tgt gtg ctg ccc gcg gcc cgg ccc ccg tct Asn Tyr Lys Val Arg Arg Cys Val Leu Pro Ala Ala Arg Pro Pro Ser 428 433 438 443	1407
cct gtg ctg ccc aca gct gac ctg ggc ctg tct ctc ctg ttt cag ttg Pro Val Leu Pro Thr Ala Asp Leu Gly Leu Ser Leu Leu Phe Gln Leu 444 449 454 459	1455
aag tca gtg gca cat ctg ccc tgg aag gcc ttc acc tac aag gct ttc Lys Ser Val Ala His Leu Pro Trp Lys Ala Phe Thr Tyr Lys Ala Phe 460 465 470 475	1503
aac acc ttc att gat gac gtc ttt gcc ttc atc atc acc atg ccc acg Asn Thr Phe Ile Asp Asp Val Phe Ala Phe Ile Ile Thr Met Pro Thr 476 481 486 491	1551

tct cac cgg ctg gcc tgc ttc cgg gac gac gtg gtg ttt ctg gtc tac		1599
Ser His Arg Leu Ala Cys Phe Arg Asp Asp Val Val Phe Leu Val Tyr		
492 497 502 507		
ctg tac cag cgg tgg ctt tat cct gtg gat aaa cgc aga gtg aac gag		1647
Leu Tyr Gln Arg Trp Leu Tyr Pro Val Asp Lys Arg Arg Val Asn Glu		
508 513 518 523		
ttt ggg gag tcc tac gag gag aag gcc acg cgg gcg ccc cac acg gac		1695
Phe Gly Ser Tyr Glu Glu Lys Ala Thr Arg Ala Pro His Thr Asp		
524 529 534 539		
tga agg cgcgggct gcccggcc aagtgcact tgaattgtca atgagtat		1752
*		
540		
ttggaaagcat ttggaggaat tccttagacat tgcgtttct gtgttgccaa aatccctcg		1812
gacatttctc agacatctcc caagttccca tcacgtcaga tttggagctg gtagcgctta		1872
cgatgcccccc acgtgtgaac atctgtcttg gtcacagagc tgggtgctgc cggtcacctt		1932
gagctgtggt ggctccggc acacgagtgt ccggggttcg gccatgtcct cacgcggca		1992
ggggtgggag ccctcacagg caagggggct gttggatttc catttcaggt ggttttctaa		2052
gtgctcctta tgtgaatttc aaacacgtat ggaattcatt ccgcattggac tctgggatca		2112
aaggctctt cctctttgt ttgagagttg gttgtttaa agcttaatgt atgtttctat		2172
tttaaaataa attttctgg ctgtggcaaa aaaaaaaaaaaa aaaaaggcgcc gcccgtctag		2232
agtatccctc gagggggccca agttacgctg taccctgctt tcttgtacaa agtggccct		2292
atagtgagtc gtatataagc taggcagttt catccagcag tcaaccctca tccttgg		2349

<210> 110
 <211> 6674
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1312)..(6330)

<220>
 <221> misc_feature
 <222> (1)..(6674)
 <223> n = a,t,c or g

<400> 110

ccactttgtcaagaaagctgggtacgcgt aagcttgggc ccctcgaggg atactctaga	60
gcggccgccc ttctttttt ttttcccaa aggtcctgtg cctataacaa ttccaggtgg	120

gccaggagga	cctgcttcac	cctttctcc	ctgcgggccc	tggcggccta	tgagtccctgg	180										
gtacccgggt	tcaccaggaa	aaccgggact	cccttttcc	ccttgcac	cattttcc	240										
gggtttgcct	ctgggtcctg	gtttccggg	ttcaccttc	tctccgaccc	ctggcatccc	300										
ctgaaatcca	ggttcacctt	tttggccctt	ttctcccttg	gtggcgaagt	ctccttttc	360										
ttgaacttga	gcttgcctg	gtactcctgg	aggcccactg	acccttggt	cacccttgc	420										
accttttgtt	ccttggaaaac	ttaagccat	ttgtccctt	tcacctggag	ggccnggagg	480										
gcctggggga	ccntgtggtc	cggtaaatcc	tggaggccc	acaggaccc	gaagccctgg	540										
cagtcctggt	gggcctggag	tccctggat	tccggaaat	cctcttcac	cttcaacag	600										
catcccgggc	acatggccaa	gtatctcacc	tggatcaccc	ttaccatcat	caggcttcac	660										
catctcacct	tggaagcggtt	caatcttttg	gtcaatattt	ctgcaccaca	gatccaggt	720										
gcacgctctg	tgggatccct	gcccgttgg	ggcctgacct	acagaccctt	tgctgaagga	780										
cccttgctg	aaggotcctg	gcctgtggcc	atcacccggac	agacccttgc	ctgaaggctc	840										
ctggcctgtg	gccaccactg	tcatacagcg	ctgttcccttg	ggctggaggg	agagcttttg	900										
ccacccatc	tcccatccgc	caagacgctc	tggcgagga	accacccgg	cactgtcccc	960										
agcagcagcc	accgcgttag	ggcaggccg	gccaccgcgc	gctggctct	ccccatgctg	1020										
gcggttcg	cactctggc	cccggtcagt	cccacttagc	ctcgggctcg	gcttcagggg	1080										
ctgctgccc	aacgcattgg	cccttccaga	agcacccg	ggcggcacac	cgccaggccg	1140										
gccggcctt	ctgggctctc	tggcgccgg	ccccggggc	tcgggccc	ccttcgg	1200										
ctcggccccc	gacggtg	agcgctggaa	gtccggcctt	ccgagagcta	gctgtccg	1260										
gcggcccccc	cacgcgggc	agccgtccct	cgccgcctcg	ggcgccacac	c atg ggg Met Gly 1	1317										
ccc	cg	ctc	agc	gtc	tgg	ctg	ctg	ctg	ccc	gcc	gcc	ctt	ctg	ctc	1365	
Pro	Arg	Leu	Ser	Val	Trp	Leu	Leu	Leu	Leu	Pro	Ala	Ala	Leu	Leu	Leu	
3															18	
cac	gag	gag	cac	agc	cg	g	cc	g	cc	t	ct	g	t	c	1413	
His	Glu	Glu	His	Ser	Arg	Ala	Ala	Ala	Lys	Gly	Gly	Cys	Ala	Gly	Ser	
19															34	
ggc	tgt	ggc	aaa	tgt	gac	tgc	cat	gga	gtg	aag	gga	caa	aag	ggt	gaa	1461
Gly	Cys	Gly	Lys	Cys	Asp	Cys	His	Gly	Val	Lys	Gly	Gln	Lys	Gly	Glu	
35															50	
aga	ggc	ctc	ccg	ggg	tta	caa	ggt	gtc	att	ggg	ttt	cct	gga	atg	caa	1509
Arg	Gly	Leu	Pro	Gly	Leu	Gln	Gly	Val	Ile	Gly	Phe	Pro	Gly	Met	Gln	

51	56	61	66	
gga cct gag ggg cca cag gga cca cca gga caa aag ggt gat act gga Gly Pro Glu Gly Pro Gln Gly Pro Pro Gly Gln Lys Gly Asp Thr Gly				1557
67	72	77	82	
gaa cca gga cta cct gga aca aaa ggg aca aga gga cct ccg gga gca Glu Pro Gly Leu Pro Gly Thr Lys Gly Thr Arg Gly Pro Pro Gly Ala				1605
83	88	93	98	
tct ggc tac cct gga aac cca gga ctt ccc gga att cct ggc caa gac Ser Gly Tyr Pro Gly Asn Pro Gly Leu Pro Gly Ile Pro Gly Gln Asp				1653
99	104	109	114	
ggc ccg cca ggc ccc cca ggt att cca gga tgc aat ggc aca aag ggg Gly Pro Pro Gly Pro Pro Gly Ile Pro Gly Cys Asn Gly Thr Lys Gly				1701
115	120	125	130	
gag aga ggg ccg ctc ggg cct cct ggc ttg cct ggt ttc gca gga aat Glu Arg Gly Pro Leu Gly Pro Pro Gly Leu Pro Gly Phe Ala Gly Asn				1749
131	136	141	146	
ccc gga cca cca ggc tta cca ggg atg aag ggt gat cca ggt gag ata Pro Gly Pro Pro Gly Leu Pro Gly Met Lys Gly Asp Pro Gly Glu Ile				1797
147	152	157	162	
ctt ggc cat gtg ccc ggg atg ctg ttg aaa ggt gaa aga gga ttt ccc Leu Gly His Val Pro Gly Met Leu Leu Lys Gly Glu Arg Gly Phe Pro				1845
163	168	173	178	
gga atc cca ggg act cca ggc cca cca gga ctg cca ggg ctt caa ggt Gly Ile Pro Gly Thr Pro Gly Pro Pro Gly Leu Pro Gly Leu Gln Gly				1893
179	184	189	194	
cct gtt ggg cct cca gga ttt acc gga cca cca ggt ccc cca ggc cct Pro Val Gly Pro Pro Gly Phe Thr Gly Pro Pro Gly Pro Pro Gly Pro				1941
195	200	205	210	
ccc ggc cct cca ggt gaa aag gga caa atg ggc tta agt ttt caa gga Pro Gly Pro Pro Gly Glu Lys Gly Gln Met Gly Leu Ser Phe Gln Gly				1989
211	216	221	226	
cca aaa ggt gac aag ggt gac caa ggg gtc agt ggg cct cca gga gta Pro Lys Gly Asp Lys Gly Asp Gln Gly Val Ser Gly Pro Pro Gly Val				2037
227	232	237	242	
cca gga caa gct caa gtt caa gaa aaa gga gac ttc gcc acc aag gga Pro Gly Gln Ala Gln Val Gln Glu Lys Gly Asp Phe Ala Thr Lys Gly				2085
243	248	253	258	
gaa aag ggc caa aaa ggt gaa cct gga ttt cag ggg atg cca ggg gtc Glu Lys Gly Gln Lys Gly Glu Pro Gly Phe Gln Gly Met Pro Gly Val				2133
259	264	269	274	
gga gag aaa ggt gaa ccc gga aaa cca gga ccc aga ggc aaa ccc gga Gly Glu Lys Gly Glu Pro Gly Lys Pro Gly Pro Arg Gly Lys Pro Gly				2181
275	280	285	290	

aaa gat ggt gac aaa ggg gaa aaa ggg agt ccc ggt ttt cct ggt gaa Lys Asp Gly Asp Lys Gly Glu Lys Gly Ser Pro Gly Phe Pro Gly Glu 291 296 301 306	2229
ccc ggg tac cca gga ctc ata ggc cgc cag ggc ccg cag gga gaa aag Pro Gly Tyr Pro Gly Leu Ile Gly Arg Gln Gly Pro Gln Gly Glu Lys 307 312 317 322	2277
ggt gaa gca ggt cct cct ggc cca cct gga att gtt ata ggc aca gga Gly Glu Ala Gly Pro Pro Gly Pro Pro Gly Ile Val Ile Gly Thr Gly 323 328 333 338	2325
cct ttg gga gaa aaa gga gag agg ggc tac cct gga act ccg ggg cca Pro Leu Gly Glu Lys Gly Glu Arg Gly Tyr Pro Gly Thr Pro Gly Pro 339 344 349 354	2373
aga gga gag cca ggc cca aaa ggt ttc cca gga cta cca ggc caa ccc Arg Gly Glu Pro Gly Pro Lys Gly Phe Pro Gly Leu Pro Gly Gln Pro 355 360 365 370	2421
gga cct cca ggc ctc cct gta cct ggg cag gct ggt gcc cct ggc ttc Gly Pro Pro Gly Leu Pro Val Pro Gly Gln Ala Gly Ala Pro Gly Phe 371 376 381 386	2469
cct ggt gaa aga gga gaa aaa ggt gac cga gga ttt cct ggt aca tct Pro Gly Glu Arg Gly Glu Lys Gly Asp Arg Gly Phe Pro Gly Thr Ser 387 392 397 402	2517
ctg cca gga cca agt gga aga gat ggg ctc ccg ggt cct cct ggt tcc Leu Pro Gly Pro Ser Gly Arg Asp Gly Leu Pro Gly Pro Pro Gly Ser 403 408 413 418	2565
cct ggg ccc cct ggg cag cct ggc tac aca aat gga att gtg gaa tgt Pro Gly Pro Pro Gly Gln Pro Gly Tyr Thr Asn Gly Ile Val Glu Cys 419 424 429 434	2613
cag ccc gga cct cca ggt gac cag ggt cct cct gga att aca ggg cag Gln Pro Gly Pro Pro Gly Asp Gln Gly Pro Pro Gly Ile Thr Gly Gln 435 440 445 450	2661
cca gga ttt ata ggc gaa att gga gag aaa gga caa aaa gga gag agt Pro Gly Phe Ile Gly Glu Ile Gly Glu Lys Gly Gln Lys Gly Glu Ser 451 456 461 466	2709
tgc ctc atc tgt gat ata gac gga tat cgg ggg cct ccc ggg cca cag Cys Leu Ile Cys Asp Ile Asp Gly Tyr Arg Gly Pro Pro Gly Pro Gln 467 472 477 482	2757
gga ccc ccg gga gaa ata ggt ttc cca ggg cag cca ggg gcc aag ggc Gly Pro Pro Gly Glu Ile Gly Phe Pro Gly Gln Pro Gly Ala Lys Gly 483 488 493 498	2805
gac aga ggt ttg cct ggc aga gat ggt gtt gca gga gtg cca ggc cgt Asp Arg Gly Leu Pro Gly Arg Asp Gly Val Ala Gly Val Pro Gly Arg 499 504 509 514	2853

caa ggt aca cca ggg ctg ata ggc cag cca gga gcc aag ggg gag cct		2901
Gln Gly Thr Pro Gly Leu Ile Gly Gln Pro Gly Ala Lys Gly Glu Pro		
515 520 525 530		
ggt gag ttt tat ttc gac ttg cgg ctc aaa ggt gac aaa gga gac cca		2949
Gly Glu Phe Tyr Phe Asp Leu Arg Leu Lys Gly Asp Lys Gly Asp Pro		
531 536 541 546		
ggc ttt cca gga cag ccc ggc atg cca ggg aga gcg ggt tct cct gga		2997
Gly Phe Pro Gly Gln Pro Gly Met Pro Gly Arg Ala Gly Ser Pro Gly		
547 552 557 562		
aga gat ggc cat ccg ggt ctt cct ggc ccc aag ggc tcg ccg ggt tct		3045
Arg Asp Gly His Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro Gly Ser		
563 568 573 578		
gta gga ttg aaa gga gag cgt ggc ccc cct gga gga gtt gga ttc cca		3093
Val Gly Leu Lys Gly Glu Arg Gly Pro Pro Gly Gly Val Gly Phe Pro		
579 584 589 594		
ggc agt cgt ggt gac acc ggc ccc cct ggg cct cca gga tat ggt cct		3141
Gly Ser Arg Gly Asp Thr Gly Pro Pro Gly Pro Pro Gly Tyr Gly Pro		
595 600 605 610		
gct ggt ccc att ggt gac aaa gga caa gca ggc ttt cct gga ggc cct		3189
Ala Gly Pro Ile Gly Asp Lys Gly Gln Ala Gly Phe Pro Gly Gly Pro		
611 616 621 626		
gga tcc cca ggc ctg cca ggt cca aag ggc tcg ccg ggt tct gta gga		3237
Gly Ser Pro Gly Leu Pro Gly Pro Lys Gly Ser Pro Gly Ser Val Gly		
627 632 637 642		
aaa att gtt cct tta cca ggc ccc cct gga gca gaa gga ctg ccg ggg		3285
Lys Ile Val Pro Leu Pro Gly Pro Pro Gly Ala Glu Gly Leu Pro Gly		
643 648 653 658		
tcc cca ggc ttc cca ggt ccc caa gga gac cga ggc ttt ccc gga acc		3333
Ser Pro Gly Phe Pro Gly Pro Gln Gly Asp Arg Gly Phe Pro Gly Thr		
659 664 669 674		
gca gga ggg cca ggc ctg cca gga gag aag ggc gct gtg ggc cag cca		3381
Ala Gly Gly Pro Gly Leu Pro Gly Glu Lys Gly Ala Val Gly Gln Pro		
675 680 685 690		
ggc att gga ttt cca ggg ccc ccc ggc ccc aaa ggt gtt gac ggc tta		3429
Gly Ile Gly Phe Pro Gly Pro Pro Gly Pro Lys Gly Val Asp Gly Leu		
691 696 701 706		
cct gga gac atg ggg cca ccg ggg act cca ggt cgc ccg gga ttt aat		3477
Pro Gly Asp Met Gly Pro Pro Gly Thr Pro Gly Arg Pro Gly Phe Asn		
707 712 717 722		
ggc tta cct ggg aac cca ggt gtg cag ggc cag aag gga gag cct gga		3525
Gly Leu Pro Gly Asn Pro Gly Val Gln Gly Gln Lys Gly Glu Pro Gly		
723 728 733 738		
gtt ggt cta ccg gga ctc aaa ggt ttg cca ggt ctt ccc ggc att cct		3573

Val	Gly	Leu	Pro	Gly	Leu	Lys	Gly	Leu	Pro	Gly	Leu	Pro	Gly	Ile	Pro
739				744				749				754			
ggc	aca	ccc	ggg	gag	aag	ggg	agc	att	ggg	gta	cca	ggc	gtt	cct	gga
Gly	Thr	Pro	Gly	Glu	Lys	Gly	Ser	Ile	Gly	Val	Pro	Gly	Val	Pro	Gly
755				760					765				770		
gaa	cat	gga	gca	atc	gga	ccc	cct	ggg	ctt	cag	ggg	atc	aga	ggt	gaa
Glu	His	Gly	Ala	Ile	Gly	Pro	Pro	Gly	Leu	Gln	Gly	Ile	Arg	Gly	Glu
771				776					781				786		
ccg	gga	cct	cct	gga	ttg	cca	ggc	tcc	gtg	ggg	tct	cca	gga	gtt	cca
Pro	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Ser	Val	Gly	Ser	Pro	Gly	Val	Pro
787				792					797				802		
gga	ata	ggc	ccc	cct	gga	gct	agg	ggt	ccc	cct	gga	gga	cag	gga	cca
Gly	Ile	Gly	Pro	Pro	Gly	Ala	Arg	Gly	Pro	Pro	Gly	Gly	Gln	Gly	Pro
803				808					813				818		
ccg	ggg	ttg	tca	ggc	cct	cct	gga	ata	aaa	gga	gag	aag	ggt	ttc	ccc
Pro	Gly	Leu	Ser	Gly	Pro	Pro	Gly	Ile	Lys	Gly	Glü	Lys	Gly	Phe	Pro
819				824					829				834		
gga	ttc	cct	gga	ctg	gac	atg	ccg	ggc	cct	aaa	gga	gat	aaa	ggg	gct
Gly	Phe	Pro	Gly	Leu	Asp	Met	Pro	Gly	Pro	Lys	Gly	Asp	Lys	Gly	Ala
835				840					845				850		
caa	gga	ctc	cct	ggc	ata	acg	gga	cag	tgc	ggg	ctc	cct	ggc	ctt	cct
Gln	Gly	Leu	Pro	Gly	Ile	Thr	Gly	Gln	Ser	Gly	Leu	Pro	Gly	Leu	Pro
851				856					861				866		
gga	cag	cag	ggg	gct	cct	ggg	att	cct	ggg	ttt	cca	ggt	tcc	aag	gga
Gly	Gln	Gly	Ala	Pro	Gly	Ile	Pro	Gly	Phe	Pro	Gly	Ser	Lys	Gly	
867				872					877				882		
gaa	atg	ggc	gtc	atg	ggg	acc	ccc	ggg	cag	ccg	ggc	tca	cca	gga	cca
Glu	Met	Gly	Val	Met	Gly	Thr	Pro	Gly	Gln	Pro	Gly	Ser	Pro	Gly	Pro
883				888					893				898		
gtg	ggt	gct	cct	gga	tta	ccg	ggg	gat	aaa	ggg	gac	cat	ggc	ttt	ccg
Val	Gly	Ala	Pro	Gly	Leu	Pro	Gly	Glu	Lys	Gly	Asp	His	Gly	Phe	Pro
899				904					909				914		
ggc	tcc	tca	gga	ccc	agg	gga	gac	cct	ggc	ttg	aaa	ggt	gat	aag	ggg
Gly	Ser	Ser	Gly	Pro	Arg	Gly	Asp	Pro	Gly	Leu	Lys	Gly	Asp	Lys	Gly
915				920					925				930		
gat	gtc	ggt	ctc	cct	ggc	aag	cct	ggc	tcc	atg	gat	aag	gtg	gac	atg
Asp	Val	Gly	Leu	Pro	Gly	Lys	Pro	Gly	Ser	Met	Asp	Lys	Val	Asp	Met
931				936					941				946		
ggc	agc	atg	aag	ggc	cag	aaa	gga	gac	caa	gga	gag	aaa	gga	caa	att
Gly	Ser	Met	Lys	Gly	Gln	Lys	Gly	Asp	Gln	Gly	Glu	Lys	Gly	Gln	Ile
947				952					957				962		
gga	cca	att	ggt	gag	aag	gga	tcc	cga	gga	gac	cct	ggg	acc	cca	gga
Gly	Pro	Ile	Gly	Glu	Lys	Gly	Ser	Arg	Gly	Asp	Pro	Gly	Thr	Pro	Gly

963	968	973	978	
gtg cct gga aag gac ggg cag gca gga cag cct ggg cag cca gga cct Val Pro Gly Lys Asp Gly Gln Ala Gly Gln Pro Gly Gln Pro Gly Pro	979	984	989	4293
994				
aaa ggt gat cca ggt ata agt gga acc cca ggt gct cca gga ctt ccg Lys Gly Asp Pro Gly Ile Ser Gly Thr Pro Gly Ala Pro Gly Leu Pro	995	1000	1005	4341
1010				
gga cca aaa gga tct gtt ggt gga atg ggc ttg cca gga aca cct gga Gly Pro Lys Gly Ser Val Gly Gly Met Gly Leu Pro Gly Thr Pro Gly	1011	1016	1021	4389
1026				
gag aaa ggt gtg cct ggc atc cct ggc cca caa ggt tca cct ggc tta Glu Lys Gly Val Pro Gly Ile Pro Gly Pro Gln Gly Ser Pro Gly Leu	1027	1032	1037	4437
1042				
cct gga gac aaa ggt gca aaa gga gag aaa ggg cag gca ggc cca cct Pro Gly Asp Lys Gly Ala Lys Gly Glu Lys Gly Gln Ala Gly Pro Pro	1043	1048	1053	4485
1058				
ggc ata ggc atc cca gga ctg cgt ggt gaa aag gga gat caa ggg ata Gly Ile Gly Ile Pro Gly Leu Arg Gly Glu Lys Gly Asp Gln Gly Ile	1059	1064	1069	4533
1074				
gcg ggt ttc cca gga agc cct gga gag aag gga gaa aaa gga agc att Ala Gly Phe Pro Gly Ser Pro Gly Glu Lys Gly Glu Lys Gly Ser Ile	1075	1080	1085	4581
1090				
ggg atc cca gga atg cca ggg tcc cca ggc ctt aaa ggg tct ccc ggg Gly Ile Pro Gly Met Pro Gly Ser Pro Gly Leu Lys Gly Ser Pro Gly	1091	1096	1101	4629
1106				
agt gtt ggc tat cca gga agt cct ggg cta cct gga gaa aaa ggt gac Ser Val Gly Tyr Pro Gly Ser Pro Gly Leu Pro Gly Glu Lys Gly Asp	1107	1112	1117	4677
1122				
aaa ggc ctc cca gga ttg gat ggc atc cct ggt gtc aaa gga gaa gca Lys Gly Leu Pro Gly Leu Asp Gly Ile Pro Gly Val Lys Gly Glu Ala	1123	1128	1133	4725
1138				
ggc ctt cct ggg act cct ggc ccc aca ggc cca gct ggc cag aaa ggg Gly Leu Pro Gly Thr Pro Gly Pro Thr Gly Pro Ala Gly Gln Lys Gly	1139	1144	1149	4773
1154				
gag cca ggc agt gat gga atc ccg ggg tca gca gga gag aag ggt gaa Glu Pro Gly Ser Asp Gly Ile Pro Gly Ser Ala Gly Glu Lys Gly Glu	1155	1160	1165	4821
1170				
cca ggt cta cca gga aga gga ttc cca ggg ttt cca ggg gcc aaa gga Pro Gly Leu Pro Gly Arg Gly Phe Pro Gly Phe Pro Gly Ala Lys Gly	1171	1176	1181	4869
1186				
gac aaa ggt tca aag ggt gag gtg ggt ttc cca gga tta gcc ggg agc Asp Lys Gly Ser Lys Gly Glu Val Gly Phe Pro Gly Leu Ala Gly Ser	1187	1192	1197	4917
1202				

cca	gga	att	cct	gga	tcc	aaa	gga	gag	caa	gga	ttc	atg	ggt	cct	ccg	4965
Pro	Gly	Ile	Pro	Gly	Ser	Lys	Gly	Glu	Gln	Gly	Phe	Met	Gly	Pro	Pro	
1203			1208						1213					1218		
ggg	ccc	cag	gga	cag	ccg	ggg	tta	ccg	gga	tcc	cca	ggc	cat	gcc	acg	5013
Gly	Pro	Gln	Gly	Gln	Pro	Gly	Leu	Pro	Gly	Ser	Pro	Gly	His	Ala	Thr	
1219			1224						1229					1234		
gag	ggg	ccc	aaa	gga	gac	cgc	gga	cct	cag	ggc	cag	cct	ggc	ctg	cca	5061
Glu	Gly	Pro	Lys	Gly	Asp	Arg	Gly	Pro	Gln	Gly	Gln	Pro	Gly	Leu	Pro	
1235			1240						1245					1250		
gga	ctt	ccg	gga	ccc	atg	ggg	cct	cca	ggg	ctt	cct	ggg	att	gat	gga	5109
Gly	Leu	Pro	Gly	Pro	Met	Gly	Pro	Pro	Gly	Leu	Pro	Gly	Ile	Asp	Gly	
1251			1256						1261					1266		
gtt	aaa	ggt	gac	aaa	gga	aat	cca	ggc	tgg	cca	gga	gca	ccc	ggt	gtc	5157
Val	Lys	Gly	Asp	Lys	Gly	Asn	Pro	Gly	Trp	Pro	Gly	Ala	Pro	Gly	Val	
1267			1272						1277					1282		
cca	ggg	ccc	aag	gga	gac	cct	gga	ttc	cag	ggc	atg	cct	ggt	att	ggt	5205
Pro	Gly	Pro	Lys	Gly	Asp	Pro	Gly	Phe	Gln	Gly	Met	Pro	Gly	Ile	Gly	
1283			1288						1293					1298		
ggc	tct	cca	gga	atc	aca	ggc	tct	aag	ggt	gat	atg	ggg	cct	cca	gga	5253
Gly	Ser	Pro	Gly	Ile	Thr	Gly	Ser	Lys	Gly	Asp	Met	Gly	Pro	Pro	Gly	
1299			1304						1309					1314		
gtt	cca	gga	ttt	caa	ggt	cca	aaa	ggt	cct	cct	ggc	ctc	cag	gga	att	5301
Val	Pro	Gly	Phe	Gln	Gly	Pro	Lys	Gly	Leu	Pro	Gly	Leu	Gln	Gly	Ile	
1315			1320						1325					1330		
aaa	ggt	gat	caa	ggc	gat	caa	ggc	gtc	ccg	gga	gct	aaa	ggt	ctc	ccg	5349
Lys	Gly	Asp	Gln	Gly	Asp	Gln	Gly	Val	Pro	Gly	Ala	Lys	Gly	Leu	Pro	
1331			1336						1341					1346		
ggc	cct	ccc	ccc	cca	ggt	cct	tac	gac	atc	atc	aaa	ggg	gag	ccc	5397	
Gly	Pro	Pro	Gly	Pro	Pro	Gly	Pro	Tyr	Asp	Ile	Ile	Lys	Gly	Glu	Pro	
1347			1352						1357					1362		
ggg	ctc	cct	ggt	cct	gag	ggc	ccc	cca	ggg	ctg	aaa	ggg	ctt	cag	gga	5445
Gly	Leu	Pro	Gly	Pro	Glu	Gly	Pro	Pro	Gly	Leu	Lys	Gly	Leu	Gln	Gly	
1363			1368						1373					1378		
ctg	cca	ggc	ccg	aaa	ggc	cag	caa	ggt	gtt	aca	gga	ttg	gtg	ggt	ata	5493
Leu	Pro	Gly	Pro	Lys	Gly	Gln	Gln	Gly	Val	Thr	Gly	Leu	Val	Gly	Ile	
1379			1384						1389					1394		
cct	gga	cct	cca	ggt	att	cct	ggg	ttt	gac	ggt	gcc	cct	ggc	cag	aaa	5541
Pro	Gly	Pro	Pro	Gly	Ile	Pro	Gly	Phe	Asp	Gly	Ala	Pro	Gly	Gln	Lys	
1395			1400						1405					1410		
gga	gag	atg	gga	cct	gcc	ggg	cct	act	ggt	cca	aga	gga	ttt	cca	ggt	5589
Gly	Glu	Met	Gly	Pro	Ala	Gly	Pro	Thr	Gly	Pro	Arg	Gly	Phe	Pro	Gly	
1411			1416						1421					1426		

cca cca ggc ccc gat ggg ttg cca gga tcc atg ggg ccc cca ggc acc Pro Pro Gly Pro Asp Gly Leu Pro Gly Ser Met Gly Pro Pro Gly Thr 1427 1432 1437 1442	5637
cca tct gtt gat cac ggc ttc ctt gtg acc agg cat agt caa aca ata Pro Ser Val Asp His Gly Phe Leu Val Thr Arg His Ser Gln Thr Ile 1443 1448 1453 1458	5685
gat gac cca cag tgt cct tct ggg acc aaa att ctt tac cac ggg tac Asp Asp Pro Gln Cys Pro Ser Gly Thr Lys Ile Leu Tyr His Gly Tyr 1459 1464 1469 1474	5733
tct ttg ctc tac gtg caa ggc aat gaa cgg gcc cat ggc cag gac ttg Ser Leu Leu Tyr Val Gln Gly Asn Glu Arg Ala His Gly Gln Asp Leu 1475 1480 1485 1490	5781
ggc acg gcc ggc agc tgc ctg cgc aag ttc agc aca atg ccc ttc ctg Gly Thr Ala Gly Ser Cys Leu Arg Lys Phe Ser Thr Met Pro Phe Leu 1491 1496 1501 1506	5829
ttc tgc aat att aac aac gtg tgc aac ttt gca tca cga aat gac tac Phe Cys Asn Ile Asn Asn Val Cys Asn Phe Ala Ser Arg Asn Asp Tyr 1507 1512 1517 1522	5877
tcg tac tgg ctg tcc acc cct gag ccc atg ccc atg tca atg gca ccc Ser Tyr Trp Leu Ser Thr Pro Glu Pro Met Pro Met Ser Met Ala Pro 1523 1528 1533 1538	5925
atc acg ggg gaa aac ata aga cca ttt att agt agg tgt gct gtg tgt Ile Thr Gly Glu Asn Ile Arg Pro Phe Ile Ser Arg Cys Ala Val Cys 1539 1544 1549 1554	5973
gag gcg cct gcc atg gtg atg gcc gtg cac agc cag acc att cag atc Glu Ala Pro Ala Met Val Met Ala Val His Ser Gln Thr Ile Gln Ile 1555 1560 1565 1570	6021
cca ccg tgc ccc agc ggg tgg tcc tcg ctg tgg atc ggc tac tct ttt Pro Pro Cys Pro Ser Gly Trp Ser Ser Leu Trp Ile Gly Tyr Ser Phe 1571 1576 1581 1586	6069
gtg atg cac acc agc gct ggt gca gaa ggc tct ggc caa gcc ctg gcg Val Met His Thr Ser Ala Gly Ala Glu Gly Ser Gly Gln Ala Leu Ala 1587 1592 1597 1602	6117
tcc ccc ggc tcc tgc ctg gag gag ttt aga agt gcg cca ttc atc gag Ser Pro Gly Ser Cys Leu Glu Glu Phe Arg Ser Ala Pro Phe Ile Glu 1603 1608 1613 1618	6165
tgt cac ggc cgt ggg acc tgc aat tac tac gca aac gct tac agc ttt Cys His Gly Arg Gly Thr Cys Asn Tyr Tyr Ala Asn Ala Tyr Ser Phe 1619 1624 1629 1634	6213
tgg ctc gcc acc ata gag agg agc gag atg ttc aag aag cct acg ccg Trp Leu Ala Thr Ile Glu Arg Ser Glu Met Phe Lys Lys Pro Thr Pro 1635 1640 1645 1650	6261
tcc acc ttg aag gca ggg gag ctg cgc acg cac gtc agc cgc tgc caa	6309

Ser	Thr	Leu	Lys	Ala	Gly	Glu	Leu	Arg	Thr	His	Val	Ser	Arg	Cys	Gln
1651				1656					1661			1666			
gtc tgt atg aga aga aca taa tg aaggctgact cagctaattgt cacaacatgg															6362
Val	Cys	Met	Arg	Arg	Thr	*									
1667				1672											
tgctacttct tctttttttt gttaacagca acgaacccta gaaaatatatac ctgtgtaccc															6422
cactgtccaa tatgaaaacc gtaaaagtgcc ttataggaat ttgcgttaact aacacaccct															6482
gccttcattga cctctacttg ctgaaggaga aaaagacagc gataagctt caatagtggc															6542
ataccaaatg gcactttga taaaataaaa tatcaatatt ttctgcaaaa aaaaaaaaaa															6602
aaggcgcc gctctagagt atccctcgag gggcccaagc ttacgcgtac ccagcttct															6662
tgtacaaagt gg															6674
<210> 111															
<211> 1421															
<212> DNA															
<213> Homo sapiens															
<220>															
<221> CDS															
<222> (217)..(1230)															
<400> 111															
ataaaattaga acgcctgtgg taccgctccg gaattcccg gtcgaccac gcgtccggag															60
ggagtgggaga acgcataagc aagctggttt gaccagaaac agaactgcct gtgacagatt															120
aagagacaag caaggcttgg aatctgagag caagcaaaga gagtgaaaat ttacagctgc															180
cctatcattc catattggaa gaagagattt ctacac atg aaa aaa atg cct ttg															234
Met Lys Lys Met Pro Leu															
1															
ttt agt aaa tca cac aaa aat cca gca gaa att gtg aaa atc ctg aaa															282
Phe	Ser	Lys	Ser	His	Lys	Asn	Pro	Ala	Glu	Ile	Val	Lys	Ile	Leu	Lys
7				12					17			22			
gac aat ttg gcc att ttg gaa aag caa gac aaa aag aca gac aag gct															330
Asp	Asn	Leu	Ala	Ile	Leu	Glu	Lys	Gln	Asp	Lys	Thr	Asp	Lys	Ala	
23				28					33			38			
tca gaa gaa gtg tct aaa tca ctg caa gca atg aaa gaa att ctg tgt															378
Ser	Glu	Glu	Val	Ser	Lys	Ser	Leu	Gln	Ala	Met	Lys	Glu	Ile	Leu	Cys
39				44					49			54			
ggtaacaacgaaa gaa ccc cca aca gaa gca gtg gct cag cta gca															426
Gly	Thr	Asn	Glu	Lys	Glu	Pro	Pro	Thr	Glu	Ala	Val	Ala	Gln	Leu	Ala
55				60					65			70			

caa gaa ctc tac agc agt ggc ctg cta gtg aca ctg ata gct gac ctg			474
Gln Glu Leu Tyr Ser Ser Gly Leu Leu Val Thr Leu Ile Ala Asp Leu			
71	76	81	86
cag ctg ata gac ttt gag gga aaa aaa gat gtg acc cag ata ttt aac			522
Gin Leu Ile Asp Phe Glu Gly Lys Lys Asp Val Thr Gln Ile Phe Asn			
87	92	97	102
aac atc ttg aga aga cag ata ggc act cg ^g agt cct act gtg gag tat			570
Asn Ile Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro Thr Val Glu Tyr			
103	108	113	118
att agt gct cat cct cat atc ctg ttt atg ctc ctc ^g aaa gga tat gaa			618
Ile Ser Ala His Pro His Ile Leu Phe Met Leu Leu Lys Gly Tyr Glu			
119	124	129	134
gcc cca cag att gcc tta cgt tgt ggg att atg ctg aga gaa tgt att			666
Ala Pro Gln Ile Ala Leu Arg Cys Gly Ile Met Leu Arg Glu Cys Ile			
135	140	145	150
cga cat gaa cca ctt gcc aaa atc atc ctc ttt tct aat caa ttc aga			714
Arg His Glu Pro Leu Ala Lys Ile Ile Leu Phe Ser Asn Gln Phe Arg			
151	156	161	166
gat ttc ttt aag tac gtg gag ttg tca aca ttt gat att gct tca gat			762
Asp Phe Phe Lys Tyr Val Glu Leu Ser Thr Phe Asp Ile Ala Ser Asp			
167	172	177	182
gcc ttt gct act ttc aag gat tta cta acc aga cat aaa gtg ttg gta			810
Ala Phe Ala Thr Phe Lys Asp Leu Leu Thr Arg His Lys Val Leu Val			
183	188	193	198
gca gac ttc tta gaa caa aat tac gac act att ttt gaa gac tat gag			858
Ala Asp Phe Leu Glu Gln Asn Tyr Asp Thr Ile Phe Glu Asp Tyr Glu			
199	204	209	214
aaa ttg ctt cag tct gag aat tat gtt act aag aga cag tct tta aag			906
Lys Leu Leu Gln Ser Glu Asn Tyr Val Thr Lys Arg Gln Ser Leu Lys			
215	220	225	230
ctg cta ggg gag ctg atc ctg gac cgt cac aac ttt gcc atc atg aca			954
Leu Leu Gly Glu Leu Ile Leu Asp Arg His Asn Phe Ala Ile Met Thr			
231	236	241	246
aag tat atc agc aag ccg gag aac ctg aaa ctc atg atg aac ctc ctt			1002
Lys Tyr Ile Ser Lys Pro Glu Asn Leu Lys Leu Met Met Asn Leu Leu			
247	252	257	262
cgg gat aaa agt ccc aac atc cag ttt gaa gcc ttt cat gtt ttt aag			1050
Arg Asp Lys Ser Pro Asn Ile Gln Phe Glu Ala Phe His Val Phe Lys			
263	268	273	278
gtg ttt gtg gcc agt cct cac aaa aca cag cct att gtg gag atc ctg			1098
Val Phe Val Ala Ser Pro His Lys Thr Gln Pro Ile Val Glu Ile Leu			
279	284	289	294

tta aaa aat cag ccc aaa ctc att gag ttt ctg agc agc ttc caa aaa Leu Lys Asn Gln Pro Lys Leu Ile Glu Phe Leu Ser Ser Phe Gln Lys 295 300 305 310	1146
gaa agg acg gat gat gag cag ttc gct gac gag aag aac tac ttg att Glu Arg Thr Asp Asp Glu Gln Phe Ala Asp Glu Lys Asn Tyr Leu Ile 311 316 321 326	1194
aaa cag atc cga gac ttg aag aaa acg gcc cct tga agag ctccccggcc Lys Gln Ile Arg Asp Leu Lys Thr Ala Pro * 327 332 337	1244
cctgtcacag tcagtcgtct catttgccta gtttgcacag tgtgtcattt cagaaagtca tcattcttgg gaagactttg gaggtgccta tttttctgc tgtaattgtt ctgggttagat	1304
ggagtataaa catttgaatg gaaaaaaatt aacctagaat aatataaaaa aaaaaaaa	1364
	1421

<210> 112
<211> 2416
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (59) .. (952)

<400> 112

ccggaattcc cgggtcgacc cacgcgtccg cggacgcgtg ggctgggagc tgtggtgc atg tac atc agc ccc cca aaa gac tgg tgg tac gcc gga gac cct tct Met Tyr Ile Ser Pro Pro Lys Asp Trp Trp Tyr Ala Gly Asp Pro Ser 1 5 10 15	58
	106

ctc ccc atc agg acc cca gcc atg ata ggc tgc tcg ttc gtg gtc aac Leu Pro Ile Arg Thr Pro Ala Met Ile Gly Cys Ser Phe Val Val Asn 17 22 27 32	154
--	-----

agg aag ttc ttc ggt gaa att ggt ctt ctg gat cct ggc atg gat gta Arg Lys Phe Phe Gly Glu Ile Gly Leu Leu Asp Pro Gly Met Asp Val 33 38 43 48	202
--	-----

tac gga gga gaa aat att gaa ctg gga atc aag gta tgg ctc tgt ggg Tyr Gly Gly Glu Asn Ile Glu Leu Gly Ile Lys Val Trp Leu Cys Gly 49 54 59 64	250
--	-----

ggc agc atg gag gtc ctt cct tgc tca cgg gtg gcc cac att gag cgg Gly Ser Met Glu Val Leu Pro Cys Ser Arg Val Ala His Ile Glu Arg 65 70 75 80	298
--	-----

aag aag aag cca tat aat agc aac att ggc ttc tac acc aag agg aat Lys Lys Lys Pro Tyr Asn Ser Asn Ile Gly Phe Tyr Thr Lys Arg Asn 81 86 91 96	346
--	-----

gct ctt cgc gtt gct gag gtc tgg atg gac gat tac aag tct cat gtg	394
---	-----

Ala Leu Arg Val Ala Glu Val Trp Met Asp Asp Tyr Lys Ser His Val			
97	102	107	112
tac ata gcg tgg aac ctg ccg ctg gag aat ccg gga att gac atc ggt			442
Tyr Ile Ala Trp Asn Leu Pro Leu Glu Asn Pro Gly Ile Asp Ile Gly			
113	118	123	128
gat gtc tcc gaa aga aga gca tta agg aaa agt tta aag tgt aag aat			490
Asp Val Ser Glu Arg Arg Ala Leu Arg Lys Ser Leu Lys Cys Lys Asn			
129	134	139	144
ttc cag tgg tac ctg gac cat gtt tac cca gaa atg aga aga tac aat			538
Phe Gln Trp Tyr Leu Asp His Val Tyr Pro Glu Met Arg Arg Tyr Asn			
145	150	155	160
aat acc gtt gct tac ggg gag ctt cgc aac aac aag gca aaa gac gtc			586
Asn Thr Val Ala Tyr Gly Glu Leu Arg Asn Asn Lys Ala Lys Asp Val			
161	166	171	176
tgc ttg gac cag ggg ccg ctg gag aac cac aca gca ata ttg tat ccg			634
Cys Leu Asp Gln Gly Pro Leu Glu Asn His Thr Ala Ile Leu Tyr Pro			
177	182	187	192
tgc cat ggc tgg gga cca cag ctt gcc cgc tac acc aag gaa ggc ttc			682
Cys His Gly Trp Gly Pro Gln Leu Ala Arg Tyr Thr Lys Glu Gly Phe			
193	198	203	208
ctg cac ttg ggt gcc ctg ggg acc acc aca ctc ctc cct gac acc cgc			730
Leu His Leu Gly Ala Leu Gly Thr Thr Leu Leu Pro Asp Thr Arg			
209	214	219	224
tgc ctg gtg gac aac tcc aag agt cgg ctg ccc cag ctc ctg gac tgc			778
Cys Leu Val Asp Asn Ser Lys Ser Arg Leu Pro Gln Leu Leu Asp Cys			
225	230	235	240
gac aag gtc aag agc agc ctg tac aag cgc tgg aac ttc atc cag aat			826
Asp Lys Val Lys Ser Ser Leu Tyr Lys Arg Trp Asn Phe Ile Gln Asn			
241	246	251	256
gga gcc atc atg aac aag ggc acg gga cgc tgc ctg gag gtg gag aac			874
Gly Ala Ile Met Asn Lys Gly Thr Gly Arg Cys Leu Glu Val Glu Asn			
257	262	267	272
cgg ggc ctg gct ggc atc gac ctc atc ctc cgc agc tgc aca ggt cag			922
Arg Gly Leu Ala Gly Ile Asp Leu Ile Leu Arg Ser Cys Thr Gly Gln			
273	278	283	288
agg tgg acc att aag aac tcc atc aag tag a gggagggagc tggggcactg			973
Arg Trp Thr Ile Lys Asn Ser Ile Lys *			
289	294		
gagcctggcc cccaggacat ggctgctccc cccaaatctt ggaccagctg ccctggcgga			1033
gagacagcaa gggccggca ggtgctcgat gggccccca gggcttctcc agggcagcac			1093
agggaccccg gatgaagact ctgtcccccc tcaggcattc agctgcccac aagttcctg			1153

caccctggaa aagcccccca cccttcctct gggaaaactga cagctgtctt ccacagcctc	1213
tgatgtggac ctggtaactga ggagcaagac tgtccagttc tcctccacat ctccccatccc	1273
agaatcagga tctgggactg gcagggtccc ctccctgtgtc tcatctcttg cagcagcagc	1333
tgctgaactc cagccatcaa cacgggtggga ggcagcgggg gcttcagcca tgtcctagct	1393
ccccgccta aaaggaggca gtgaggacca ggcactattt cctccgaggt tacttctacc	1453
cagatgacac ctgcctgttc acgccccaaag qcagctactg cccctaaccctt tttccaccag	1513
ggtagcttg ggcaactgcag ctctggactt ttctggcccc tcctgagatg acctgatgga	1573
gctgatgctt tctctcctaa tccctgggca cttaggtctt atcagtgtgc ttgggccagc	1633
tctcctgcct gtgtctagag gaagccagag acagaaatag gctaaggctg cagtaggatc	1693
tcagccacaa gggccccgca ggatggagct gggtaagga ccagggagcc ctgactccca	1753
gaggctgcca ccggggagaa gcagcggtcc tccatccaga acctaagggc tgaagcaaag	1813
gctgccagga cccttgaaga tgctttggc tcacctcatt tcacccacg ctctgctggc	1873
tggcagagga gaaggcagtc gtttcctctc tgaagagtat tttttcgat tgccctctgg	1933
ttagggtgca catataaattc agagtttata tatgaacgcg tgtgcatttca caagtgtgt	1993
tgtgcctgcg tgctgtgcgt ggcagggtgt gtgtgtgtgt gtctggctgt gcgttccggaa	2053
gtgtgtgacg atgctgaccc agctgtgtgg ccttgggctt gctgcttcat tactcacctg	2113
gatggggacg agggatgaga aggggtgtggg tttggccca tgtcaactggc cggaaaggatg	2173
tgtctcagcc ctgccccctgtg gggtgccccca gatgggaggc tgtcccatctt cccagtc	2233
atctctttt ccccacactg tccctggcca agccctgccc agagctgaac cctgttagctg	2293
cccccttgcc ctgtgtggga ttgcagttgt ctcatgggt gacgtcttac tggtgatcat	2353
ctcctcacccttccatctccac cttgtgaaat aaatacatgt tagcacttcc caaaaaaaaaaa	2413
aaa	2416

```
<210> 113  
<211> 1007  
<212> DNA  
<213> Homo sapiens
```

<220>
<221> CDS
<222> (58) .. (786)

<400> 113

atggccct cgaggccaag aattcgac gagcaagttg aaaaccagct gctaaaa	57
atg aag gtg gaa tcg tcc caa gaa gcc aat gct gag gtg atg cga gag	105
Met Lys Val Glu Ser Ser Gln Glu Ala Asn Ala Glu Val Met Arg Glu	
1 5 10 15	
atg acc aag aag ctg tac agc cag tat gag gag aag ctg cag gaa gaa	153
Met Thr Lys Lys Leu Tyr Ser Gln Tyr Glu Glu Lys Leu Gln Glu Glu	
17 22 27 32	
cag agg aag cac agt gct gag aag gag gct ctt ttg gaa gaa acc aat	201
Gln Arg Lys His Ser Ala Glu Lys Glu Ala Leu Leu Glu Glu Thr Asn	
33 38 43 48	
agt ttt ctg aaa gcg att gaa gaa gcc aat aaa aag atg caa gca gca	249
Ser Phe Leu Lys Ala Ile Glu Glu Ala Asn Lys Lys Met Gln Ala Ala	
49 54 59 64	
gag atc agc cta gag gag aaa gac cag agg atc ggg gag ctg gac agg	297
Glu Ile Ser Leu Glu Glu Lys Asp Gln Arg Ile Gly Glu Leu Asp Arg	
65 70 75 80	
ctg att gag cgc atg gaa aag gaa cgt cat caa ctg caa ctt caa ctc	345
Leu Ile Glu Arg Met Glu Lys Glu Arg His Gln Leu Gln Leu Gln Leu	
81 86 91 96	
cta gaa cat gaa aca gaa atg tct ggg gag tta act gat tct gac aag	393
Leu Glu His Glu Thr Glu Met Ser Gly Glu Leu Thr Asp Ser Asp Lys	
97 102 107 112	
gaa agg tat cag cag ttg gag gag gca tca gcc agc ctc cgt gag cgg	441
Glu Arg Tyr Gln Gln Leu Glu Glu Ala Ser Ala Ser Leu Arg Glu Arg	
113 118 123 128	
atc aga cac cta gat gac atg gtg cat tgc cag cag aag aaa gtc aag	489
Ile Arg His Leu Asp Asp Met Val His Cys Gln Gln Lys Lys Val Lys	
129 134 139 144	
cag atg gtc gag gag att gaa tca tta aag aaa aag ttgcaa cag aaa	537
Gln Met Val Glu Glu Ile Glu Ser Leu Lys Lys Lys Leu Gln Gln Lys	
145 150 155 160	
cag ctc tta ata ctg cag ctt tta gaa aag ata tct ttc tta gaa gga	585
Gln Leu Leu Ile Leu Gln Leu Leu Glu Lys Ile Ser Phe Leu Glu Gly	
161 166 171 176	
gag aat aat gaa cta caa agc agg ttg gac tat tta aca gaa acc cag	633
Glu Asn Asn Glu Leu Gln Ser Arg Leu Asp Tyr Leu Thr Glu Thr Gln	
177 182 187 192	
gcc aag acc gaa gtg gaa acc aga gag ata gga gtg ggc tgt gat ctt	681
Ala Lys Thr Glu Val Glu Thr Arg Glu Ile Gly Val Gly Cys Asp Leu	
193 198 203 208	
ctc ccc agc caa aca ggc agg act cgt gaa att gtg atg cct tct agg	729
Leu Pro Ser Gln Thr Gly Arg Thr Arg Glu Ile Val Met Pro Ser Arg	
209 214 219 224	

aac tac acc cca tac aca aga gtc ctg gag tta acc atg aag aaa act	777
Asn Tyr Thr Pro Tyr Thr Arg Val Leu Glu Leu Thr Met Lys Lys Thr	
225 230 235 240	
ctg act tag gcactca gaggcataca cttttacag atggacaaaa gctctgaaac	833
Leu Thr *	
241	
cctgtggctt caaatccttt gggaaagggtg actgttgttt cccctacaca cagtgtaaac	893
cggaatggga atcgctgagg ctctgatcca cttctaagac aggaaggaaa gtgaaggcag	953
agtgagcagg taagagaggg atataacaagg tcacattca gacacccact cggg	1007

<210> 114
 <211> 3074
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (366)..(2213)

<400> 114

ccggaattcc cgggtcgacg atttcgtgga cacctggcaa gtcctgcctt gcctgtcccc	60
caaccttggt cggcccgccc ggcgcacggct ggcctcccta ggccacattc ttgcacaaag	120
ttcgagagggc tgtggaaaaa gcaaccctga accggccaag ggccggcgaa gctgatcccg	180
caatggcatt ttgtttgaa cagttgctgg ggttgacgtt tcctcataag aggggtactg	240
gacaccagcg cagagtgcag actgaatggg gaaaggagat gcagagaaaa tctggcaaca	300
tacctattct tcacatccta ctcgtgggg agggtgcta gtggccctct gcaccaaccc	360

aaaga atg tct tcc aag caa gcc acc tct cca ttt gcc tgt gca gct	407
Met Ser Ser Lys Gln Ala Thr Ser Pro Phe Ala Cys Ala Ala	
1 5 10	

gat gga gag gat gca atg acc cag gat tta acc tca agg gaa aag gaa	455
Asp Gly Glu Asp Ala Met Thr Gln Asp Leu Thr Ser Arg Glu Lys Glu	
15 20 25 30	

gag ggc agt gat caa cat gtg gcc tcc cat ctg cct ctg cac ccc ata	503
Glu Gly Ser Asp Gln His Val Ala Ser His Leu Pro Leu His Pro Ile	
31 36 41 46	

atg cac aac aaa cct cac tct gag gag cta cca aca ctt gtc agt acc	551
Met His Asn Lys Pro His Ser Glu Glu Leu Pro Thr Leu Val Ser Thr	
47 52 57 62	

att caa caa gat gct gac tgg gac agc gtt ctg tca tct cag caa aga	599
Ile Gln Gln Asp Ala Asp Trp Asp Ser Val Leu Ser Ser Gln Gln Arg	

63	68	73	78	
atg gaa tca gag aat aat aag tta tgt tcc cta tat tcc ttc cga aat Met Glu Ser Glu Asn Asn Lys Leu Cys Ser Leu Tyr Ser Phe Arg Asn				647
79	84	89	94	
acc tct acc tca cca cat aag cct gac gaa ggg agt cgg gac cgt gag Thr Ser Thr Ser Pro His Lys Pro Asp Glu Gly Ser Arg Asp Arg Glu				695
95	100	105	110	
ata atg acc agt gtt act ttt gga acc cca gag cgc cgc aaa ggg agt Ile Met Thr Ser Val Thr Phe Gly Thr Pro Glu Arg Arg Lys Gly Ser				743
111	116	121	126	
ctt gcc gat gtg gtg gac aca ctg aaa cag aag aag ctt gag gaa atg Leu Ala Asp Val Val Asp Thr Leu Lys Gln Lys Lys Leu Glu Glu Met				791
127	132	137	142	
act cg g act gaa caa gag gat tcc tcc tgc atg gaa aaa cta ctt tca Thr Arg Thr Glu Gln Glu Asp Ser Ser Cys Met Glu Lys Leu Leu Ser				839
143	148	153	158	
aaa gat tgg aag gaa aaa atg gaa aga cta aat acc agt gaa ctt ctt Lys Asp Trp Lys Glu Lys Met Glu Arg Leu Asn Thr Ser Glu Leu Leu				887
159	164	169	174	
gga gaa att aaa ggt aca cct gag agc ctg gca gaa aaa gaa cgg cag Gly Glu Ile Lys Gly Thr Pro Glu Ser Leu Ala Glu Lys Glu Arg Gln				935
175	180	185	190	
ctc tcc acc atg att acc cag ctg atc agt tta cgg gag cag cta ctg Leu Ser Thr Met Ile Thr Gln Leu Ile Ser Leu Arg Glu Gln Leu Leu				983
191	196	201	206	
gca gcg cat gat gaa cag aaa aaa ctg gca gc g tca caa att gag aaa Ala Ala His Asp Glu Gln Lys Lys Leu Ala Ala Ser Gln Ile Glu Lys				1031
207	212	217	222	
caa cg g cag caa atg gac ctt gct cgc caa cag caa gaa cag att g c Gln Arg Gln Gln Met Asp Leu Ala Arg Gln Gln Glu Gln Ile Ala				1079
223	228	233	238	
aga caa cag cag caa ctt ctg caa cag cag cac aaa att aat ctc ctg Arg Gln Gln Gln Leu Leu Gln Gln His Lys Ile Asn Leu Leu				1127
239	244	249	254	
cag caa cag atc cag cag gtt cag ggt cac atg cct ccg ctc atg atc Gln Gln Gln Ile Gln Gln Val Gln Gly His Met Pro Pro Leu Met Ile				1175
255	260	265	270	
cca att ttt cca cat gac cag cgg act ctg gca gca gct gct gct gcc Pro Ile Phe Pro His Asp Gln Arg Thr Leu Ala Ala Ala Ala Ala				1223
271	276	281	286	
caa cag gga ttc ctc ttc ccc cct gga ata aca tac aaa cca ggt gat Gln Gln Gly Phe Leu Phe Pro Pro Gly Ile Thr Tyr Lys Pro Gly Asp				1271
287	292	297	302	

aac tac ccc gta cag ttc att cca tca aca atg gca gct gct gct Asn Tyr Pro Val Gln Phe Ile Pro Ser Thr Met Ala Ala Ala Ala Ala 303 308 313 318	1319
tct gga ctc agc cct tta cag ctc cag aag ggt cat gtc tcc cac cca Ser Gly Leu Ser Pro Leu Gln Leu Gln Lys Gly His Val Ser His Pro 319 324 329 334	1367
caa att aac caa agg cta aag ggc cta agt gac cgt ttt ggc agg aat Gln Ile Asn Gln Arg Leu Lys Gly Leu Ser Asp Arg Phe Gly Arg Asn 335 340 345 350	1415
ttg gac acc ttt gaa cat ggt ggc cac tct tac aac cac aaa cag Leu Asp Thr Phe Glu His Gly Gly His Ser Tyr Asn His Lys Gln 351 356 361 366	1463
att gag cag ctc tat gcc gct cag ctg gcc agc atg cag gtg tca cct Ile Glu Gln Leu Tyr Ala Ala Gln Leu Ala Ser Met Gln Val Ser Pro 367 372 377 382	1511
gga gca aag atg cca tca act cca cag cca aac aca gca ggg acg Gly Ala Lys Met Pro Ser Thr Pro Gln Pro Pro Asn Thr Ala Gly Thr 383 388 393 398	1559
gtc tca cct act ggg ata aaa aat gaa aag aga ggg acc agc cct gta Val Ser Pro Thr Gly Ile Lys Asn Glu Lys Arg Gly Thr Ser Pro Val 399 404 409 414	1607
act caa gtt aag gat gaa gca gca cag cct ctg aat ctc tca tcc Thr Gln Val Lys Asp Glu Ala Ala Gln Pro Leu Asn Leu Ser Ser 415 420 425 430	1655
cga ccc aag aca gca gag cct gta aag tcc cca acg tct ccc acc cag Arg Pro Lys Thr Ala Glu Pro Val Lys Ser Pro Thr Ser Pro Thr Gln 431 436 441 446	1703
aac ctc ttc cca gcc agc aaa acc agc cct gtc aat ctg cca aac aaa Asn Leu Phe Pro Ala Ser Lys Thr Ser Pro Val Asn Leu Pro Asn Lys 447 452 457 462	1751
agc agc atc cct agc ccc att gga gga agc ctg gga aga gga tcc tct Ser Ser Ile Pro Ser Pro Ile Gly Gly Ser Leu Gly Arg Gly Ser Ser 463 468 473 478	1799
tta gat atc cta tct agt ctc aac tcc cct gcc ctt ttt ggg gat cag Leu Asp Ile Leu Ser Ser Leu Asn Ser Pro Ala Leu Phe Gly Asp Gln 479 484 489 494	1847
gat aca gtg atg aaa gcc att cag gag gcg cggt aag atg cga gag cag Asp Thr Val Met Lys Ala Ile Gln Glu Ala Arg Lys Met Arg Glu Gln 495 500 505 510	1895
atc cag cgg gag caa cag cag caa cag cca cat ggt gtt gac ggg aaa Ile Gln Arg Glu Gln Gln Gln Gln Pro His Gly Val Asp Gly Lys 511 516 521 526	1943

ctg tcc tcc ata aat aat atg ggg ctg aat agc tgc agg aat gaa aag Leu Ser Ser Ile Asn Asn Met Gly Leu Asn Ser Cys Arg Asn Glu Lys 527 532 537 542	1991
gaa aga acg cgc ttt gag aat ttg ggg ccc cag tta acg gga aag tca Glu Arg Thr Arg Phe Glu Asn Leu Gly Pro Gln Leu Thr Gly Lys Ser 543 548 553 558	2039
aat gaa gat gga aaa ctg ggc cca ggt gtc atc gac ctt act cgg cca Asn Glu Asp Gly Lys Leu Gly Pro Gly Val Ile Asp Leu Thr Arg Pro 559 564 569 574	2087
gaa gat gca gag gga ggt gcc act gtg gct gaa gca cga gtc tac agg Glu Asp Ala Glu Gly Gly Ala Thr Val Ala Glu Ala Arg Val Tyr Arg 575 580 585 590	2135
gac gcc cgc ggc ctg cca gca gcg agc cac aca tta agc gac cat atg Asp Ala Arg Gly Leu Pro Ala Ala Ser His Thr Leu Ser Asp His Met 591 596 601 606	2183
aat gca ttc ata ggt ttg ggc aaa gga tga g aggagaaaaa tccttcaggc Asn Ala Phe Ile Gly Leu Gly Lys Gly * 607 612	2234
cttccccgac atgcataact ccaacattag caaaatctta ggatctcgct ggaaatcaat	2294
gtccaaccag gagaagcaac cttattatga agagcaggcc cggctaagca agatccactt	2354
agagaagtac ccaaactata aatacaaacc ccgaccgaaa cgcacctgca ttgttgatgg	2414
caaaaagctt cggattgggg agtataagca actgtatgagg tctcgagac aggagatgag	2474
gcagttcttt actgtggggc aacagcctca gattccaatc accacaggaa caggttgtt	2534
gtatcctggt gctatcacta tggcaactac cacaccatcg cctcagatga catctgactg	2594
ctctagcacc tcggccagcc cggagcccag cctccggtc atccagagca cttatggtat	2654
gaagacagat ggcggaaagcc tagctggaaa tgaaatgatc aatggagagg atgaaatgga	2714
aatgtatgat gactatgaag atgaccccaa atcagactat agcagtgaaa atgaagcccc	2774
ggaggctgtc agtgccaact gaggagttt tgtttgctga attaaagtac tctgacattt	2834
caccccccctc cccaaacaaag agtttattaaa gagcccgcat gcatttgtgg ctccacaatt	2894
acatcagcag aatggtctta attgtttcgt aaagtgtgag acagattaag tttccctga	2954
tttttcatga acttgagttt ttgttgtta ttgttattgt tggtgttgg tttttttaa	3014
tttaggtgaa gacatattaa atatgagaca ccaggacttg aaacttaaaa aaaaaaaaaa	3074

<210> 115
<211> 3442

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (145)..(3078)

<400> 115

gttacccggtc	cggaattccc	gggtcgacga	tttcgtctcg	gctccttggc	gctgcctggg	60
gtcctttccg	cccggtcccc	gcttgccagc	ccccgctgct	ctgtgccctg	tccggccagg	120
cctggagccg	acaccaccgc	catc	atg ccg gcc gtg tcc	aag ggc gat ggg	Met Pro Ala Val Ser Lys Gly Asp Gly	171
			1	5		
atg cgg ggg ctc	gctg ttc atc	tcc gac atc	cg aac tgc aag	agc		219
Met Arg Gly Leu	Ala Val Phe Ile	Ser Asp Ile Arg	Asn Cys Lys Ser			
10	15	20	25			
aaa gag gcg gaa	att aag aga atc	aac aag gaa	ctg gcc aac atc	cgc		267
Lys Glu Ala Glu	Ile Lys Arg Ile	Asn Lys Glu	Leu Ala Asn Ile	Arg		
26	31	36	41			
tcc aag ttc aaa	gga gac aaa	gcc ttg gat	ggc tac agt aag	aaa		315
Ser Lys Phe Lys	Gly Asp Lys Ala	Leu Asp Gly Tyr	Ser Lys Lys Lys			
42	47	52	57			
tat gtg tgt aaa	ctg ctt ttc atc	ttc ctg ctt	ggc cat gac att	gac		363
Tyr Val Cys Lys	Leu Phe Ile	Phe Leu Leu	Gly His Asp Ile	Asp		
58	63	68	73			
ttt ggg cac atg	gag gct gtg aat	ctg ttg agt	tcc aat aaa tac	aca		411
Phe Gly His Met	Glu Ala Val Asn	Leu Leu Ser	Ser Asn Lys Tyr	Thr		
74	79	84	89			
gag aag caa ata	ggt tac ctg ttc	att tct gtg ctg	gtg aac tcg aac			459
Glu Lys Gln Ile	Gly Tyr Leu Phe Ile	Ser Val Leu Val	Asn Ser Asn			
90	95	100	105			
tcg gag ctg atc	cgc ctc atc	aac aac gcc	atc aag aat gac	ctg gcc		507
Ser Glu Leu Ile	Arg Leu Ile	Asn Ala Ile	Lys Asn Asp	Leu Ala		
106	111	116	121			
agc cgc aac ccc	acc ttc atg tgc	ctg gcc ctg	cac tgc atc	gcc aac		555
Ser Arg Asn Pro	Thr Phe Met	Cys Leu Ala	Leu His Cys Ile	Ala Asn		
122	127	132	137			
gtg ggc agc	cgg gag atg	ggc gag gcc	ttt gcc gct	gac atc ccc	cgc	603
Val Gly Ser Arg	Glu Met Gly	Glu Ala Phe	Ala Ala Asp	Ile Pro	Arg	
138	143	148	153			
atc ctg gtg	gcc ggg gac	agc atg gac	agt gtc aag	cag agt	gct ggc	651
Ile Leu Val	Ala Gly Asp	Ser Met Asp	Ser Val Lys	Gln Ser	Ala Ala	
154	159	164	169			
ctg tgc ctc	ctt cga ctg	tac aag	gcc tcg	cct gac	ctg gtg ccc atg	699

Leu	Cys	Leu	Leu	Arg	Leu	Tyr	Lys	Ala	Ser	Pro	Asp	Leu	Val	Pro	Met	
170					175					180					185	
ggc	gag	tgg	acg	gcg	cgt	gtg	gta	cac	ctg	ctc	aat	gac	cag	cac	atg	747
Gly	Glu	Trp	Thr	Ala	Arg	Val	Val	His	Leu	Leu	Asn	Asp	Gln	His	Met	
186						191				196					201	
ggt	gtg	gtc	acg	gcc	gcc	gtc	agc	ctc	atc	acc	tgt	ctc	tgc	aag	aag	795
Gly	Val	Val	Thr	Ala	Ala	Val	Ser	Leu	Ile	Thr	Cys	Leu	Cys	Lys	Lys	
202						207				212					217	
aac	cca	gat	gac	ttc	aag	acg	tgc	gtc	tct	ctg	gct	gtg	tcg	cgc	ctg	843
Asn	Pro	Asp	Asp	Phe	Lys	Thr	Cys	Val	Ser	Leu	Ala	Val	Ser	Arg	Leu	
218					223					228					233	
agc	cgg	atc	gtc	tcc	tct	gcc	tcc	acc	gac	ctc	cag	gac	tac	acc	tac	891
Ser	Arg	Ile	Val	Ser	Ser	Ala	Ser	Thr	Asp	Leu	Gln	Asp	Tyr	Thr	Tyr	
234					239					244					249	
- tac	- ttc	- gtc	- cca	- gca	- ccc	- tgg	- ctc	- tcg	- gtg	- aag	- ctc	- ctg	- cgg	- ctg	- ctg	939
Tyr	Phe	Val	Pro	Ala	Pro	Trp	Leu	Ser	Val	Lys	Leu	Leu	Arg	Leu	Leu	
250					255					260					265	
cag	tgc	tac	ccg	cct	cca	gag	gat	gcf	gct	gtg	aag	ggg	cgg	ctg	gtg	987
Gln	Cys	Tyr	Pro	Pro	Pro	Glu	Asp	Ala	Ala	Val	Lys	Gly	Arg	Leu	Val	
266						271				276					281	
gaa	tgt	ctg	gag	act	gtg	ctc	aac	aag	gcc	cag	gag	ccc	ccc	aaa	tcc	1035
Glu	Cys	Leu	Glu	Thr	Val	Leu	Asn	Lys	Ala	Gln	Glu	Pro	Pro	Lys	Ser	
282					287					292					297	
aag	aag	gtg	cag	cat	tcc	aac	gcc	aag	aac	gcc	atc	ctc	tcc	gag	acc	1083
Lys	Lys	Val	Gln	His	Ser	Asn	Ala	Lys	Asn	Ala	Ile	Leu	Phe	Glu	Thr	
298					303					308					313	
atc	agc	ctc	atc	atc	cac	tat	gac	agt	gag	ccc	aac	ctc	ctg	gtt	cgg	1131
Ile	Ser	Leu	Ile	Ile	His	Tyr	Asp	Ser	Glu	Pro	Asn	Leu	Leu	Val	Arg	
314					319					324					329	
gcc	tgc	aac	cag	ctg	ggc	cag	tcc	ctg	cag	cac	cg	gag	acc	aac	ctg	1179
Ala	Cys	Asn	Gln	Leu	Gly	Gln	Phe	Leu	Gln	His	Arg	Glu	Thr	Asn	Leu	
330					335					340					345	
cgc	tac	ctg	gcc	ctg	gag	agc	atg	tgc	acg	ctg	gcc	agc	tcc	gag	tcc	1227
Arg	Tyr	Leu	Ala	Leu	Glu	Ser	Met	Cys	Thr	Leu	Ala	Ser	Ser	Glu	Phe	
346					351					356					361	
tcc	cat	gaa	gcc	gtc	aag	acg	cac	att	gac	acc	gtc	atc	aat	gcc	ctc	1275
Ser	His	Glu	Ala	Val	Lys	Thr	His	Ile	Asp	Thr	Val	Ile	Asn	Ala	Leu	
362					367					372					377	
aag	acg	gag	cg	gac	gtc	acg	gtg	cg	cag	cg	gct	gac	ctc	ctc		1323
Lys	Thr	Glu	Arg	Asp	Val	Ser	Val	Arg	Gln	Arg	Ala	Ala	Asp	Leu	Leu	
378					383					388					393	
tac	gcc	atg	tgt	gac	cg	agc	aat	gcc	aag	cag	atc	gtg	tcg	gag	atg	1371
Tyr	Ala	Met	Cys	Asp	Arg	Ser	Asn	Ala	Lys	Gln	Ile	Val	Ser	Glu	Met	

394	399	404	409														
ctg	cg	tac	ctg	gag	acg	gca	gac	tac	gcc	atc	cgc	gag	gag	atc	gtc		1419
Leu	Arg	Tyr	Leu	Glu	Thr	Ala	Asp	Tyr	Ala	Ile	Arg	Glu	Glu	Ile	Val		
410				415					420					425			
ctg	aag	gtg	gcc	atc	ctg	gcc	gag	aag	tac	gcc	gtg	gac	tac	agc	tgg		1467
Leu	Lys	Val	Ala	Ile	Leu	Ala	Glu	Lys	Tyr	Ala	Val	Asp	Tyr	Ser	Trp		
426					431					436				441			
tac	gtg	gac	acc	atc	ctc	aac	ctc	atc	cgc	att	gcf	ggc	gac	tac	gtg		1515
Tyr	Val	Asp	Thr	Ile	Leu	Asn	Leu	Ile	Arg	Ile	Ala	Gly	Asp	Tyr	Val		
442					447					452				457			
agt	gag	gag	gtg	tgg	tac	cgt	gtg	cta	cag	atc	gtc	acc	aac	cgt	gat		1563
Ser	Glu	Glu	Val	Trp	Tyr	Arg	Val	Leu	Gln	Ile	Val	Thr	Asn	Arg	Asp		
458						463				468				473			
gac	gtc	cag	ggc	tat	gcc	gcc	aag	acc	gtc	ttt	gag	gcf	ctc	cag	gcc		1611
Asp	Val	Gln	Gly	Tyr	Ala	Ala	Lys	Thr	Val	Phe	Glu	Ala	Leu	Gln	Ala		
474					479					484				489			
cct	gcc	tgt	cac	gag	aac	atg	gtg	aag	gtt	ggc	ggc	tac	atc	ctt	ggg		1659
Pro	Ala	Cys	His	Glu	Asn	Met	Val	Lys	Val	Gly	Gly	Tyr	Ile	Leu	Gly		
490						495				500				505			
gag	ttt	ggg	aaa	ctg	att	gct	ggg	gac	ccc	cgc	tcc	agc	ccc	cca	gtg		1707
Glu	Phe	Gly	Asn	Leu	Ile	Ala	Gly	Asp	Pro	Arg	Ser	Ser	Pro	Pro	Val		
506						511				516				521			
cag	tcc	tcc	ctg	ctc	cac	tcc	aag	ttc	cat	ctg	tgc	agc	gtg	gcc	acg		1755
Gln	Phe	Ser	Leu	Leu	His	Ser	Lys	Phe	His	Leu	Cys	Ser	Val	Ala	Thr		
522						527				532				537			
cg	gc	ctg	ctg	tcc	acc	tac	atc	aag	ttc	atc	aa	ctc	tcc	ccc		1803	
Arg	Ala	Leu	Leu	Leu	Ser	Thr	Tyr	Ile	Lys	Phe	Ile	Asn	Leu	Ser	Pro		
538						543				548				553			
gag	acc	aag	gcc	acc	atc	cag	ggc	gtc	ctg	cg	ggc	ggc	tcc	cag	ctg		1851
Glu	Thr	Lys	Ala	Thr	Ile	Gln	Gly	Val	Leu	Arg	Ala	Gly	Ser	Gln	Leu		
554						559				564				569			
cgc	aat	gct	gac	gtg	gag	ctg	cag	cag	cga	gcc	gtg	gag	tac	ctc	acc		1899
Arg	Asn	Ala	Asp	Val	Glu	Leu	Gln	Gln	Arg	Ala	Val	Glu	Tyr	Leu	Thr		
570						575				580				585			
ctc	agc	tca	gtg	gcc	agc	acc	gac	gtc	ctg	gcc	acg	gtg	ctg	gag	gag		1947
Leu	Ser	Ser	Val	Ala	Ser	Thr	Asp	Val	Leu	Ala	Thr	Val	Leu	Glu	Glu		
586						591				596				601			
atg	ccg	ccc	ttc	ccc	gag	cgc	gag	tcg	tcc	atc	ctg	gcc	aag	ctg	aaa		1995
Met	Pro	Pro	Phe	Pro	Glu	Arg	Glu	Ser	Ser	Ile	Leu	Ala	Lys	Leu	Lys		
602						607				612				617			
cgc	aag	aag	ggg	cca	ggg	gcc	agc	gcc	ctg	gac	gat	ggc	cg	agg		2043	
Arg	Lys	Lys	Gly	Pro	Gly	Ala	Gly	Ser	Ala	Leu	Asp	Asp	Gly	Arg	Arg		
618						623				628				633			

gac ccc agc agc aac gac atc aac ggg ggc atg gag ccc acc ccc agc		2091
Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro Ser		
634 639 644 649		
act gtg tcg acg ccc tcg ccc tcc gcc gac ctc ctg ggg ctg cg ^g gca		2139
Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg Ala		
650 655 660 665		
gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac ctt		2187
Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn Leu		
666 671 676 681		
ctg gtg gac gtc ttc gat ggc ccg gcc cag ccc agc ctg ggg ccc		2235
Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly Pro		
682 687 692 697		
acc ccc gag gag gcc ttc ctc agc gag ctg gag ccg cct gcc ccc gag		2283
Thr Pro Glu Glu Ala Phe Leu Ser Glu Leu Glu Pro Pro Ala Pro Glu		
698 703 708 713		
agc ccc atg gct ttg ctg gct gac cca gct cca gct gct gac cca ggt		2331
Ser Pro Met Ala Leu Leu Ala Asp Pro Ala Pro Ala Asp Pro Gly		
714 719 724 729		
cct gag gac atc ggc cct ccc att ccg gaa gcc gat gag ttg ctg aat		2379
Pro Glu Asp Ile Gly Pro Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn		
730 735 740 745		
aag ttt gtg tgt aag aac aac ggg gtc ctg ttc gag aac cag ctg ctg		2427
Lys Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu Asn Gln Leu Leu		
746 751 756 761		
cag atc gga gtc aag tca gag ttc cga cag aac ctg ggc cgc atg tat		2475
Gln Ile Gly Val Lys Ser Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr		
762 767 772 777		
ctc ttc tat ggc aac aag acc tcg gtg cag ttc cag aat ttc tca ccc		2523
Leu Phe Tyr Gly Asn Lys Thr Ser Val Gln Phe Gln Asn Phe Ser Pro		
778 783 788 793		
act gtg gtt cac ccg gga gac ctc cag act cag ctg gct gtg cag acc		2571
Thr Val Val His Pro Gly Asp Leu Gln Thr Gln Leu Ala Val Gln Thr		
794 799 804 809		
aag cgc gtg gcg gcg cag gtg gac ggc ggc gcg cag gtg cag cag gtg		2619
Lys Arg Val Ala Ala Gln Val Asp Gly Gly Ala Gln Val Gln Gln Val		
810 815 820 825		
ctc aat atc gag tgc ctg cgg gac ttc ctg acg ccc ccg ctg ctg tcc		2667
Leu Asn Ile Glu Cys Leu Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser		
826 831 836 841		
gtg cgc ttc cgg tac ggt ggc gcc ccc cag gcc ctc acc ctg aag ctc		2715
Val Arg Phe Arg Tyr Gly Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu		
842 847 852 857		

cca gtg acc atc aac aag ttc ttc cag ccc acc gag atg gcg gcc cag Pro Val Thr Ile Asn Lys Phe Phe Gln Pro Thr Glu Met Ala Ala Gln 858 863 868 873	2763
gat ttc ttc cag cgc tgg aag cag ctg agc ctc cct caa cag gag gcg Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala 874 879 884 889	2811
cag aaa atc ttc aaa gcc aac cac ccc atg gac gca gaa gtt act aag Gln Lys Ile Phe Lys Ala Asn His Pro Met Asp Ala Glu Val Thr Lys 890 895 900 905	2859
gcc aag ctt ctg ggg ttt ggc tct gct ctc ctg gac aat gtg gac ccc Ala Lys Leu Leu Gly Phe Gly Ser Ala Leu Leu Asp Asn Val Asp Pro 906 911 916 921	2907
aac cct gag aac ttc gtg ggg gcg ggg atc atc cag act aaa gcc ctg Asn Pro Glu Asn Phe Val Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu 922 927 932 937	2955
cag gtg ggc tgt ctg ctt cg ^g ctg gag ccc aat gcc cag gcc cag atg Gln Val Gly Cys Leu Leu Arg Leu Glu Pro Asn Ala Gln Ala Gln Met 938 943 948 953	3003
tac cgg ctg acc ctg cgc acc agc aag gag ccc gtc tcc cgt cac ctg Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Pro Val Ser Arg His Leu 954 959 964 969	3051
tgt gag ctg ctg gca cag cag ttc tga gccct ggactctgcc ccggggatg Cys Glu Leu Leu Ala Gln Gln Phe *970 975	3103
tggccggcac tggcagccc cttggactga ggcagtttg gtggatgggg gacctccact ggtagacagag aagacaccag gtttgggg atgcctggga ctttcctccg gcctttgt tttttatattt tgccatctg ctgctgtta cattctgggg gtttaggggg agtccccctc cctcccttcc cccccaagc acagagggga gaggggcccag ggaagtggat gtctccccc ctcccccccc accctgttgt agccctccct accccctccc catccagggg ctgtgttata ttgtgagcga ataaacagag agacgctaaa aaaaaaaaaa	3163 3223 3283 3343 3403 3442

<210> 116
<211> 3376
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (145)..(3012)

<400> 116

gctaccggtc	cggaattccc	gggtcgacga	tttcgtctcg	gctccttggc	gctgcctggg	60
gtccttccg	cccggtcccc	gcttgccagc	ccccgctgct	ctgtgccctg	tccggccagg	120
cctggagccg	acaccaccgc	catc	atg ccg gcc gtg tcc aag ggc gat ggg			171
			Met Pro Ala Val Ser Lys Gly Asp Gly			
			1	5		
atg cgg ggg ctc	gctg ttc atc	tcc gac atc	cg aac tgt aag agc			219
Met Arg Gly	Leu Ala Val	Phe Ile Ser	Asp Ile Arg Asn Cys Lys Ser			
10	15	20	25			
aaa gag gcg gaa att aag	aga atc aac aag	gaa ctg	gcc aac atc cgc			267
Lys Glu Ala Glu Ile	Lys Arg Ile Asn	Lys Glu Leu	Ala Asn Ile Arg			
26	31	36	41			
tcc aag ttc aaa gga	gac aaa gcc ttg	gat ggc tac	agt aag aaa aaa			315
Ser Lys Phe Lys Gly	Asp Lys Ala Leu Asp	Gly Tyr Ser Lys Lys	Lys			
42	47	52	57			
tat gtg tgt aaa	ctg ctt ttc atc	ttc ctg ctt	ggc cat gac att gac			363
Tyr Val Cys Lys	Leu Phe Ile	Phe Leu Leu	Gly His Asp Ile Asp			
58	63	68	73			
ttt ggg cac atg	gag gct gtg aat	ctg ttg	agt tcc aat aaa tac aca			411
Phe Gly His Met	Glu Ala Val Asn	Leu Ser Ser	Asn Lys Tyr Thr			
74	79	84	89			
gag aag caa ata	ggt tac ctg ttc	att tct	gtg ctg gtg aac tcg aac			459
Glu Lys Gln Ile	Gly Tyr Leu Phe Ile	Ser Val	Leu Val Asn Ser Asn			
90	95	100	105			
tcg gag ctg atc	cgc ctc atc	aac aac	gcc atc aag aat gac	ctg gcc		507
Ser Glu Leu Ile	Arg Leu Ile	Asn Asn	Ala Ile	Lys Asn Asp Leu Ala		
106	111	116	121			
agc cgc aac ccc acc	ttc atg tgc	ctg gcc	ctg cac tgc atc	gcc aac		555
Ser Arg Asn Pro	Thr Phe Met	Cys Leu Ala	Leu His Cys Ile	Ala Asn		
122	127	132	137			
gtg ggc agc	cg ggg gag	atg ggc gag	gcc ttt	gcc gct gac	atc ccc cgc	603
Val Gly Ser Arg	Glu Met Gly	Ala Phe	Ala Ala	Asp Ile	Pro Arg	
138	143	148	153			
atc ctg gtg	gcc ggg gac	agc atg gac	agt gtc	aag cag	agt gcg gcc	651
Ile Leu Val	Ala Gly Asp	Ser Met	Asp Ser	Val Lys	Gln Ser Ala	
154	159	164	169			
ctg tgc ctc	ctt cga ctg	tac aag	gcc tcg	cct gac	ctg gtg ccc atg	699
Leu Cys Leu	Leu Arg	Leu Tyr	Lys Ala	Ser Pro	Asp Leu Val	
170	175	180	185			
gac gag tgg acg	gct cgt gtg	gta cac	ctg ctc	aat gac	cag cac atg	747
Gly Glu Trp Thr	Ala Arg Val	Val His	Leu Leu	Asn Asp	Gln His Met	
186	191	196	201			
ggt gtg gtc	acg gcc	gtc agc	ctc atc	acc tgt	ctc tgc aag aag	795

Gly Val Val Thr Ala Ala Val Ser Leu Ile Thr Cys Leu Cys Lys Lys			
202	207	212	217
aac cca gat gac ttc aag acg tgc gtc tct ctg gct gtg tcg cgc ctg			843
Asn Pro Asp Asp Phe Lys Thr Cys Val Ser Leu Ala Val Ser Arg Leu			
218	223	228	233
agc cggtatcgtctcc tct gcc tcc acc gac ctc cag gac tac acc tac			891
Ser Arg Ile Val Ser Ser Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr			
234	239	244	249
tac ttc gtc cca gca ccc tgg ctc tcg gtg aag ctc ctg cgg ctg ctg			939
Tyr Phe Val Pro Ala Pro Trp Leu Ser Val Lys Leu Leu Arg Leu Leu			
250	255	260	265
cag tgc tac ccg cct cca gag gat gcg gct gtg aag ggg cgg ctg gtg			987
Gln Cys Tyr Pro Pro Glu Asp Ala Ala Val Lys Gly Arg Leu Val			
266	271	276	281
gaa tgt ctg gag act gtg ctc aac aag gcc cag gag ccc ccc aaa tcc			1035
Glu Cys Leu Glu Thr Val Leu Asn Lys Ala Gln Glu Pro Pro Lys Ser			
282	287	292	297
aag aag gtg cag cat tcc aac gcc aag aac gcc atc ctc ttc gag acc			1083
Lys Lys Val Gln His Ser Asn Ala Lys Asn Ala Ile Leu Phe Glu Thr			
298	303	308	313
atc agc ctc atc atc cac tat gac agt gag ccc aac ctc ctg gtt cgg			1131
Ile Ser Leu Ile Ile His Tyr Asp Ser Glu Pro Asn Leu Leu Val Arg			
314	319	324	329
gcc tgc aac cag ctg ggc cag ttc ctg cag cac cgg gag acc aac ctg			1179
Ala Cys Asn Gln Leu Gly Gln Phe Leu Gln His Arg Glu Thr Asn Leu			
330	335	340	345
cgc tac ctg gcc ctg gag agc atg tgc acg ctg gcc agc tcc gag ttc			1227
Arg Tyr Leu Ala Leu Glu Ser Met Cys Thr Leu Ala Ser Ser Glu Phe			
346	351	356	361
tcc cat gaa gcc gtc aag acg cac att gac acc gtc atc aat gcc ctc			1275
Ser His Glu Ala Val Lys Thr His Ile Asp Thr Val Ile Asn Ala Leu			
362	367	372	377
aag acg gag cgg gac gtc agc gtg cgg cag cgg gcg gct gac ctc ctc			1323
Lys Thr Glu Arg Asp Val Ser Val Arg Gln Arg Ala Ala Asp Leu Leu			
378	383	388	393
tac gcc atg tgt gac cgg agc aat gcc aag cag atc gtg tcg gag atg			1371
Tyr Ala Met Cys Asp Arg Ser Asn Ala Lys Gln Ile Val Ser Glu Met			
394	399	404	409
ctg cgg tac ctg gag acg gca gac tac gcc atc cgc gag gag atc gtc			1419
Leu Arg Tyr Leu Glu Thr Ala Asp Tyr Ala Ile Arg Glu Glu Ile Val			
410	415	420	425
ctg aag gtg gcc atc ctg gcc gag aag tac gcc gtg gac tac agc tgg			1467
Leu Lys Val Ala Ile Leu Ala Glu Lys Tyr Ala Val Asp Tyr Ser Trp			

426	431	436	441	
tac gtg gac acc atc ctc aac ctc atc cgc att gcg ggc gac tac gtg Tyr Val Asp Thr Ile Leu Asn Leu Ile Arg Ile Ala Gly Asp Tyr Val				1515
442	447	452	457	
agt gag gag gtg tgg tac cgt gtg cta cag atc gtc acc aac cgt gat Ser Glu Glu Val Trp Tyr Arg Val Leu Gln Ile Val Thr Asn Arg Asp				1563
458	463	468	473	
gac gtc cag ggc tat gcc gcc aag acc gtc ttt gag gcg ctc cag gcc Asp Val Gln Gly Tyr Ala Ala Lys Thr Val Phe Glu Ala Leu Gln Ala				1611
474	479	484	489	
cct gcc tgt cac gag aac atg gtg aag gtt ggc ggc tac atc ctt ggg Pro Ala Cys His Glu Asn Met Val Lys Val Gly Gly Tyr Ile Leu Gly				1659
490	495	500	505	
gag ttt ggg aac ctg att gct ggg gac ccc cgc tcc agc ccc cca gtg Glu Phe Gly Asn Leu Ile Ala Gly Asp Pro Arg Ser Ser Pro Pro Val				1707
506	511	516	521	
cag ttc tcc ctg ctc cac tcc aag ttc cat ctg tgc agc gtg gcc acg Gln Phe Ser Leu Leu His Ser Lys Phe His Leu Cys Ser Val Ala Thr				1755
522	527	532	537	
cg ^g gc ^g ct ^g ct ^g ct ^g tcc acc tac atc aag ttc atc aac ctc tcc ccc Arg Ala Leu Leu Leu Ser Thr Tyr Ile Lys Phe Ile Asn Leu Ser Pro				1803
538	543	548	553	
gag acc aag gcc acc atc cag ggc gtc ctg cg ^g gcc gg ^c tcc cag ctg Glu Thr Lys Ala Thr Ile Gln Gly Val Leu Arg Ala Gly Ser Gln Leu				1851
554	559	564	569	
cg ^c aat gct gac gt ^g gag ctg cag cag cga gc ^c gt ^g gag tac ctc acc Arg Asn Ala Asp Val Glu Leu Gln Gln Arg Ala Val Glu Tyr Leu Thr				1899
570	575	580	585	
ctc agc tca gt ^g gcc agc acc gac gtc ctg gcc acg gt ^g ctg gag gag Leu Ser Ser Val Ala Ser Thr Asp Val Leu Ala Thr Val Leu Glu Glu				1947
586	591	596	601	
at ^g cc ^g cc ^c tt ^c cc ^c gag cg ^c gag tc ^g tcc atc ctg gcc aag ctg aaa Met Pro Pro Phe Pro Glu Arg Glu Ser Ser Ile Leu Ala Lys Leu Lys				1995
602	607	612	617	
cg ^c aag aag gg ^c cc ^a gg ^c gc ^c agc gc ^c ctg gac gat gg ^c cg ^g agg Arg Lys Lys Gly Pro Gly Ala Gly Ser Ala Leu Asp Asp Gly Arg Arg				2043
618	623	628	633	
gac ccc agc agc aac gac atc aac gg ^c gg ^c at ^g gag ccc acc ccc agc Asp Pro Ser Ser Asn Asp Ile Asn Gly Gly Met Glu Pro Thr Pro Ser				2091
634	639	644	649	
act gt ^g tc ^g ac ^g cc ^c tc ^g cc ^c tcc gc ^c gac ctc ctg gg ^c cg ^g gca Thr Val Ser Thr Pro Ser Pro Ser Ala Asp Leu Leu Gly Leu Arg Ala				2139
650	655	660	665	

gcc cct ccc ccg gca gca ccc ccg gct tct gca gga gca ggg aac ctt		2187
Ala Pro Pro Pro Ala Ala Pro Pro Ala Ser Ala Gly Ala Gly Asn Leu		
666 671 676 681		
ctg gtg gac gtc ttc gat ggc ccg gcc cag ccc agc ctg ggg ccc		2235
Leu Val Asp Val Phe Asp Gly Pro Ala Ala Gln Pro Ser Leu Gly Pro		
682 687 692 697		
acc ccc gag gag gcc ttc ctc agc cca ggt cct gag gac atc ggc cct		2283
Thr Pro Glu Glu Ala Phe Leu Ser Pro Gly Pro Glu Asp Ile Gly Pro		
698 703 708 713		
ccc att ccg gaa gcc gat gag ttg ctg aat aag ttt gtg tgt aag aac		2331
Pro Ile Pro Glu Ala Asp Glu Leu Leu Asn Lys Phe Val Cys Lys Asn		
714 719 724 729		
aac ggg gtc ctg ttc gag aac cag ctg ctg cag atc gga gtc aag tca		2379
Asn Gly Val Leu Phe Glu Asn Gln Leu Leu Gln Ile Gly Val Lys Ser		
730 735 740 745		
gag ttc cga cag aac ctg ggc cgc atg tat ctc ttc tat ggc aac aag		2427
Glu Phe Arg Gln Asn Leu Gly Arg Met Tyr Leu Phe Tyr Gly Asn Lys		
746 751 756 761		
acc tcg gtg cag ttc cag aat ttc tca ccc act gtg gtt cac ccg gga		2475
Thr Ser Val Gln Phe Gln Asn Phe Ser Pro Thr Val Val His Pro Gly		
762 767 772 777		
gac ctc cag act cag ctg gct gtg cag acc aag cgc gtg gcg gcg cag		2523
Asp Leu Gln Thr Gln Leu Ala Val Gln Thr Lys Arg Val Ala Ala Gln		
778 783 788 793		
gtg gac ggc ggc gcg cag gtg cag cag gtg ctc aat atc gag tgc ctg		2571
Val Asp Gly Gly Ala Gln Val Gln Gln Val Leu Asn Ile Glu Cys Leu		
794 799 804 809		
cgg gac ttc ctg acg ccc ccg ctg ctg tcc gtg cgc ttc cggt tac ggt		2619
Arg Asp Phe Leu Thr Pro Pro Leu Leu Ser Val Arg Phe Arg Tyr Gly		
810 815 820 825		
ggc gcc ccc cag gcc ctc acc ctg aag ctc cca gtg acc atc aac aag		2667
Gly Ala Pro Gln Ala Leu Thr Leu Lys Leu Pro Val Thr Ile Asn Lys		
826 831 836 841		
tcc ttc cag ccc acc gag atg gcg gcc cag gat ttc ttc cag cgc tgg		2715
Phe Phe Gln Pro Thr Glu Met Ala Ala Gln Asp Phe Phe Gln Arg Trp		
842 847 852 857		
aag cag ctg agc ctc cct caa cag gag gcg cag aaa atc ttc aaa gcc		2763
Lys Gln Leu Ser Leu Pro Gln Gln Glu Ala Gln Lys Ile Phe Lys Ala		
858 863 868 873		
aac cac ccc atg gac gca gaa gtt act aag gcc aag ctt ctg ggg ttt		2811
Asn His Pro Met Asp Ala Glu Val Thr Lys Ala Lys Leu Leu Gly Phe		
874 879 884 889		

ggc tct gct ctc ctg gac aat gtg gac ccc aac cct gag aac ttc gtg		2859	
Gly Ser Ala Leu Leu Asp Asn Val Asp Pro Asn Pro Glu Asn Phe Val			
890	895	900	905
ggg gcg ggg atc atc cag act aaa gcc ctg cag gtg ggc tgt ctg ctt		2907	
Gly Ala Gly Ile Ile Gln Thr Lys Ala Leu Gln Val Gly Cys Leu Leu			
906	911	916	921
cgg ctg gag ccc aat gcc cag gcc cag atg tac cgg ctg acc ctg cgc		2955	
Arg Leu Glu Pro Asn Ala Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg			
922	927	932	937
acc agc aag gag ccc gtc tcc cgt cac ctg tgt gag ctg ctg gca cag		3003	
Thr Ser Lys Glu Pro Val Ser Arg His Leu Cys Glu Leu Leu Ala Gln			
938	943	948	953
cag ttc tga gccctgg actctgcccc gggggatgtg gccggcactg ggcagcccc		3059	
Gln Phe *			
954			
tggactgagg=cagtttggt=ggatggggga=cctccactgg=tgacagagaa=gacaccagg		3119	
tttggggat gcctggact ttccctccggc ctttgtatt ttatatttg ttcatctgct		3179	
gctgtttaca ttctgggggg ttagggggag tccccctccc tccctttccc cccaaagcac		3239	
agaggggaga ggggccaggg aagtggatgt ctcctccct cccacccac cctgtttag		3299	
cccttcctac ccctccccca tccaggggct gtgtattatt gtgagcgaat aaacagagag		3359	
acgctaaaaa aaaaaaaaa		3376	

<210> 117
 <211> 2616
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (261)..(2159)

<400> 117

caccggcccc	gaattccccgg	gtcgacgatt	tcgtgtggct	ccttgcgttc	ctacatcctc	60
tcatctgaga	atcagagagc	ataatcttct	tacggggcccg	tgattttatta	acgtggctta	120
atctgaagg	tctcagtcaa	attctttgtg	atctactgat	tgtggggca	tggcaaggtt	180
tgcttaaagg	agcttggctg	gtttggccc	ttgttagctga	cagaagggtgg	ccagggagaa	240
ggcagcacac	tgctcggaga	atg aag	gctt ctg	ttg ctg	gtc ttg	290
/		Met Lys	Ala Leu	Leu Leu	Leu Val	Leu Pro

tgg ctc agt cct gct aac tac att gac aat gtg ggc aac ctg cac ttc			338
Trp Leu Ser Pro Ala Asn Tyr Ile Asp Asn Val Gly Asn Leu His Phe			
11	16	21	26
ctg tat tca gaa ctc tgt aaa ggt gcc tcc cac tac ggc ctg acc aaa			386
Leu Tyr Ser Glu Leu Cys Lys Gly Ala Ser His Tyr Gly Leu Thr Lys			
27	32	37	42
gat agg aag agg cgc tca caa gat ggc tgt cca gac ggc tgt gcg agc			434
Asp Arg Lys Arg Arg Ser Gln Asp Gly Cys Pro Asp Gly Cys Ala Ser			
43	48	53	58
ctc aca gcc acg gct ccc tcc cca gag gtt tct gca gct gcc acc atc			482
Leu Thr Ala Thr Ala Pro Ser Pro Glu Val Ser Ala Ala Ala Thr Ile			
59	64	69	74
tcc tta atg aca gac gag cct ggc cta gac aac cct gcc tac gtg tcc			530
Ser Leu Met Thr Asp Glu Pro Gly Leu Asp Asn Pro Ala Tyr Val Ser			
75	80	85	90
tcg gca gag gac ggg cag cca gca atc agc cca gtg gac tct ggc cgg			578
Ser Ala Glu Asp Gly Gln Pro Ala Ile Ser Pro Val Asp Ser Gly Arg			
91	96	101	106
agc aac cga act agg gca cgg ccc ttt gag aga tcc act att aga agc			626
Ser Asn Arg Thr Arg Ala Arg Pro Phe Glu Arg Ser Thr Ile Arg Ser			
107	112	117	122
aga tca ttt aaa aaa ata aat cga gct ttg agt gtt ctt cga agg aca			674
Arg Ser Phe Lys Lys Ile Asn Arg Ala Leu Ser Val Leu Arg Arg Thr			
123	128	133	138
aag agc ggg agt gca gtt gcc aac cat gcc gac cag ggc agg gaa aat			722
Lys Ser Gly Ser Ala Val Ala Asn His Ala Asp Gln Gly Arg Glu Asn			
139	144	149	154
tct gaa aac acc act gcc cct gag gtc ttt cca agg ttg tac cac ctg			770
Ser Glu Asn Thr Thr Ala Pro Glu Val Phe Pro Arg Leu Tyr His Leu			
155	160	165	170
att cca gat ggt gaa att acc agc atc aag atc aat cga gta gat ccc			818
Ile Pro Asp Gly Glu Ile Thr Ser Ile Lys Ile Asn Arg Val Asp Pro			
171	176	181	186
agt gaa agc ctc tct att atg ctg gtg gga ggt agc gaa acc cca ctg			866
Ser Glu Ser Leu Ser Ile Met Leu Val Gly Gly Ser Glu Thr Pro Leu			
187	192	197	202
gtc cat atc att atc caa cac att tat cgt gat ggg gtg atc gcc aga			914
Val His Ile Ile Ile Gln His Ile Tyr Arg Asp Gly Val Ile Ala Arg			
203	208	213	218
gac ggc cgg cta ctg cca gga gac atc att cta aag gtc aac ggg atg			962
Asp Gly Arg Leu Leu Pro Gly Asp Ile Ile Leu Lys Val Asn Gly Met			
219	224	229	234
gac atc agc aat gtc cct cac aac tac gct gtg cgt ctc ctg cgg cag			1010

Asp Ile Ser Asn Val Pro His Asn Tyr Ala Val Arg Leu Leu Arg Gln			
235	240	245	250
ccc tgc cag gtg ctg tgg ctg act gtg atg cgt gaa cag aag ttc cgc			1058
Pro Cys Gln Val Leu Trp Leu Thr Val Met Arg Glu Gln Lys Phe Arg			
251	256	261	266
agc agg aac aat gga cag gcc ccg gat gcc tac aga ccc cga gat gac			1106
Ser Arg Asn Asn Gly Gln Ala Pro Asp Ala Tyr Arg Pro Arg Asp Asp			
267	272	277	282
agc ttt cat gtg att ctc aac aaa agt agc ccc gag gag cag ctt gga			1154
Ser Phe His Val Ile Leu Asn Lys Ser Ser Pro Glu Glu Gln Leu Gly			
283	288	293	298
ata aaa ctg gtg cgc aag gtg gat gag cct ggg gtt ttc atc ttc aat			1202
Ile Lys Leu Val Arg Lys Val Asp Glu Pro Gly Val Phe Ile Phe Asn			
299	304	309	314
gtg ctg gat ggc ggt gtg gca tat cga cat ggt cag ctt gag gag aat			1250
Val Leu Asp Gly Gly Val Ala Tyr Arg His Gly Gln Leu Glu Glu Asn			
315	320	325	330
gac cgt gtg tta gcc atc aat gga cat gat ctt cga tat ggc agc cca			1298
Asp Arg Val Leu Ala Ile Asn Gly His Asp Leu Arg Tyr Gly Ser Pro			
331	336	341	346
gaa agt gcg gct cat ctg att cag gcc agt gaa aga cgt gtt cac ctc			1346
Glu Ser Ala Ala His Leu Ile Gln Ala Ser Glu Arg Arg Val His Leu			
347	352	357	362
gtc gtg tcc cgc cag gtt cg ^g cag cg ^g agc cct gac atc ttt cag gaa			1394
Val Val Ser Arg Gln Val Arg Gln Arg Ser Pro Asp Ile Phe Gln Glu			
363	368	373	378
gcc ggc tgg aac agc aat ggc agc tgg tcc cca ggg cca ggg gag agg			1442
Ala Gly Trp Asn Ser Asn Gly Ser Trp Ser Pro Gly Pro Gly Glu Arg			
379	384	389	394
agc aac act ccc aag ccc ctc cat cct aca att act tgt cat gag aag			1490
Ser Asn Thr Pro Lys Pro Leu His Pro Thr Ile Thr Cys His Glu Lys			
395	400	405	410
gtg gta aat atc caa aaa gac ccc ggt gaa tct ctc ggc atg acc gtc			1538
Val Val Asn Ile Gln Lys Asp Pro Gly Glu Ser Leu Gly Met Thr Val			
411	416	421	426
gca ggg gga gca tca cat aga gaa tgg gat ttg cct atc tat gtc atc			1586
Ala Gly Gly Ala Ser His Arg Glu Trp Asp Leu Pro Ile Tyr Val Ile			
427	432	437	442
agt gtt gag ccc gga gga gtc ata agc aga gat gga aga ata aaa aca			1634
Ser Val Glu Pro Gly Gly Val Ile Ser Arg Asp Gly Arg Ile Lys Thr			
443	448	453	458
ggt gac att ttg ttg aat gtg gat ggg gtc gaa ctg aca gag gtc agc			1682
Gly Asp Ile Leu Leu Asn Val Asp Gly Val Glu Leu Thr Glu Val Ser			

459	464	469	474	
cgg agt gag gca gtg gca tta ttg aaa aga aca tca tcc tcg ata gta Arg Ser Glu Ala Val Ala Leu Leu Lys Arg Thr Ser Ser Ser Ile Val 475	480	485	490	1730
ctc aaa gct ttg gaa gtc aaa gag tat gag ccc cag gaa gac tgc agc Leu Lys Ala Leu Glu Val Lys Glu Tyr Glu Pro Gln Glu Asp Cys Ser 491	496	501	506	1778
agc cca gca gcc ctg gac tcc aac cac aac atg gcc cca ccc agt gac Ser Pro Ala Ala Leu Asp Ser Asn His Asn Met Ala Pro Pro Ser Asp 507	512	517	522	1826
tgg tcc cca tcc tgg gtc atg tgg ctg gaa tta cca cgg tgc ttg tat Trp Ser Pro Ser Trp Val Met Trp Leu Glu Leu Pro Arg Cys Leu Tyr 523	528	533	538	1874
aac tgt aaa gat att gta tta cga aga aac aca gct gga agt ctg ggc Asn Cys Lys Asp Ile Val Leu Arg Arg Asn Thr Ala Gly Ser Leu Gly 539	544	549	554	1922
ttc tgc att gta gga ggt tat gaa gaa tac aat gga aac aaa cct ttt Phe Cys Ile Val Gly Gly Tyr Glu Glu Tyr Asn Gly Asn Lys Pro Phe 555	560	565	570	1970
ttc atc aaa tcc att gtt gaa gga aca cca gca tac aat gat gga aga Phe Ile Lys Ser Ile Val Glu Gly Thr Pro Ala Tyr Asn Asp Gly Arg 571	576	581	586	2018
att aga tgt ggt gat att ctt ctt gct gtc aat ggt aga agt aca tca Ile Arg Cys Gly Asp Ile Leu Leu Ala Val Asn Gly Arg Ser Thr Ser 587	592	597	602	2066
gga atg ata cat gct tgc ttg gca aga ctg ctg aaa gaa ctt aaa gga Gly Met Ile His Ala Cys Leu Ala Arg Leu Leu Lys Glu Leu Lys Gly 603	608	613	618	2114
aga att act cta act att gtt tct tgg cct ggc act ttt tta tag aat Arg Ile Thr Leu Thr Ile Val Ser Trp Pro Gly Thr Phe Leu *619	624	629		2162
caatgatggg tcagaggaaa acagaaaaat cacaaatagg ctaagaagtt gaaacactat				2222
atttatcttg tcagtttta tatttaaga aagaatacat tgaaaaatg tcaggaaaag				2282
tatgatcatc taatgaaagc cagttacacc tcagaaaata tgattccaaa aaaattaaaa				2342
ctactagttt ttttcagtg tggaggattt ctcattactc tacaacattg tttatattt				2402
ttcttattcaa taaaaagccc taaaacaact aaaatgattt gtataccccca ctgaattcaa				2462
gctgatttaa atttaaaatt tggatatgc tgaagtctgc caagggtaca ttatggccat				2522
tttaattta cagctaaaat atttttaaa atgcattgct gagaaacggt gctttcatca				2582
aacaagaata aatatttttc agaaaaaaaaaaa aaaa				2616

<210> 118

<211> 1431

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (481)..(969)

<400> 118

ttttagatgt	gtacgcctgc	aggtaaccgg	ccggaattcc	cgggtcgacg	atttcgtgga	60
ggctgcggcg	acgggtcctc	ctccgccgtc	cggtcgcgcc	ctcgccgaaag	ctcgccagtg	120
cgcgtgcgcc	cgcacccgca	ctccaaatta	gaaaggggac	gtctagtggg	ttgcccggga	180
gggggtggcg	gagcggtcct	ggaaataatc	tgtcccttgt	cgcgcggaaac	tggcgaggta	240
gttccttcgc	ggtggagaga	cctggaatgg	ccaaatatca	aggtaagtt	caaagtttga	300
aactggatga	tgattcagtt	atagaaggag	taagcgacca	agtacttgtg	gcagttgtgg	360
tcagtttcgc	tttgattgct	accctggat	atgcactttt	cagaaatgta	catcaaaaca	420
ttcacccaga	aaaccaggag	ctagtaaggg	tacttcgaga	acagcttcaa	acagaacagg	480
atg cac ctg ctg cca ctc gac agc agt tct aca ctg aca tgt act gtc						528
Met His Leu Leu Pro Leu Asp Ser Ser Ser Thr Leu Thr Cys Thr Val						
1	5	10	15			
cca tct gcc tgc acc aag cct cct tcc cgg tgg aga cca act gtg gac						576
Pro Ser Ala Cys Thr Lys Pro Pro Ser Arg Trp Arg Pro Thr Val Asp						
17	22	27	32			
atc ttt ttt gtg gta acc tta ctc cta aca gta ttt ggt gaa gat gat						624
Ile Phe Phe Val Val Thr Leu Leu Leu Thr Val Phe Gly Glu Asp Asp						
33	38	43	48			
cag tct cag gat gtt ctg aga ttg cat cag gat att aat gat tat aac						672
Gln Ser Gln Asp Val Leu Arg Leu His Gln Asp Ile Asn Asp Tyr Asn						
49	54	59	64			
cgg aga ttc tca ggg caa ccc aga tct att atg gag aga att atg gat						720
Arg Arg Phe Ser Gly Gln Pro Arg Ser Ile Met Glu Arg Ile Met Asp						
65	70	75	80			
cta ccc act tta ctg agg cat gca ttc agg gaa atg ttt tca gtc ggg						768
Leu Pro Thr Leu Leu Arg His Ala Phe Arg Glu Met Phe Ser Val Gly						
81	86	91	96			
ggc ctt ttc tgg atg ttt cgc atc agg ata ata ctt tgt tta atg gga						816
Gly Leu Phe Trp Met Phe Arg Ile Arg Ile Ile Leu Cys Leu Met Gly						
97	102	107	112			

gct ttt ttc tat ctt ata tca cct cta gat ttt gta cct gaa gcc ttg 864
 Ala Phe Phe Tyr Leu Ile Ser Pro Leu Asp Phe Val Pro Glu Ala Leu
 113 118 123 128

 ttt gga att cta ggc ttt cta gat gat ttc ttt gtc atc ttt tta ttg 912
 Phe Gly Ile Leu Gly Phe Leu Asp Asp Phe Phe Val Ile Phe Leu Leu
 129 134 139 144

 ctt atc tac atc tct att atg tat cga gaa gtg ata acc caa agg cta 960
 Leu Ile Tyr Ile Ser Ile Met Tyr Arg Glu Val Ile Thr Gln Arg Leu
 145 150 155 160

 act aga tga aaaagaa aacaaaactg agtttactag gatatctgag ctaatgtaga 1016
 Thr Arg *
 161

 acatcaaaca gaaggaccca tggcagtata aagcaatgaa gcaatggagt attatctcac 1076

 aaatataaaa ccactataag acaaacattt gattatcatt tgacaaatac ctaggtataa 1136

 ctggaaatttt catgttgaa gttctaataat taagtttaga attataatga tctacagtt 1196

 tatcttgatt ctatgttgc tggaaaaat atggaattat ataaaaaggg atgcctttat 1256

 atattttct tttccccaga attacttaga ttaatttagat gtatagtaaa atattgttaa 1316

 atgtcagttt atccatctta tccttctcag caggtaccta tatgataata tatacgatgt 1376

 aaactcatct aaatattttt gttccaataa aatattatata actaaaaaaaaaaaa 1431

<210> 119
 <211> 2236
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (80)..(1369)

<400> 119
 ccgtccggaa ttcccgac gagccacgcg tccgcagaca tggccggcgc aaggagatca 60

 gcaggacgct gcgcacaac atg ggc aac cac ctg ccg ctc ctg cct gca gag 112
 Met Gly Asn His Leu Pro Leu Leu Pro Ala Glu
 1 5

agt gag gaa gaa gat gaa atg gaa gtt gaa gac cag gat agt aaa gaa 160
 Ser Glu Glu Glu Asp Glu Met Glu Val Glu Asp Gln Asp Ser Lys Glu
 12 17 22 27

gcc aaa aaa cca aac atc ata aat ttt gac acc agt ctg ccg acá tca 208
 Ala Lys Lys Pro Asn Ile Ile Asn Phe Asp Thr Ser Leu Pro Thr Ser
 28 33 38 43

cat aca tac cta ggt gct gat atg gaa gaa ttt cat ggc agg act ttg				256
His Thr Tyr Leu Gly Ala Asp Met Glu Glu Phe His Gly Arg Thr Leu				
44	49	54	59	
 cac gat gac gac agc tgt cag gtg att cca gtt ctt cca caa gtg atg				304
His Asp Asp Asp Ser Cys Gln Val Ile Pro Val Leu Pro Gln Val Met				
60	65	70	75	
 atg atc ctg att ccc gga cag aca tta cct ctt cag ctt ttt cac cct				352
Met Ile Leu Ile Pro Gly Gln Thr Leu Pro Leu Gln Leu Phe His Pro				
76	81	86	91	
 caa gaa gtc agt atg gtg cgg aat tta att cag aaa ¹ gat aga acc ttt				400
Gln Glu Val Ser Met Val Arg Asn Leu Ile Gln Lys Asp Arg Thr Phe				
92	97	102	107	
 gct gtt ctt gca tac agc aat gta cag gaa agg gaa gca cag ttt gga				448
Ala Val Leu Ala Tyr Ser Asn Val Gln Glu Arg Glu Ala Gln Phe Gly				
108	113	118	123	
 aca aca gca gag ata tat gcc tat cga gaa gaa cag gat ttt gga att				496
Thr Thr Ala Glu Ile Tyr Ala Tyr Arg Glu Glu Gln Asp Phe Gly Ile				
124	129	134	139	
 gag ata gtg aaa gtg aaa gca att gga aga caa agg ttc aaa gtc ctt				544
Glu Ile Val Lys Val Lys Ala Ile Gly Arg Gln Arg Phe Lys Val Leu				
140	145	150	155	
 gag cta aga aca cag tca gat gga atc cag caa gct aaa gtg caa att				592
Glu Leu Arg Thr Gln Ser Asp Gly Ile Gln Gln Ala Lys Val Gln Ile				
156	161	166	171	
 ctt ccc gaa tgt gtg ttg cct tca acc atg tct gca gtt caa tta gaa				640
Leu Pro Glu Cys Val Leu Pro Ser Thr Met Ser Ala Val Gln Leu Glu				
172	177	182	187	
 tcc ctc aat aag tgc cag ata ttt cct tca aaa cct gtc tca aga gaa				688
Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser Lys Pro Val Ser Arg Glu				
188	193	198	203	
 gac caa tgt tca tat aaa tgg tgg cag aaa tac cag aag aga aag ttt				736
Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys Tyr Gln Lys Arg Lys Phe				
204	209	214	219	
 cat tgt gca aat cta act tca tgg cct cgc tgg ctg tat tcc tta tat				784
His Cys Ala Asn Leu Thr Ser Trp Pro Arg Trp Leu Tyr Ser Leu Tyr				
220	225	230	235	
 gat gct gag acc tta atg gac aga atc aag aaa cag cta cgt gaa tgg				832
Asp Ala Glu Thr Leu Met Asp Arg Ile Lys Lys Gln Leu Arg Glu Trp				
236	241	246	251	
 gat gaa aat cta aaa gat gat tct ctt cct tca aat cca ata gat ttt				880
Asp Glu Asn Leu Lys Asp Asp Ser Leu Pro Ser Asn Pro Ile Asp Phe				
252	257	262	267	

tct tac aga gta gct gct tgt ctt cct att gat gat gta ttg aga att Ser Tyr Arg Val Ala Ala Cys Leu Pro Ile Asp Asp Val Leu Arg Ile 268 273 278 283	928
cag ctc ctt aaa att ggc agt gct atc cag cga ctt cgc tgt gaa tta Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln Arg Leu Arg Cys Glu Leu 284 289 294 299	976
gac att atg aat aaa tgt act tcc ctt tgc tgt aaa caa tgt caa gaa Asp Ile Met Asn Lys Cys Thr Ser Leu Cys Cys Lys Gln Cys Gln Glu 300 305 310 315	1024
aca gaa ata aca acc aaa aat gaa ata ttc agt tta tcc tta tgt ggg Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe Ser Leu Ser Leu Cys Gly 316 321 326 331	1072
ccg atg gca gct tat gtg aat cct cat gga tat gtg cat gag aca ctt Pro Met Ala Ala Tyr Val Asn Pro His Gly Tyr Val His Glu Thr Leu 332 337 342 347	1120
act gtg tat aag gct tgc aac ttg aat ctg ata ggc cgg cct tct aca Thr Val Tyr Lys Ala Cys Asn Leu Asn Leu Ile Gly Arg Pro Ser Thr 348 353 358 363	1168
gaa cac agc tgg ttt cct ggg tat gcc tgg act gtt gcc cag tgt aag Glu His Ser Trp Phe Pro Gly Tyr Ala Trp Thr Val Ala Gln Cys Lys 364 369 374 379	1216
atc tgt gca agc cat att gga tgg aag ttt acg gcc acc aaa aaa gac Ile Cys Ala Ser His Ile Gly Trp Lys Phe Thr Ala Thr Lys Lys Asp 380 385 390 395	1264
atg tca cct caa aaa ttt tgg ggc tta acg cga tct gct ctg ttg ccc Met Ser Pro Gln Lys Phe Trp Gly Leu Thr Arg Ser Ala Leu Leu Pro 396 401 406 411	1312
acg atc cca gac act gaa gat gaa ata agt cca gac aaa gta ata ctt Thr Ile Pro Asp Thr Glu Asp Glu Ile Ser Pro Asp Lys Val Ile Leu 412 417 422 427	1360
tgc ttg taa acagatg tgatagagat aaagtttagtt atctaacaaa ttggttatat Cys Leu *	1416
428	
tctaagatct gctttggaaa ttattgcctc tgatacatac ctaagtaaac ataacattaa	1476
taccttaagta aacataacat tactggagg gttgcagttt ctaagtgaaa ctgtatgttga	1536
aacttttaag tatacttttag gaaacaagca tgaacggcag tctagaatac cagaaacatc	1596
tacttgggta gcttggtgcc attatcctgt ggaatctgat atgtctggta gcatgtcatt	1656
gatgggacat gaagacatct ttggaaatga tgagattatt tcctgtgtta aaaaaaaaaa	1716
aaatcttaaa ttcttacaat gtgaaactga aactaataat ttgatcctga tgtatggac	1776
agcgatctg taccagtgtct ctaaataaca aaagcttaggg tgacaagttac atgttccttt	1836

tggaaagaag caaggcaatg tatattaatt attctaaaag ggctttgttc ctttccattt	1896
tctttaactt ctctgagata ctgatttgc aattttgaaa attagttaaa atatgcagtt	1956
ttttgagccc acgaatagtt gtcatttcct ttatgtgcct gtttagtaaaa agtagtattg	2016
tgtatggct cagtatctga actataagcc catttatact gttccataca aaagctattt	2076
ttcaaaaatt aatttgaacc aaaactacta ctataggaa aagatgccaa aacatgtccc	2136
ctcacccagg ctaaacttga tactgtatta ttttggcaa tgtaaattga agaaaaatctg	2196
taagtaagta aaccttaagt gtgaaactaa aaaaaaaaaa	2236

<210> 120
 <211> 2507
<212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (256)..(2091)

<400> 120

catgcagtac gcgtgccgga actgccgcgg agatcccgac tcgacccacg cgtccgcgg	60
cgcgtgggtc gcccacgcgt ccggccggctg gagcagaagt gttagccggc agagctccc	120
gacccttacc cacagccagg cgggacgcgc acagtcctc cacgcggaaa gaagtacctt	180
cgcgggtcac cggctcctgc agggtgcaaa tatatacaga gcttcataat cagccaaaga	240
ccacatagag caaac atg aat gat att tcc caa aag gct gag att aaa gaa	291
Met Asn Asp Ile Ser Gln Lys Ala Glu Ile Lys Glu	
1 5 10	

atg ctt gct tct gat gat gag gaa gat gta tct tct aaa gta gaa aag	339
Met Leu Ala Ser Asp Asp Glu Glu Asp Val Ser Ser Lys Val Glu Lys	
13 18 23 28	

gct tat gtt cca aaa tta aca gga act gtg aag ggt aga ttt gct gaa	387
Ala Tyr Val Pro Lys Leu Thr Gly Thr Val Lys Gly Arg Phe Ala Glu	
29 34 39 44	

atg gag aaa caa aga caa gag gaa caa agg aag aga acg gag gag gaa	435
Met Glu Lys Gln Arg Gln Glu Glu Gln Arg Lys Arg Thr Glu Glu Glu	
45 50 55 60	

cga aaa cgc aga att gag cag gat atg tta gaa aag agg aaa ata cag	483
Arg Lys Arg Arg Ile Glu Gln Asp Met Leu Glu Lys Arg Lys Ile Gln	
61 66 71 76	

cgt gaa tta gca aaa agg gct gaa cag att gag gac ata aac aat acg	531
---	-----

Arg Glu Leu Ala Lys Arg Ala Glu Gln Ile Glu Asp Ile Asn Asn Thr				
77	82	87	92	
gga act gaa tca gca tca gag gaa gga gat gat tca cta ctt ata act				579
Gly Thr Glu Ser Ala Ser Glu Glu Gly Asp Asp Ser Leu Leu Ile Thr				
93	98	103	108	
gtg gta cct gtc aaa tca tat aaa aca tct gga aaa atg aaa aag aat				627
Val Val Pro Val Lys Ser Tyr Lys Thr Ser Gly Lys Met Lys Lys Asn				
109	114	119	124	
ttt gag gat cta gaa aaa gaa cgt gaa gag aaa gaa agg atc aag tac				675
Phe Glu Asp Leu Glu Lys Glu Arg Glu Glu Lys Glu Arg Ile Lys Tyr				
125	130	135	140	
gag gaa gat aaa aga ata aga tat gaa gaa caa cga cca tct ctc aag				723
Glu Glu Asp Lys Arg Ile Arg Tyr Glu Glu Gln Arg Pro Ser Leu Lys				
141	146	151	156	
gaa gca aag tgt ctt tca tta gtt atg gat gat gaa ata gaa agt gaa				771
Glu Ala Lys Cys Leu Ser Leu Val Met Asp Asp Glu Ile Glu Ser Glu				
157	162	167	172	
gca aaa aaa gaa tca ctt tct ccc gga aaa ttg aaa cta act ttt gaa				819
Ala Lys Lys Glu Ser Leu Ser Pro Gly Lys Leu Lys Leu Thr Phe Glu				
173	178	183	188	
gaa ctg gag cga caa aga caa gaa aac cga aag aag caa gct gaa gag				867
Glu Leu Glu Arg Gln Arg Gln Glu Asn Arg Lys Lys Gln Ala Glu Glu				
189	194	199	204	
gaa gca aga aaa cgt tta gaa gaa gag aag cgt gct ttt gaa gaa gca				915
Glu Ala Arg Lys Arg Leu Glu Glu Lys Arg Ala Phe Glu Glu Ala				
205	210	215	220	
agg cgg caa atg gta aat gaa gat gag gaa aac caa gac aca gca aaa				963
Arg Arg Gln Met Val Asn Glu Asp Glu Glu Asn Gln Asp Thr Ala Lys				
221	226	231	236	
att ttt aaa ggg tac cgc cct ggt aaa ctc aaa ctc agt ttt gaa gaa				1011
Ile Phe Lys Gly Tyr Arg Pro Gly Lys Leu Lys Leu Ser Phe Glu Glu				
237	242	247	252	
atg gaa agg caa aga aga gaa gat gaa aaa agg aaa gca gaa gaa gaa				1059
Met Glu Arg Gln Arg Arg Glu Asp Glu Lys Arg Lys Ala Glu Glu Glu				
253	258	263	268	
gcc aga agg aga ata gag gaa gaa aag aag gcg ttt gct gaa gca agg				1107
Ala Arg Arg Arg Ile Glu Glu Lys Lys Ala Phe Ala Glu Ala Arg				
269	274	279	284	
aga aat atg gta gta gat gat gac tcc cca gag atg tat aag aca atc				1155
Arg Asn Met Val Val Asp Asp Asp Ser Pro Glu Met Tyr Lys Thr Ile				
285	290	295	300	
tct caa gaa ttt ctt aca ccg gga aaa ctg gaa att aat ttt gaa gaa				1203
Ser Gln Glu Phe Leu Thr Pro Gly Lys Leu Glu Ile Asn Phe Glu Glu				

301	306	311	316	
tta tta aaa caa aaa atg gaa gaa gaa aaa cga cga aca gag gag gaa Leu Leu Lys Gln Lys Met Glu Glu Glu Lys Arg Arg Thr Glu Glu Glu 317 322 327 332				1251
cgg aag cat aag cta gaa atg gag aaa caa gaa ttt gaa caa ctg aga Arg Lys His Lys Leu Glu Met Glu Lys Gln Glu Phe Glu Gln Leu Arg 333 338 343 348				1299
cag gaa atg gga gag gaa gag gaa aat gaa acc ttt gga ttg agc Gln Glu Met Gly Glu Glu Glu Asn Glu Thr Phe Gly Leu Ser 349 354 359 364				1347
aga gaa tat gaa gaa ctg atc aaa tta aaa agg agt ggc tct att caa Arg Glu Tyr Glu Glu Leu Ile Lys Leu Lys Arg Ser Gly Ser Ile Gln 365 370 375 380				1395
gct aaa aac cta aaa agc aag ttt gaa aaa att gga cag ttg tct gaa Ala Lys Asn Leu Lys Ser Lys Phe Glu Lys Ile Gly Gln Leu Ser Glu 381 386 391 396				1443
aaa gaa ata cag aaa aaa ata gaa gaa gag cga gca aga agg aga gca Lys Glu Ile Gln Lys Lys Ile Glu Glu Glu Arg Ala Arg Arg Arg Ala 397 402 407 412				1491
att gac ctt gaa att aaa gag cga gaa gct gaa aat ttt cat gag gaa Ile Asp Leu Glu Ile Lys Glu Arg Glu Ala Glu Asn Phe His Glu Glu 413 418 423 428				1539
gat gat gtt gat gtt agg cct gca aga aaa agc gag gct cca ttt act Asp Asp Val Asp Val Arg Pro Ala Arg Lys Ser Glu Ala Pro Phe Thr 429 434 439 444				1587
cac aaa gtg aat atg aaa gct aga ttt gaa caa atg gct aag gca aga His Lys Val Asn Met Lys Ala Arg Phe Glu Gln Met Ala Lys Ala Arg 445 450 455 460				1635
gaa gaa gaa gaa caa aga aga att gaa gaa caa aag tta cta cgc atg Glu Glu Glu Glu Gln Arg Arg Ile Glu Glu Gln Lys Leu Leu Arg Met 461 466 471 476				1683
cag ttt gaa caa agg gaa att gat gca gca cta caa aag aaa aga gaa Gln Phe Glu Gln Arg Glu Ile Asp Ala Ala Leu Gln Lys Lys Arg Glu 477 482 487 492				1731
gag gag gag gag gaa gaa ggt agc atc atg aat ggc tcc act gct gaa Glu Glu Glu Glu Glu Gly Ser Ile Met Asn Gly Ser Thr Ala Glu 493 498 503 508				1779
gat gaa gag caa acc aga tca gga gct cca tgg ttc aag aag cct ctt Asp Glu Glu Gln Thr Arg Ser Gly Ala Pro Trp Phe Lys Lys Pro Leu 509 514 519 524				1827
'aaa aac aca tca gtt gta gac agt gag cca gtc aga ttt acg gtt aaa Lys Asn Thr Ser Val Val Asp Ser Glu Pro Val Arg Phe Thr Val Lys 525 530 535 540				1875

gta aca gga gaa ccc aaa cca gaa att aca tgg tgg ttt gaa gga gaa Val Thr Gly Glu Pro Lys Pro Glu Ile Thr Trp Trp Phe Glu Gly Glu 541 546 551 556	1923
ata ctg cag gat gga gaa gac tat caa tat att gaa agg gga gaa act Ile Leu Gln Asp Gly Glu Asp Tyr Gln Tyr Ile Glu Arg Gly Glu Thr 557 562 567 572	1971
tac tgc ctt tac tta cca gaa act ttc cca gaa gat gga gga gag tat Tyr Cys Leu Tyr Leu Pro Glu Thr Phe Pro Glu Asp Gly Gly Glu Tyr 573 578 583 588	2019
atg tgt aaa gca gtc aac aat aaa gga tct gca gct agt acc tgt att Met Cys Lys Ala Val Asn Asn Lys Gly Ser Ala Ala Ser Thr Cys Ile 589 594 599 604	2067
ctt acc att gaa agt aag aat taa tcactcttt tatctttat tctattaatt Leu Thr Ile Glu Ser Lys Asn * 605 610	2121
ttttttcct taaaatcaact tttttttttc tcttttttag ctgtatgacta ctagctcccc	2181
tccctctcc ctggacttt ctcttcact ccaacttct tactacatcc atctttctg	2241
tggcgcccccc aaaaaaggaa accaggagtg ccactatgct gacttcttat tcctttcat	2301
aacagtcttc aaagcacagc tcatactaaag aatgcctact tctttccaa ataagcatca	2361
gatttatcgc ctattatgca gtaacagtca ataaaaatgta cttatggggg ggaattactc	2421
aattattcta tcagaaccta ttataaagac tgtatccc atagacgtt acagcaacta	2481
tgtttaaaaa aaaaaaaaaa aaaaaaa	2507

<210> 121
<211> 4771
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3023) .. (4771)

<400> 121 atggcaaagc aacttaacct tccagaaaaat acagatgatt ggacaaaaga ggatgtaaat	60
cagtggtag aaagtctataa gattgaccaa aaacacaggg aaattttgac tgaacaagac	120
gtgaatggag cagtctgaa gtggtaaaa aaagaacatc ttgttgatat gggcatcaca	180
catggaccag ctattcaaata agaagaacta ttcaaagaat tgccggaaaac agccattgaa	240
gattcgattc agacatctaa gatggaaag cccagtaaaa atgctcctaa agaccaaact	300

gtgtctcaa	aggaacgtag	agaaaactca	aagcaaaaac	aaaaggtaa	agagaaccca	360
gatatggcta	atccgtctgc	aatgagtaca	actgctaaag	gttctaagtc	actaaaagtt	420
gagctcatag	aagataaaat	agattataca	aaggaaaggc	aaccatccat	agacctgaca	480
tgtgtatcat	atccatttga	tgaattcagt	aatccatatc	gttacaagtt	ggatttttagt	540
ctacagcctg	aaacaggacc	aggcaatctc	attgatccga	tacatgaatt	caaagccttc	600
acaaatacag	caacagccac	agaagaggat	gtcaagatga	aatttagcaa	tgaggtttc	660
cgatttgctt	cagttgtat	gaattcacgt	accaatggca	ctattcattt	tggagtcaaa	720
gacaaacccc	atggaaaaat	tgttggcatc	aaagtcacca	atgataccaa	ggaagccctc	780
attaaccatt	tcaatctgat	gataaaacaag	tattttgaag	accatcaagt	ccaacaagca	840
aagaagtgca	ttcgagagcc	aagatttgc	gaagttttac	tgccaaatag	tactctatct	900
gacagatttg	ttattgaagt	ggacatttatt	ccacagttct	ctgaatgcc	atatgattat	960
ttccagatta	aaatgcaaaa	ttacaacaac	aaaatatggg	aacaaagtaa	aaaattctca	1020
ctatttgtc	gagatggac	cagctctaag	gacattacga	aaaataaagt	tgatttcaga	1080
gcattttaag	cagattttaa	aacactggca	gagtcagaa	aagcagcaga	agaaaaattc	1140
agagcaaaaa	caaataaaaa	agaaagagag	ggaccaaagt	tggttaaatt	attgacagga	1200
aatcaagatt	tgttagataa	ttcatactat	gaacagtaca	ttcttgtaac	aaataaatgc	1260
cacccagatc	aaacaaaaca	cttagatttc	ctgaaggaaa	ttaaatggtt	tgctgtattg	1320
gagtttgatc	ctgagtc当地	catcaatgga	gtggtcaaag	cttacaaaaga	aagccgagta	1380
gcaaacccttc	actttccaag	tgtatatgta	gaacagaaaa	ccacaccaaa	tgagacgatt	1440
tctactctaa	atctttacca	tcaacccagc	tggattttct	gcaatggcag	gttagacctt	1500
gacagtgaaa	aatataaacc	cttgatcca	agttcctggc	aaagagaaag	agcttctgat	1560
gtcaggaaac	tgatttcatt	tcttacacat	gaagacataa	tgccaagagg	gaagtttttg	1620
gtggattttc	tattactgtc	ctctgtggat	gaccaagag	atcccctcat	tgagactttc	1680
tgtgctttct	accaggatct	caaaggaatg	gaaaatatac	tgtgtatttgc	tgtgcacccca	1740
cacatatttc	agggatggaa	agatctactt	gaagcaagat	taataaaaaca	ccaagatgaa	1800
atttcaagcc	aatgtatttc	tgctttaagc	cttgaagaga	tcaatggcac	tattcttaaa	1860
ctaaaatctg	tgactcaatc	ttcaaaaagg	ctttgccat	ctattggttt	atcgactgtc	1920
cttctgaaaa	aggaagaaga	tatcatgact	gctctggaaa	ttatctgtga	aatgaatgt	1980

gagggtacac tgtagagaa ggacaaaaat aaattccttg aattcaaggc atcaaaaagag	2040
gaagacttct atcgaggtgg caaagtgtca tggtaact tctacttctc ttctgaaagt	2100
tattcttcac ctttgtcaa aaggataaa tatgaaagac ttgaagcaat gattcaaaaac	2160
tgtgcagatt cttctaaacc aacaagtacc aaaattattc atctgtatca tcatccaggc	2220
tgtggggaa ctaccttggc tatgcacatt ctctggAAC taaggaagaa attcagatgt	2280
gctgtgctga aaaacaagac agtggattt tctgaaattg gagaacaggt aaccagtttta	2340
atcacctatg gggcaatgaa ccgtcaggaa tacgtacctg tactactcct tggatgat	2400
tttgaagaac aagataatgt ctatcttcg cagtactcta ttcaaacagc tatactaaa	2460
aagtacattc gatatgaaaa acctctggtg attatcctaa attgtatgat atcacaaaaat	2520
cctgaaaaaaaaa gtgcaaggat cccagacagt attgccgtaa tacagcaact ctctccaaa	2580
gaacagagag ctttgagct taaattgaaa gaaatcaaag aacagcataa aaactttgag	2640
gatttttatt ctttatgtat catgaaaacc aattttata aagaatacat agaaaatgtg	2700
gtccggata tcctgaaagg gcagaatatt ttcaccaagg aagcaaagct ctttttttt	2760
ctggctcttc ttaattcata tgtgcctgat accaccattt cactatcaca gtgtgaaaaaa	2820
ttcttaggaa ttggaaacaa gaaggcttc tggggacag aaaaatttga agacaagatg	2880
ggcacctact ctacaattcc tgataaaaac agaggtcatc gaatgtgggactactgtgg	2940
agtacgcattt attcacttt tgattgcaga gttctactg gaagaatttga agaaaagctt	3000
tcacctgaat aaaagtcaaa tt atg ttg gat atg cta act gag aat ttg ttc	3052
Met Leu Asp Met Leu Thr Glu Asn Leu Phe	
1 5	
tcc gat act ggt atg gga aaa agt aaa ttt ttg caa gat atg cac aca	3100
Phe Asp Thr Gly Met Gly Lys Ser Lys Phe Leu Gln Asp Met His Thr	
11 16 21 26	
ctc cta ctc aca aga cac cgc gat gaa cat gaa ggt gaa aca gga aat	3148
Leu Leu Leu Thr Arg His Arg Asp Glu His Glu Gly Glu Thr Gly Asn	
27 32 37 42	
tgg ttt tcc cca ttt att gaa gca tta cat aaa gat gaa gga aat gaa	3196
Trp Phe Ser Pro Phe Ile Glu Ala Leu His Lys Asp Glu Gly Asn Glu	
43 48 53 58	
gca gtt gaa gct gta ttg ctt gaa agt atc cat cgg ttc aac cca aat	3244
Ala Val Glu Ala Val Leu Leu Glu Ser Ile His Arg Phe Asn Pro Asn	
59 64 69 74	
gca ttc att tgc caa gcg ttg gca aga cat ttc tac att aaa aag aag	3292
Ala Phe Ile Cys Gln Ala Leu Ala Arg His Phe Tyr Ile Lys Lys Lys	
75 80 85 90	

gac ttt ggc aat gct cta aac tgg gca aaa caa gca aaa atc ata gaa Asp Phe Gly Asn Ala Leu Asn Trp Ala Lys Gln Ala Lys Ile Ile Glu 91 96 101 106	3340
cct gac aat tct tat atc tca gat aca ctg ggt caa gtc tac aaa agt Pro Asp Asn Ser Tyr Ile Ser Asp Thr Leu Gly Gln Val Tyr Lys Ser 107 112 117 122	3388
aaa ata aga tgg tgg ata gag gaa aac gga gga aac ggg aac att tca Lys Ile Arg Trp Trp Ile Glu Glu Asn Gly Gly Asn Gly Asn Ile Ser 123 128 133 138	3436
gtt gat gat cta att gct ctt ttg gat tta gca gaa cat gcc tca agt Val Asp Asp Leu Ile Ala Leu Leu Asp Leu Ala Glu His Ala Ser Ser 139 144 149 154	3484
gca ttc aaa gaa tct caa cag caa agt gaa gat aga gag tat gaa gtg Ala Phe Lys Glu Ser Gln Gln Ser Glu Asp Arg Glu Tyr Glu Val 155 160 165 170	3532
aag gaa aga ttg tat ccg aag tca aaa agg cggt tat gat act tac aat Lys Glu Arg Leu Tyr Pro Lys Ser Lys Arg Arg Tyr Asp Thr Tyr Asn 171 176 181 186	3580
ata gct ggt tat caa gga gag ata gaa gtt ggg ctt tac aca atc caa Ile Ala Gly Tyr Gln Gly Glu Ile Glu Val Gly Leu Tyr Thr Ile Gln 187 192 197 202	3628
att ctc cag ctc att cct ttt gat aat aaa aat gag cta tct aaa Ile Leu Gln Leu Ile Pro Phe Phe Asp Asn Lys Asn Glu Leu Ser Lys 203 208 213 218	3676
aga tat atg gtc aat ttt gta tca gga agt agt gat att cca ggg gat Arg Tyr Met Val Asn Phe Val Ser Gly Ser Ser Asp Ile Pro Gly Asp 219 224 229 234	3724
cca aac aat gaa tat aaa tta gcc ctc aaa aac tat att cct tat tta Pro Asn Asn Glu Tyr Lys Leu Ala Leu Lys Asn Tyr Ile Pro Tyr Leu 235 240 245 250	3772
act aaa ttg aaa ttt tct ttg aaa aag tcc ttt gat ttt ttt gat gaa Thr Lys Leu Lys Phe Ser Leu Lys Lys Ser Phe Asp Phe Phe Asp Glu 251 256 261 266	3820
tac ttt gtc ctg cta aaa ccc agg aac aat att aag caa aat gaa gag Tyr Phe Val Leu Leu Lys Pro Arg Asn Asn Ile Lys Gln Asn Glu Glu 267 272 277 282	3868
gcc aaa act cgg aga aag gtg gct gga tat ttt aag aaa tat gta gat Ala Lys Thr Arg Arg Lys Val Ala Gly Tyr Phe Lys Lys Tyr Val Asp 283 288 293 298	3916
ata ttt tgt ctc tta gaa gaa tca caa aac aac aca ggt ctt gga tca Ile Phe Cys Leu Leu Glu Glu Ser Gln Asn Asn Thr Gly Leu Gly Ser 299 304 309 314	3964

aag ttc agt gag cca ctt caa gta gag aga tgc agg aga aac cta gta Lys Phe Ser Glu Pro Leu Gln Val Glu Arg Cys Arg Arg Asn Leu Val 315 320 325 330	4012
gct tta aaa gca gac aag ttt tct ggg ctc ttg gaa tat ctt atc aaa Ala Leu Lys Ala Asp Lys Phe Ser Gly Leu Leu Glu Tyr Leu Ile Lys 331 336 341 346	4060
agt caa gag gat gct ata agc act atg aaa tgt ata gtg aac gaa tat Ser Gln Glu Asp Ala Ile Ser Thr Met Lys Cys Ile Val Asn Glu Tyr 347 352 357 362	4108
act ttt ctc tta gaa caa tgc act gtc aaa atc cag tca aaa gaa aag Thr Phe Leu Leu Glu Gln Cys Thr Val Lys Ile Glu Ser Lys Glu Lys 363 368 373 378	4156
cta aat ttc atc ttg gcc aac att att ctc tcc tgt atc caa cct acc Leu Asn Phe Ile Leu Ala Asn Ile Ile Leu Ser Cys Ile Gln Pro Thr 379 384 389 394	4204
tcc aga tta gta aag cca gtt gaa aaa cta aaa gat cag ctt cga gaa Ser Arg Leu Val Lys Pro Val Glu Lys Leu Lys Asp Gln Leu Arg Glu 395 400 405 410	4252
gtc ttg caa cca ata gga ctg act tat cag ttt tca gaa ccg tat ttt Val Leu Gln Pro Ile Gly Leu Thr Tyr Gln Phe Ser Glu Pro Tyr Phe 411 416 421 426	4300
cta gct tcc ctc tta ttc tgg cca gaa aat caa caa cta gat caa cat Leu Ala Ser Leu Leu Phe Trp Pro Glu Asn Gln Gln Leu Asp Gln His 427 432 437 442	4348
tct gaa caa atg aaa gag tat gct caa gca cta aaa aat tct ttc aag Ser Glu Gln Met Lys Glu Tyr Ala Gln Ala Leu Lys Asn Ser Phe Lys 443 448 453 458	4396
ggg caa tat aaa cat atg cat cgt aca aag caa cca att gca tat ttc Gly Gln Tyr Lys His Met His Arg Thr Lys Gln Pro Ile Ala Tyr Phe 459 464 469 474	4444
ttt ctt gga aaa ggt aaa aga ctg gaa aga ctt gtt cac aaa gga aaa Phe Leu Gly Lys Gly Lys Arg Leu Glu Arg Leu Val His Lys Gly Lys 475 480 485 490	4492
att gac cag tgc ttt aag aag aca cca gat att aat tcc ttg tgg cag Ile Asp Gln Cys Phe Lys Lys Thr Pro Asp Ile Asn Ser Leu Trp Gln 491 496 501 506	4540
agt ggå gat gtg tgg aag gag gaa aaa gtc caa gaa ctt ttg ctt cgt Ser Gly Asp Val Trp Lys Glu Glu Lys Val Gln Glu Leu Leu Leu Arg 507 512 517 522	4588
tta caa ggt cga gct gaa aac aat tgt tat ata gaa tat gga atc, Leu Gln Gly Arg Ala Glu Asn Asn Cys Leu Tyr Ile Glu Tyr Gly Ile 523 528 533 538	4636
aat gaa aaa atc aca ata ccc atc act ccc gct ttt tta ggt caa ctt	4684

Asn Glu Lys Ile Thr Ile Pro Ile Thr Pro Ala Phe Leu Gly Gln Leu			
539	544	549	554
aga agt ggc aga agc ata gag aag gtg tct ttt tac ctg gga ttt tcc			4732
Arg Ser Gly Arg Ser Ile Glu Lys Val Ser Phe Tyr Leu Gly Phe Ser			
555	560	565	570
att gga ggc cca ctt gct tat gac att gaa att gtt taa			4771
Ile Gly Gly Pro Leu Ala Tyr Asp Ile Glu Ile Val *			
571	576	581	
<210> 122			
<211> 1470			
<212> DNA			
<213> Homo sapiens			
<220>			
<221> CDS			
<222> (141)..(869)			
<400> 122			
tttgagcac gctgtaccgg tccggaattc ccgggtcgac ccacgcgtcc gcccacgcgt			60
ccgccttagc cagagaactg ggtgcacatctg agccagtgg aatttgtgac ttctccttct			120
tctaggagtg cgtgatcaga atg gtg tct gga cgg ttc tac ttg tcc tgc			170
Met Val Ser Gly Arg Phe Tyr Leu Ser Cys			
1	5		
ctg ctg ctg ggg tcc ctg ggc tct atg tgc atc ctc ttc act atc tac			218
Leu Leu Leu Gly Ser Leu Gly Ser Met Cys Ile Leu Phe Thr ile Tyr			
11	16	21	26
tgg atg cag tac tgg cgt ggt ggc ttt gcc tgg aat ggc agc atc tac			266
Trp Met Gln Tyr Trp Arg Gly Gly Phe Ala Trp Asn Gly Ser Ile Tyr			
27	32	37	42
atg ttc aac tgg cac cca gtg ctt atg gtt gct ggc atg gtg gta ttc			314
Met Phe Asn Trp His Pro Val Leu Met Val Ala Gly Met Val Val Phe			
43	48	53	58
tat gga ggt gcg tca ctg gtg tac cgc ctg ccc cag tcg tgg gtg ggg			362
Tyr Gly Gly Ala Ser Leu Val Tyr Arg Leu Pro Gln Ser Trp Val Gly			
59	64	69	74
ccc aaa ctg ccc tgg aaa ctc ctc cat gca gcg ctg cac ctg atg gcc			410
Pro Lys Leu Pro Trp Lys Leu Leu His Ala Ala Leu His Leu Met Ala			
75	80	85	90
ttc gtc ctc act gtt gtg ggg ctg gtt gct gtc ttt acg ttt cac aac			458
Phe Val Leu Thr Val Val Gly Leu Val Ala Val Phe Thr Phe His Asn			
91	96	101	106

cat gga agg act gcc aac ctc tac tcc ctt cac agc tgg ctg ggc atc His Gly Arg Thr Ala Asn Leu Tyr Ser Leu His Ser Trp Leu Gly Ile 107 112 117 122	506
acc act gtc ttc ctc ttc gcc tgc cag tgg ttc ctg ggc ttt gct gtc Thr Thr Val Phe Leu Phe Ala Cys Gln Trp Phe Leu Gly Phe Ala Val 123 128 133 138	554
ttc ctc ctg ccc tgg gcg tcc atg tgg ctg cgc agc ctc cta aaa cct Phe Leu Leu Pro Trp Ala Ser Met Trp Leu Arg Ser Leu Leu Lys Pro 139 144 149 154	602
atc cac gtc ttt ttt gga gcc gcc atc ctc tct ctg tcc atc gca tcc Ile His Val Phe Phe Gly Ala Ala Ile Leu Ser Leu Ser Ile Ala Ser 155 160 165 170	650
gtc att tcg ggc att aat gag aag ctt ttc ttc agt ttg aaa aac acc Val Ile Ser Gly Ile Asn Glu Lys Leu Phe Phe Ser Leu Lys Asn Thr 171 176 181 186	698
acc agg cca tac cac agc ctg ccc agt gag gcg gtc ttt gcc aac agc Thr Arg Pro Tyr His Ser Leu Pro Ser Glu Ala Val Phe Ala Asn Ser 187 192 197 202	746
acc ggg atg ctg gtg gtg gcc ttt ggg ctg ctg gtg ctc tac atc ctt Thr Gly Met Leu Val Val Ala Phe Gly Leu Leu Val Leu Tyr Ile Leu 203 208 213 218	794
ctg gct tca tct tgg aag cgc cca gag ccg ggg atc ctg acc gac aga Leu Ala Ser Ser Trp Lys Arg Pro Glu Pro Gly Ile Leu Thr Asp Arg 219 224 229 234	842
cag ccc ctg ctg cat gat ggg gag tga agcag caggaagggg ctccccaaagag Gln Pro Leu Leu His Asp Gly Glu *	894
235 240	
ctccctgggtgg tgcagccctgt gctccctca gaagctctgc tcttcccagg gctccggct	954
ggtttcagca ggccgactttc ttccaatgct gggcccagac ttcttgctg ggtgctggcc	1014
tgcctctcc ggccgcttgc tgcctgtctg ctttccttgg tggctttgcg tgggtgctgg	1074
gcctgccttc tctggctgct tgctgcctgt ctgcttcct tggtggttt ggcttctgca	1134
ctccttggcg tcagcccttc aggtcccaag cttcagactg ctgtgcttag taagcaagtg	1194
agaaggcctgg ggtttggagc ccacctactc tctggcagca tcagcatcct actcctggca	1254
acatcaggcc aacgtccacc ccagcctcac attgccagat gttggcagaa gggctaataat	1314
tgaccgtctt gactggctgg agccttcaa gcccactggga tgtcctccag gcacctgggt	1374
cccatgacca gctccccgtc tccatagggg taggcatttc actggtttat gaagctcgag	1434
tttcattaaa tatgttaaga atcaaaaaaaa aaaaaaa	1470

<210> 123
<211> 1650
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (88)..(1005)

<400> 123

ccggccgagct	cgctgtggcc	cggatgttcg	gtgcagctgc	cagatccgct	gatctagcgc	60
ttctcgaaaa	aaacaccttag	gcggcccc	atg gca tgc ctt gga ctt tat tgt	Met Ala Cys Leu Gly Leu Tyr Cys	111	
			1	5		
ggg aag acc cta tta ttt aaa aat ggc tca act gaa ata tat gga gaa	Gly Lys Thr Leu Leu Phe Lys Asn Gly Ser Thr Glu Ile Tyr Gly Glu	159				
9	14		19	24		
tgt ggg gta tgc cca aga gga cag aga acg aat gca cag aaa tat tgt	Cys Gly Val Cys Pro Arg Gly Gln Arg Thr Asn Ala Gln Lys Tyr Cys	207				
25	30		35	40		
cag cct tgc aca gaa tct cct gaa ctt tat gat tgg ctc tat ctt gga	Gln Pro Cys Thr Glu Ser Pro Glu Leu Tyr Asp Trp Leu Tyr Leu Gly	255				
41	46		51	56		
ttt atg gca atg ctt cct ctg gtt tta cat tgg ttc att gaa tgg	Phe Met Ala Met Leu Pro Leu Val Leu His Trp Phe Phe Ile Glu Trp	303				
57	62		67	72		
tac tcg ggg aaa aag agt tcc agc gca ctt ttc caa cac atc act gca	Tyr Ser Gly Lys Ser Ser Ala Leu Phe Gln His Ile Thr Ala	351				
73	78		83	88		
tta ttt gaa tgc agc atg gca gct att atc acc tta ctt gtg agt gat	Leu Phe Glu Cys Ser Met Ala Ala Ile Ile Thr Leu Leu Val Ser Asp	399				
89	94		99	104		
cca gtt ggt gtt ctt tat att cgt tca tgt cga gta ttg atg ctt tct	Pro Val Gly Val Leu Tyr Ile Arg Ser Cys Arg Val Leu Met Leu Ser	447				
105	110		115	120		
gac tgg tac acg atg ctt tac aac cca agt cca gat tac gtt acc aca	Asp Trp Tyr Thr Met Leu Tyr Asn Pro Ser Pro Asp Tyr Val Thr Thr	495				
121	126		131	136		
gta cac tgt act cat gaa gcc gtc tac cca cta tat acc att gta ttt	Val His Cys Thr His Glu Ala Val Tyr Pro Leu Tyr Thr Ile Val Phe	543				
137	142		147	152		
atc tat tac gca ttc tgc ttg gta tta atg atg ctg ctc cga cct ctt	Ile Tyr Tyr Ala Phe Cys Leu Val Leu Met Met Leu Leu Arg Pro Leu	591				
153	158		163	168		

ctg gtg aag aag att gca tgt ggg tta ggg aaa tct gat cga ttt aaa Leu Val Lys Lys Ile Ala Cys Gly Leu Gly Lys Ser Asp Arg Phe Lys 169 174 179 184	639
agt att tat gct gca ctt tac ttc ttc cca att tta acc gtg ctt cag Ser Ile Tyr Ala Ala Leu Tyr Phe Phe Pro Ile Leu Thr Val Leu Gln 185 190 195 200	687
gca gtt ggt gga ggc ctt tta tat tac gcc ttc cca tac att ata tta Ala Val Gly Gly Leu Leu Tyr Tyr Ala Phe Pro Tyr Ile Ile Leu 201 206 211 216	735
gtg tta tct ttg gtt act ctg gct gtg tac atg tct gct tct gaa ata Val Leu Ser Leu Val Thr Leu Ala Val Tyr Met Ser Ala Ser Glu Ile 217 222 227 232	783
gag aac tgc tat gat ctt ctg gtc aga aag aaa aga ctt att gtt ctc Glu Asn Cys Tyr Asp Leu Leu Val Arg Lys Lys Arg Leu Ile Val Leu 233 238 243 248	831
ttc agc cac tgg tta ctt cat gcc tat gga ata atc tcc att tcc aga Phe Ser His Trp Leu Leu His Ala Tyr Gly Ile Ile Ser Ile Ser Arg 249 254 259 264	879
gtg gat aaa ctt gag caa gat ttg ccc ctt ttg gct ttg gta cct aca Val Asp Lys Leu Glu Gln Asp Leu Pro Leu Leu Ala Leu Val Pro Thr 265 270 275 280	927
cca gcc ctt ttt tac ttg ttc act gca aaa ttt acc gaa cct tca agg Pro Ala Leu Phe Tyr Leu Phe Thr Ala Lys Phe Thr Glu Pro Ser Arg 281 286 291 296	975
ata ctc tca gaa gga gcc aat gga cac tga g tgttagacatg tgaaatgcc Ile Leu Ser Glu Gly Ala Asn Gly His *	1026
297 302	
aaaacctgag aagtgcctt aataaaaaag taaatcaatc ttaacagtgt atgagaacta	1086
ttctatcata tatggaca agattgtcag tatatcttaa tgtttgggtt tgtctttgtt	1146
ttgttatgg ttagacttac agacttggaa aatgcaaaac tctgtataac tctgttacac	1206
aggtaatat tatctgctac actggaaggc cgcttaggaag cccttgcttc tctcaacagt	1266
tcaagctgttc tttagggcaa aatcatgtt ctgtgtaccc agcaatgtt tccatttttta	1326
ttaagaaaaag ctttaacacg tgtaatctgc agtcottaac agtggcgtaa ttgtacgtac	1386
ctgttgtt tcagttgtt ttccacctat aatgaattgt aaaaacaaac atacttgttgg	1446
ggtctgatag caaacataga aatgatgtat attgtttttt gttatctatt tattttcatc	1506
aatacagtat tttgatgtat tgcaaaaata gataataatt tatataacag gttttctgtt	1566
tatagattgg ttcaagattt gtttggatta ttgttcctgt aaagaaaaaca ataataaaaa	1626

gcttacctac ataaaaaaaaaaa aaaa

1650

<210> 124
<211> 1534
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(1334)

<400> 124

ggaattcttt	ctgtcttgcc	ttgcagttat	aagttttaaa	ggttttat	ttgtcttctg	60
ctttaggcaa	tcctttatca	caggatattc	tcaacttata	ccaggacc	ca gatggAACCC	120
gaaagctact	gaacttc	atg ctt gac aat ctc	gca gtt cat cca	gag cag	Met Leu Asp Asn Leu Ala Val His Pro Glu Gln	170
		1		5		
ctt cct ccg agg cca tgg att aca tta aaa gaa	cga gac caa att ctg					218
Leu Pro Pro Arg Pro Trp Ile Thr Leu Lys	Glu Arg Asp Gln Ile Leu	12	17	22	27	
ccg tca gca tca ttc acg gtt atg tgt tac aat	gtg tta tgt gat aaa					266
Pro Ser Ala Ser Phe Thr Val Met Cys Tyr Asn Val Leu Cys Asp Lys		28	33	38	43	
tac gct acc cgg cag cta tat ggc tat tgc cca tcc tgg	gca tta aac					314
Tyr Ala Thr Arg Gln Leu Tyr Gly Tyr Cys Pro Ser Trp Ala Leu Asn		44	49	54	59	
tgg gaa tac agg aaa aag gga att atg gaa gaa att	gtt aac tgt gac					362
Trp Glu Tyr Arg Lys Lys Gly Ile Met Glu Glu Ile Val Asn Cys Asp		60	65	70	75	
gca gat atc att agt ctt cag gaa gtg gaa aca gag caa	tac ttc act					410
Ala Asp Ile Ile Ser Leu Gln Glu Val Thr Glu Gln Tyr Phe Thr		76	81	86	91	
ctc ttt ctg cca gca ttg aag gag cgt gga tat gat	gga ttt ttt tct					458
Leu Phe Leu Pro Ala Leu Lys Glu Arg Gly Tyr Asp Gly Phe Phe Ser		92	97	102	107	
cca aag tca cgt gcc aaa atc atg tct gag cag gag aga	aag cat gta					506
Pro Lys Ser Arg Ala Lys Ile Met Ser Glu Gln Glu Arg Lys His Val		108	113	118	123	
gat ggt tgt gca ata ttc ttc aaa aca gaa aaa ttt aca ttg	gtg cag					554
Asp Gly Cys Ala Ile Phe Phe Lys Thr Glu Lys Phe Thr Leu Val Gln		124	129	134	139	
aag cat aca gtg gaa ttt aac caa gtg gcg atg gct aat	tca gat gga					602
Lys His Thr Val Glu Phe Asn Gln Val Ala Met Ala Asn Ser Asp Gly						

140	145	150	155	
tcc gaa gct atg ctg aac aga gtg atg aca aaa gat aac att ggt gtc Ser Glu Ala Met Leu Asn Arg Val Met Thr Lys Asp Asn Ile Gly Val				650
156	161	166	171	
gct gtg gta tta gag gtc cac aaa gaa cta ttt gga gca ggt atg aag Ala Val Val Leu Glu Val His Lys Glu Leu Phe Gly Ala Gly Met Lys				698
172	177	182	187	
cct att cat gct gca gac aaa cag ctg ctt ata gtg gca aat gcc cac Pro Ile His Ala Ala Asp Lys Gln Leu Leu Ile Val Ala Asn Ala His				746
188	193	198	203	
atg cat tgg gac cca gag tat tct gat gtg aag ctc atc cag acc atg Met His Trp Asp Pro Glu Tyr Ser Asp Val Lys Leu Ile Gln Thr Met				794
204	209	214	219	
atg ttt gtc tca gag gtt aaa aac att ctg gag aaa gcc tct agt agg Met Phe Val Ser Glu Val Lys Asn Ile Leu Glu Lys Ala Ser Ser Arg				842
220	225	230	235	
cct gga agc cca act gca gat cct aat tcc atc ccg ctg gtg cta tgt Pro Gly Ser Pro Thr Ala Asp Pro Asn Ser Ile Pro Leu Val Leu Cys				890
236	241	246	251	
gca gat ctt aac tca ttg cca gat tca ggt gtt gtg gaa tac tta agc Ala Asp Leu Asn Ser Leu Pro Asp Ser Gly Val Val Glu Tyr Leu Ser				938
252	257	262	267	
aat gga gga gta gct gac aac cat aaa gac ttc aag gaa cta agg tac Asn Gly Gly Val Ala Asp Asn His Lys Asp Phe Lys Glu Leu Arg Tyr				986
268	273	278	283	
aat gag tgt ctt atg aac ttc agc tgc aat gga aag aat gga agc tca Asn Glu Cys Leu Met Asn Phe Ser Cys Asn Gly Lys Asn Gly Ser Ser				1034
284	289	294	299	
gaa ggg aga atc aca cat ggc ttc caa ctt aag agc gcc tat gaa aat Glu Gly Arg Ile Thr His Gly Phe Gln Leu Lys Ser Ala Tyr Glu Asn				1082
300	305	310	315	
aac ttg atg cct tac acc aat tac acc ttt gat ttc aaa ggc gtg att Asn Leu Met Pro Tyr Thr Asn Tyr Thr Phe Asp Phe Lys Gly Val Ile				1130
316	321	326	331	
gac tac att ttc tat tcc aag act cat atg aac gtg ctt ggt gtc ctg Asp Tyr Ile Phe Tyr Ser Lys Thr His Met Asn Val Leu Gly Val Leu				1178
332	337	342	347	
ggg cct tta gat cct caa tgg ctg gtt gag aac aac atc act ggg tgt Gly Pro Leu Asp Pro Gln Trp Leu Val Glu Asn Asn Ile Thr Gly Cys				1226
348	353	358	363	
cca cac cct cac atc cct tca gac cac ttc tca ctg tta aca caa ctt Pro His Pro His Ile Pro Ser Asp His Phe Ser Leu Leu Thr Gln Leu				1274
364	369	374	379	

gaa ctc cac cct cca ctc ctg cct ctt gtc aat ggt gtt cac ttg cct	1322
Glu Leu His Pro Pro Leu Leu Pro Leu Val Asn Gly Val His Leu Pro	
380 . 385 390 395	
aat cg ^g agg tag tgg agtactgcccgcccaagacggggatctgtt gctatggacc	1377
Asn Arg Arg *	
396	
tgtacagttg taaatcaaag tatgttaggag tgaagtatgg ccattcctaa gctgcttctt	1437
caggtttctt tcatttatgtg gttgctgtaa gactttgtac atttttgtgc atattggat	1497
catttggcag tagggctgga accaaagtat tactctt	1534

<210> 125
 <211> 2850
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (635) .. (2422)

<400> 125

cggttcgacg atttcgtact atacctaatac tgccctggaac taaatccaga tctaggctct	60
actttttattt attccattct tgcaatgatt gaatgacctt ctctttgtta aaaaatttgag	120
ctatagttta cataccatca aattcaccct tttgatgtat acaactcagg ggtgattagt	180
atattcacaa aagggtgtct agcatcacca ctgtctcatt ttggagcatt ttcatgcccc	240
caccatgaag accatgtcca ctggcagcca ttcccatgac ctttccttgt gagatctcca	300
gttatactt tgcacaagct gatgaattgc tgttcttgat aatactgagc tttcacaatc	360
acagttgcca gagaaacatc agcgggcttt agctggggca gagcttagca agtgttgggg	420
tatcagcagt tagtcaactgt ttgcctggaa ccacaggatg tgaatccttag ttccctggatt	480
ccaaggaatc ctgcatccag gtgtttattt tgctttgcag agtcaacatc aagctcagga	540
gctggttgca gacatagatg agtgtgaagt ttctggcctg tgcaggcatg gagggcgatg	600
cgtgaacact catggagact ttgaatgcta ctgt atg gat gga tac ttg cca	652
Met Asp Gly Tyr Leu Pro	
1	

agg aat gga cct gaa cct ttc cac ccg acc acc gat gcc aca tca tgc	700
Arg Asn Gly Pro Glu Pro Phe His Pro Thr Thr Asp Ala Thr Ser Cys	
7 12 17 22	

aca gaa ata gac tgt ggt acc cct cct gag gtt cca gat ggc tat atc	748
---	-----

Thr	Glu	Ile	Asp	Cys	Gly	Thr	Pro	Pro	Glu	Val	Pro	Asp	Gly	Tyr	Ile	
23																38
ata	gga	aat	tat	acg	tct	agt	ctg	ggc	agc	cag	gtt	cgt	tat	gct	tgc	796
Ile	Gly	Asn	Tyr	Thr	Ser	Ser	Leu	Gly	Ser	Gln	Val	Arg	Tyr	Ala	Cys	
39																54
aga	gaa	gga	tcc	tcc	agt	gtt	cca	gaa	gat	aca	gtt	tca	agc	tgc	aca	844
Arg	Glu	Gly	Phe	Phe	Ser	Ser	Val	Pro	Glu	Asp	Thr	Val	Ser	Ser	Cys	
55																70
ggc	ctg	ggc	aca	tgg	gag	tcc	cca	aaa	tta	cat	tgc	caa	gag	atc	aac	892
Gly	Leu	Gly	Thr	Trp	Glu	Ser	Pro	Lys	Leu	His	Cys	Gln	Glu	Ile	Asn	
71																86
tgt	ggc	aac	cct	cca	gaa	atg	cgg	cac	gcc	atc	ttg	gta	gga	aat	cac	940
Cys	Gly	Asn	Pro	Pro	Glu	Met	Arg	His	Ala	Ile	Leu	Val	Gly	Asn	His	
87																102
agc	tcc	agg	ctg	ggc	ggt	gtg	gct	cgc	tat	gtc	tgt	caa	gag	ggc	ttt	988
Ser	Ser	Arg	Leu	Gly	Gly	Val	Ala	Arg	Tyr	Val	Cys	Gln	Glu	Gly	Phe	
103																118
gag	agc	cct	gga	gga	aag	atc	act	tct	gtc	aca	gag	aaa	ggc	acc		1036
Glu	Ser	Pro	Gly	Gly	Lys	Ile	Thr	Ser	Val	Cys	Thr	Glu	Lys	Gly	Thr	
119																134
tgg	aga	gaa	agt	act	tta	aca	tgc	aca	gaa	att	ctg	aca	aag	att	aat	1084
Trp	Arg	Glu	Ser	Thr	Leu	Thr	Cys	Thr	Glu	Ile	Leu	Thr	Lys	Ile	Asn	
135																150
gat	gta	tca	ctg	ttt	aat	gat	acc	tgt	gtg	aga	tgg	caa	ata	aac	tca	1132
Asp	Val	Ser	Leu	Phe	Asn	Asp	Thr	Cys	Val	Arg	Trp	Gln	Ile	Asn	Ser	
151																166
aga	aga	ata	aac	ccc	aag	atc	tca	tat	gtg	ata	tcc	ata	aaa	gga	caa	1180
Arg	Arg	Ile	Asn	Pro	Lys	Ile	Ser	Tyr	Val	Ile	Ser	Ile	Lys	Gly	Gln	
167																182
cgg	ttg	gac	cct	atg	gaa	tca	gtt	cgt	gag	aca	gtc	aac	ttg	acc		1228
Arg	Leu	Asp	Pro	Met	Glu	Ser	Val	Arg	Glu	Glu	Thr	Val	Asn	Leu	Thr	
183																198
aca	gac	agc	agg	acc	cca	gaa	gtg	tgc	cta	gcc	ctg	tac	cca	ggc	acc	1276
Thr	Asp	Ser	Arg	Thr	Pro	Glu	Val	Cys	Leu	Ala	Leu	Tyr	Pro	Gly	Thr	
199																214
aac	tac	acc	gtg	aac	atc	tcc	aca	gca	cct	ccc	agg	cgc	tcg	atg	cca	1324
Asn	Tyr	Thr	Val	Asn	Ile	Ser	Thr	Ala	Pro	Pro	Arg	Arg	Ser	Met	Pro	
215																230
gcc	gtc	atc	ggt	ttc	cag	aca	gct	gaa	gtt	gat	ctc	tta	gaa	gat	gat	1372
Ala	Val	Ile	Gly	Phe	Gln	Thr	Ala	Glu	Val	Asp	Leu	Leu	Glu	Asp	Asp	
231																246
gga	agt	ttc	aat	att	tca	ata	ttt	aat	gaa	act	tgt	ttg	aaa	ttg	aac	1420
Gly	Ser	Phe	Asn	Ile	Ser	Ile	Phe	Asn	Glu	Thr	Cys	Leu	Lys	Leu	Asn	

247	252	257	262	
agg cgt tct agg aaa gtt gga tca gaa cac atg tac caa ttt acc gtt Arg Arg Ser Arg Lys Val Gly Ser Glu His Met Tyr Gln Phe Thr Val 263 268 273 278				1468
ctg ggt cag agg tgg tat ctg gct aac ttt tct cat gca aca tcg ttt Leu Gly Gln Arg Trp Tyr Leu Ala Asn Phe Ser His Ala Thr Ser Phe 279 284 289 294				1516
aac ttc aca acg agg gaa caa gtg cct gta gtg tgt ttg gat ctg tac Asn Phe Thr Thr Arg Glu Gln Val Pro Val Val Cys Leu Asp Leu Tyr 295 300 305 310				1564
cct acg act gat tat acg gtg aat gtg acc ctg ctg aga tct cct aag Pro Thr Thr Asp Tyr Thr Val Asn Val Thr Leu Leu Arg Ser Pro Lys 311 316 321 326				1612
cg g cac tca gtg caa ata aca ata gca act ccc cca gca gta aaa cag Arg His Ser Val Gln Ile Thr Ile Ala Thr Pro Pro Ala Val Lys Gln 327 332 337 342				1660
acc atc agt aac att tca gga ttt aat gaa acc tgc ttg aga tgg aga Thr Ile Ser Asn Ile Ser Gly Phe Asn Glu Thr Cys Leu Arg Trp Arg 343 348 353 358				1708
agc atc aag aca gct gat atg gag gag atg tat tta ttc cac att tgg Ser Ile Lys Thr Ala Asp Met Glu Glu Met Tyr Leu Phe His Ile Trp 359 364 369 374				1756
ggc cag aga tgg tat cag aag gaa ttt gcc cag gaa atg acc ttt aat Gly Gln Arg Trp Tyr Gln Lys Glu Phe Ala Gln Glu Met Thr Phe Asn 375 380 385 390				1804
atc agt agc agc cga gat ccc gag gtg tgc ttg gac cta cgt ccg Ile Ser Ser Ser Arg Asp Pro Glu Val Cys Leu Asp Leu Arg Pro 391 396 401 406				1852
gg t acc aac tac aat gtc agt ctc cgg gct ctg tct tcg gaa ctt cct Gly Thr Asn Tyr Asn Val Ser Leu Arg Ala Leu Ser Ser Glu Leu Pro 407 412 417 422				1900
gtg gtc atc tcc ctg aca acc cag ata aca gag cct ccc ctc ccg gaa Val Val Ile Ser Leu Thr Thr Gln Ile Thr Glu Pro Pro Leu Pro Glu 423 428 433 438				1948
gta gaa ttt ttt acg gtg cac aga gga cct cta cca cgc ctc aga ctg Val Glu Phe Phe Thr Val His Arg Gly Pro Leu Pro Arg Leu Arg Leu 439 444 449 454				1996
agg aaa gcc aag gag aaa aat gga cca atc agt tca tat cag gtg tta Arg Lys Ala Lys Glu Lys Asn Gly Pro Ile Ser Ser Tyr Gln Val Leu 455 460 465 470				2044
gtg ctt ccc ctg gcc ctc caa agc aca ttt tct tgt gat tct gaa ggc Val Leu Pro Leu Ala Leu Gln Ser Thr Phe Ser Cys Asp Ser Glu Gly 471 476 481 486				2092

gct tcc tcc ttc ttt agc aac gcc tct gat gct gat gga tac gtg gct Ala Ser Ser Phe Phe Ser Asn Ala Ser Asp Ala Asp Gly Tyr Val Ala 487 492 497 502	2140
gca gaa cta ctg gcc aaa gat gtt cca gat gat gcc atg gag ata cct Ala Glu Leu Leu Ala Lys Asp Val Pro Asp Asp Ala Met Glu Ile Pro 503 508 513 518	2188
ata gga gac agg ctg tac tat ggg gaa tat tat aat gca ccc ttg aaa Ile Gly Asp Arg Leu Tyr Tyr Gly Glu Tyr Tyr Asn Ala Pro Leu Lys 519 524 529 534	2236
aga ggg agt gat tac tgc att ata tta cga atc ac ^a agt gaa tgg aat Arg Gly Ser Asp Tyr Cys Ile Ile Leu Arg Ile Thr Ser Glu Trp Asn 535 540 545 550	2284
aag gtg aga aga cac tcc tgt gca gtt tgg gct cag gtg aaa gat tcg Lys Val Arg Arg His Ser Cys Ala Val Trp Ala Gln Val Lys Asp Ser 551 556 561 566	2332
tca ctc atg ctg ctg cag atg gcg ggt gtt gga ctg ggt tcc ctg gct Ser Leu Met Leu Leu Gln Met Ala Gly Val Gly Leu Gly Ser Leu Ala 567 572 577 582	2380
gtt gtg atc att ctc aca ttc ctc tcc ttc tca gcg gtg tga tggcaga Val Val Ile Ile Leu Thr Phe Leu Ser Phe Ser Ala Val *583 588 593	2429
tggacactga gtggggagga tgcactgctg ctggcaggt gttctggcag cttctcaggt	2489
gcccccacag aggctccgtg tgacttccgt ccagggagca tgtgggcctg caactttctc	2549
cattcccagc tgggccccat tcctggattt aagatggtgg ctatccctga ggagtcacca	2609
taaggagaaa actcaggaat tctgagtctt ccctgctaca ggaccagtcc tgtgcaatga	2669
acttgagact cctgatgtac actgtgatat tgaccgaagg ctacatacag atctgtgaat	2729
cttggctggg acttcctctg agtgatgcct gagggtcagc tcctcttagac attgactgca	2789
agagaatctc tgcaacctcc tatataaaag catttctgtt aattcaaaaa aaaaaaaaaa	2849
a	2850

<210> 126
 <211> 3423
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (53)...(2800)

<400> 126

gcacgaggtt	tcaaaggaca	caaagagaga	tgtggactca	aagtcaccgg	gg	atg	55
						Met	
						1	
cct tta ttt gaa gca gag gaa gga gtt cta tca cga acc cag ata ttt							103
Pro Leu Phe Glu Ala Glu Gly Val Leu Ser Arg Thr Gln Ile Phe							
2	7		12			17	
cct acc act att aaa gtc att gat cca gaa ttt ctg gag gag cca cct							151
Pro Thr Thr Ile Lys Val Ile Asp Pro Glu Phe Leu Glu Glu Pro Pro							
18	23		28			33	
gca ctt gca ttt tta tat aag gat ctg tat gaa gaa gca gtt gga gag							199
Ala Leu Ala Phe Leu Tyr Lys Asp Leu Tyr Glu Glu Ala Val Gly Glu							
34	39		44			49	
aaa aag aag gaa gag gag aca gct tct gaa ggt gac agt gtg aat tct							247
Lys Lys Glu Glu Thr Ala Ser Glu Gly Asp Ser Val Asn Ser							
50	55		60			65	
gag gca tca ttt ccc agc aga aat tct gac act gat gat gga aca gga							295
Glu Ala Ser Phe Pro Ser Arg Asn Ser Asp Thr Asp Asp Gly Thr Gly							
66	71		76			81	
ata tat ttt gag aag tac ata ctc aaa gat gac att ctc cat gac aca							343
Ile Tyr Phe Glu Lys Tyr Ile Leu Lys Asp Asp Ile Leu His Asp Thr							
82	87		92			97	
tct cta act caa aag gac cag ggc caa ggt ctg gaa gaa aaa cga gtt							391
Ser Leu Thr Gln Lys Asp Gln Gly Gln Gly Leu Glu Glu Lys Arg Val							
98	103		108			113	
ggt aag gat gat tca tac caa ccg ata gct gca gaa ggg gaa att tgg							439
Gly Lys Asp Asp Ser Tyr Gln Pro Ile Ala Ala Glu Gly Glu Ile Trp							
114	119		124			129	
gga aag ttt gga act att tgc agg gag aag agt ctg gaa gaa cag aaa							487
Gly Lys Phe Gly Thr Ile Cys Arg Glu Lys Ser Leu Glu Glu Gln Lys							
130	135		140			145	
ggt gtt tat ggg gaa gga gaa tca gta gac cat gtg gag acc gtt ggt							535
Gly Val Tyr Gly Glu Gly Ser Val Asp His Val Glu Thr Val Gly							
146	151		156			161	
aac gta gcg atg cag aag aaa gct ccc atc aca gag gac gtc aga gtg							583
Asn Val Ala Met Gln Lys Ala Pro Ile Thr Glu Asp Val Arg Val							
162	167		172			177	
gct acc cag aaa ata agt tat gcg gtt cca ttt gaa gac acc cat cat							631
Ala Thr Gln Lys Ile Ser Tyr Ala Val Pro Phe Glu Asp Thr His His							
178	183		188			193	
gtt ctg gag cgt gca gat gaa gca ggc agt cac ggt aat gaa gtc gga							679
Val Leu Glu Arg Ala Asp Glu Ala Gly Ser His Gly Asn Glu Val Gly							
194	199		204			209	

aat gca agt cca gag gtc aat ctg aat gtc cca gta caa gtg tcc ttc Asn Ala Ser Pro Glu Val Asn Leu Asn Val Pro Val Gln Val Ser Phe 210 215 220 225	727
ccg gag gaa gaa ttt gca tct ggt gca act cat gtt caa gaa aca tca Pro Glu Glu Glu Phe Ala Ser Gly Ala Thr His Val Gln Glu Thr Ser 226 231 236 241	775
cta gaa gaa cct aaa atc ctg gtc cca cct gag cca agt gaa gag agg Leu Glu Glu Pro Lys Ile Leu Val Pro Pro Glu Pro Ser Glu Glu Arg 242 247 252 257	823
ctc cgt aat agc cct gtt cag gat gag tat gaa ttt aca gaa tcc ctg Leu Arg Asn Ser Pro Val Gln Asp Glu Tyr Glu Phe Thr Glu Ser Leu 258 263 268 273	871
cat aat gaa gtg gtt cct caa gac ata tta tca gaa gaa ctg tct tca His Asn Glu Val Val Pro Gln Asp Ile Leu Ser Glu Glu Leu Ser Ser 274 279 284 289	919
gaa=tcc aca=cct gaa=gat gtc=tta=tct=caa=gga=aag=gaa=tcc=ttt=gag Glu Ser Thr Pro Glu Asp Val Leu Ser Gln Gly Lys Glu Ser Phe Glu 290 295 300 305	967
cac atc agt gaa aat gaa ttt gcg agt gag gca gaa caa agt aca cct His Ile Ser Glu Asn Glu Phe Ala Ser Glu Ala Glu Gln Ser Thr Pro 306 311 316 321	1015
gct gaa caa aaa gag ttg ggc agc gag agg aaa gaa gaa gac caa tta Ala Glu Gln Lys Glu Leu Gly Ser Glu Arg Lys Glu Glu Asp Gln Leu 322 327 332 337	1063
tca tct gag gta gta act gaa aag gca caa aaa gag ctg aaa aag tcc Ser Ser Glu Val Val Thr Glu Lys Ala Gln Lys Glu Leu Lys Lys Ser 338 343 348 353	1111
cag att gac aca tac tgt tac acc tgc aaa tgt cca att tct gcc act Gln Ile Asp Thr Tyr Cys Tyr Cys Lys Cys Pro Ile Ser Ala Thr 354 359 364 369	1159
gac aag gtg ttt ggc acc cac aaa gac cat gaa gtt tca acg ctt gac Asp Lys Val Phe Gly Thr His Lys Asp His Glu Val Ser Thr Leu Asp 370 375 380 385	1207
aca gct ata agt gct gta aag gtt caa tta gca gaa ttt cta gaa aat Thr Ala Ile Ser Ala Val Lys Val Gln Leu Ala Glu Phe Leu Glu Asn 386 391 396 401	1255
tta caa gaa aag tcc ttg agg att gaa gcc ttt gtt agt gag ata gaa Leu Gln Glu Lys Ser Leu Arg Ile Glu Ala Phe Val Ser Glu Ile Glu 402 407 412 417	1303
tcc ttt ttt aat acc att gag gaa aac tgt agt aaa aat gag aaa agg Ser Phe Phe Asn Thr Ile Glu Glu Asn Cys Ser Lys Asn Glu Lys Arg 418 423 428 433	1351
cta gaa gaa cag aat gag gaa atg atg aag aag gtt tta gca cag tat	1399

Leu Glu Glu Gln Asn Glu Glu Met Met Lys Lys Val Leu Ala Gln Tyr			
434	439	444	449
gat gag aaa gcc cag agc ttt gag gaa gtg aag aag aag atg gag			1447
Asp Glu Lys Ala Gln Ser Phe Glu Glu Val Lys Lys Lys Met Glu			
450	455	460	465
ttc ctg cat gag cag atg gtc cac ttt ctg cag agc atg gac act gcc			1495
Phe Leu His Glu Gln Met Val His Phe Leu Gln Ser Met Asp Thr Ala			
466	471	476	481
aaa gac acc ctg gag acc atc gtg aga gaa gca gag gag ctt gat gag			1543
Lys Asp Thr Leu Glu Thr Ile Val Arg Glu Ala Glu Glu Leu Asp Glu			
482	487	492	497
gcc gtc ttc ctg act tcg ttt gag gaa atc aat gaa agg ttg ctt tct			1591
Ala Val Phe Leu Thr Ser Phe Glu Glu Ile Asn Glu Arg Leu Leu Ser			
498	503	508	513
gca atg gag agc act gct tct tta gag aaa atg cct gct gcg ttt tcc			1639
Ala Met Glu Ser Thr Ala Ser Leu Glu Lys Met Pro Ala Ala Phe Ser			
514	519	524	529
ctt ttc gaa cat tat gat gac agc tcg gca aga agt gac cag atg tta			1687
Leu Phe Glu His Tyr Asp Asp Ser Ser Ala Arg Ser Asp Gln Met Leu			
530	535	540	545
aaa caa gtg gct gtt cca cag cct cct aga tta gaa cct cag gaa cca			1735
Lys Gln Val Ala Val Pro Gln Pro Pro Arg Leu Glu Pro Gln Glu Pro			
546	551	556	561
aat tct gcc acc agc aca aca att gca gtt tac tgg agc atg aac aag			1783
Asn Ser Ala Thr Ser Thr Ile Ala Val Tyr Trp Ser Met Asn Lys			
562	567	572	577
gaa gat gtc att gat tca ttt cag gtt tac tgc atg gag gag cca caa			1831
Glu Asp Val Ile Asp Ser Phe Gln Val Tyr Cys Met Glu Glu Pro Gln			
578	583	588	593
gat gat caa gaa gta aat gag ttg gta gaa gaa tac aga ctg aca gtg			1879
Asp Asp Gln Glu Val Asn Glu Leu Val Glu Glu Tyr Arg Leu Thr Val			
594	599	604	609
aaa gaa agc tac tgc att ttt gaa gat ctg gaa cct gac cga tgc tat			1927
Lys Glu Ser Tyr Cys Ile Phe Glu Asp Leu Glu Pro Asp Arg Cys Tyr			
610	615	620	625
caa gtg tgg gtg atg gct gtg aac ttc act gga tgt agc ctg ccc agt			1975
Gln Val Trp Val Met Ala Val Asn Phe Thr Gly Cys Ser Leu Pro Ser			
626	631	636	641
gaa agg gcc atc ttt agg aca gca ccc tcc acc cct gtg atc cgc gct			2023
Glu Arg Ala Ile Phe Arg Thr Ala Pro Ser Thr Pro Val Ile Arg Ala			
642	647	652	657
gag gac tgt act gtg tgt tgg aac aca gcc act atc cga tgg cgg ccc			2071
Glu Asp Cys Thr Val Cys Trp Asn Thr Ala Thr Ile Arg Trp Arg Pro			

658	663	668	673	
acc acc cca gag gcc acg gag acc tac act ctg gag tac tgc aga cag Thr Thr Pro Glu Ala Thr Glu Thr Tyr Thr Leu Glu Tyr Cys Arg Gln 674 679 684 689				2119
cac tct cct gag gga gag ggc ctc aga tct ttc tct gga atc aaa gga His Ser Pro Glu Gly Glu Gly Leu Arg Ser Phe Ser Gly Ile Lys Gly 690 695 700 705				2167
ctc cag ctg aaa gtt aac ctc caa ccc aat gat aac tac ttt ttc tat Leu Gln Leu Lys Val Asn Leu Gln Pro Asn Asp Asn Tyr Phe Phe Tyr 706 711 716 721				2215
gtg agg gcc atc aat gca ttt ggg aca agt gaa cag agt gaa gct gct Val Arg Ala Ile Asn Ala Phe Gly Thr Ser Glu Gln Ser Glu Ala Ala 722 727 732 737				2263
ctc atc tcc acc aga gga acc aga ttt ctc ttg ttg aga gaa aca gct Leu Ile Ser Thr Arg Gly Thr Arg Phe Leu Leu Leu Arg Glu Thr Ala 738 743 748 753				2311
cat cct gct cta cac att tcc tca agt ggg aca gtg atc agc ttt ggt His Pro Ala Leu His Ile Ser Ser Ser Gly Thr Val Ile Ser Phe Gly 754 759 764 769				2359
gag agg aga cgg ctg acg gaa atc ccg tca gtg ctg ggt gag gag ctg Glu Arg Arg Arg Leu Thr Glu Ile Pro Ser Val Leu Gly Glu Glu Leu 770 775 780 785				2407
cct tcc tgt ggc cag cat tac tgg gaa acc aca gtc aca gac tgc cca Pro Ser Cys Gly Gln His Tyr Trp Glu Thr Thr Val Thr Asp Cys Pro 786 791 796 801				2455
gca tat cga ctc ggc atc tgc tcc agc tcg gct gtg cag gca ggt gcc Ala Tyr Arg Leu Gly Ile Cys Ser Ser Ala Val Gln Ala Gly Ala 802 807 812 817				2503
cta gga caa ggg gag acc tca tgg tac atg cac tgc tct gag cca cag Leu Gly Gln Gly Glu Thr Ser Trp Tyr Met His Cys Ser Glu Pro Gln 818 823 828 833				2551
aga tac aca ttt ttc tac agt ggt att gtg agt gat gtt cat gtg act Arg Tyr Thr Phe Phe Tyr Ser Gly Ile Val Ser Asp Val His Val Thr 834 839 844 849				2599
gag cgt cca gcc aga gtg ggc atc ctg ctg gac tac aac aac cag aga Glu Arg Pro Ala Arg Val Gly Ile Leu Leu Asp Tyr Asn Asn Gln Arg 850 855 860 865				2647
ctt atc ttc atc aac gca gag agc gag cag ttg ctc ttc atc atc agg Leu Ile Phe Ile Asn Ala Glu Ser Glu Gln Leu Leu Phe Ile Ile Arg 866 871 876 881				2695
cac agg ttt aat gag ggt gtc cac cct gcc ttt gcc'ctg gag aaa cct His Arg Phe Asn Glu Gly Val His Pro Ala Phe Ala Leu Glu Lys Pro 882 887 892 897				2743

gga aaa tgt act ttg cac ctg ggg ata gag ccc ccg gat tct gta agg	2791
Gly Lys Cys Thr Leu His Leu Gly Ile Glu Pro Pro Asp Ser Val Arg	
898 903 908 913	
cac aag tga tccttgg ctttcagaat ttgcaagaac agcgatttga attttggggg	2847
His Lys *	
914	
ggtctgctgt tcattcctt aggtgctata cattattcaa aaagtctccc gcgcatttgc	2907
actaatgatg gctgcatgca tagcaatcag catgtgagca aaatcgacaa gaaaaccttg	2967
actttacaga gcagtgtgtg agtaaacaga atgaaaacaa caacctccac tcttagtt	3027
atataagttt gagttcttcc ttaaattaaa agatctacac ttgagttggg aaccgaaaga	3087
gaaaaatgga cttccatctg tttactggt aaaggaaatc ctctgatgga caggtcagag	3147
tgaaggaagg ttgtgctggt aagacatctc tgacgaagag ccatggatgc tttccacaaa	3207
atgtcacctc gctgcaactaa aggatgatga atcctaatac ttaaaggaat tgtttcagct	3267
gatttaaatt tataatgaac tctttgtaa taatgtatac tgtagaacat gagtctctcc	3327
tccctaaaat tttaaatgta gaaaagtgct atatattaga aatttccatt ttgttaata	3387
aatggtaga gtctataaag ccaaaaaaaaaaaaa	3423

<210> 127
 <211> 1668
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1668)

<400> 127

atg gcg gcc gcc ggg gct gcg gct aca cac cta gag gtg gcc cg ggc	48
Met Ala Ala Ala Gly Ala Ala Ala Thr His Leu Glu Val Ala Arg Gly	
1 5 10	

aag cgc gcc gcc ctc ttc gct gcg gtg gcc atc gtg ctg ggg cta	96
Lys Arg Ala Ala Leu Phe Ala Ala Val Ala Ile Val Leu Gly Leu	
17 22 27 32	

ccg ctc tgg tgg aag acc acg gag acc tac cgg gcc tcg ttg cct tac	144
Pro Leu Trp Trp Lys Thr Thr Glu Thr Tyr Arg Ala Ser Leu Pro Tyr	
33 38 43 48	

tcc cag atc agt ggc ctg aat gcc ctt cag ctc cgc ctc atg gtg cct	192
Ser Gln Ile Ser Gly Leu Asn Ala Leu Gln Leu Arg Leu Met Val Pro	
49 54 59 64	

gtc act gtc gtg ttt acg cgg gag tca gtg ccc ctg gac gac cag gag			240
Val Thr Val Val Phe Thr Arg Glu Ser Val Pro Leu Asp Asp Gln Glu			
65	70	75	80
aag ctg ccc ttc acc gtt gtg cat gaa aga gag att cct ctg aaa tac			288
Lys Leu Pro Phe Thr Val Val His Glu Arg Glu Ile Pro Leu Lys Tyr			
81	86	91	96
aaa atg aaa atc aaa tgc cgt ttc cag aag gcc tat cgg agg gct ttg			336
Lys Met Lys Ile Lys Cys Arg Phe Gln Lys Ala Tyr Arg Arg Ala Leu			
97	102	107	112
gac cat gag gag gag gcc ctg tca tcg ggc agt gtg caa gag gca gaa			384
Asp His Glu Glu Ala Leu Ser Ser Gly Ser Val Gln Glu Ala Glu			
113	118	123	128
gcc atg tta gat gag cct cag gaa caa gcg gag ggc tcc ctg act gtg			432
Ala Met Leu Asp Glu Pro Gln Glu Gln Ala Glu Gly Ser Leu Thr Val			
129	134	139	144
tac gtg ata tct gaa cac tcc tca ctt ctt ccc cag gac atg atg agc			480
Tyr Val Ile Ser Glu His Ser Ser Leu Leu Pro Gln Asp Met Met Ser			
145	150	155	160
tac att ggg ccc aag agg aca gca gtg gtg cgg ggg ata atg cac cgg			528
Tyr Ile Gly Pro Lys Arg Thr Ala Val Val Arg Gly Ile Met His Arg			
161	166	171	176
gag gcc ttt aac atc att ggc cgc cgc ata gtc cag gtg gcc cag gcc			576
Glu Ala Phe Asn Ile Ile Gly Arg Arg Ile Val Gln Val Ala Gln Ala			
177	182	187	192
atg tct ttg act gag gat gtg ctt gct gct ctg gct gac cac ctt			624
Met Ser Leu Thr Glu Asp Val Leu Ala Ala Leu Ala Asp His Leu			
193	198	203	208
cca gag gac aag tgg agc gct gag aag agg cgg cct ctc aag tcc agc			672
Pro Glu Asp Lys Trp Ser Ala Glu Lys Arg Arg Pro Leu Lys Ser Ser			
209	214	219	224
ttg ggc tat gag atc acc ttc agt tta ctc aac cca gac ccc aag tcc			720
Leu Gly Tyr Glu Ile Thr Phe Ser Leu Leu Asn Pro Asp Pro Lys Ser			
225	230	235	240
cat gat gtc tac tgg gac att gag ggg gct gtc cgg cgc tat gtg caa			768
His Asp Val Tyr Trp Asp Ile Glu Gly Ala Val Arg Arg Tyr Val Gln			
241	246	251	256
cct ttc ctg aat gcc ctc ggt gcc gct ggc aac ttc tct gtg gac tct			816
Pro Phe Leu Asn Ala Leu Gly Ala Ala Gly Asn Phe Ser Val Asp Ser			
257	262	267	272
cag att ctt tac tat gca atg ttg ggg gtg aat ccc cgc ttt gac tca			864
Gln Ile Leu Tyr Tyr Ala Met Leu Gly Val Asn Pro Arg Phe Asp Ser			
273	278	283	288

gct tcc tcc agc tac tat ttg gac atg cac agc ctc ccc cat gtc atc Ala Ser Ser Ser Tyr Tyr Leu Asp Met His Ser Leu Pro His Val Ile 289 294 299 304	912
aac cca gtg gag tcc cg ^g ctg gga tcc agt gct gcc tcc ttg tac cct Asn Pro Val Glu Ser Arg Leu Gly Ser Ser Ala Ala Ser Leu Tyr Pro 305 310 315 320	960
gtg ctc aac ttt cta ctc tac gtg cct gag ctt gca cac tca ccg ctg Val Leu Asn Phe Leu Leu Tyr Val Pro Glu Leu Ala His Ser Pro Leu 321 326 331 336	1008
tac att cag gac aag gat ggc gct cca gtg gcc acc aat gcc ttc cat Tyr Ile Gln Asp Lys Asp Gly Ala Pro Val Ala Thr Asn Ala Phe His 337 342 347 352	1056
agt ccc cgc tgg ggt ggc att atg gta tat aat gtt gac tcc aaa acc Ser Pro Arg Trp Gly Gly Ile Met Val Tyr Asn Val Asp Ser Lys Thr 353 358 363 368	1104
---tat aat gcc tca gtg ctg cca gtg aga gtc gag gtg gac atg gtg cga Tyr Asn Ala Ser Val Leu Pro Val Arg Val Glu Val Asp Met Val Arg 369 374 379 384	1152
gtg atg gag gtg ttc ctg gca cag ttg cgg ttg ctc ttt ggg att gct Val Met Glu Val Phe Leu Ala Gln Leu Arg Leu Leu Phe Gly Ile Ala 385 390 395 400	1200
cag ccc cag ctg cct cca aaa tgc ctg ctt tca ggg cct acg agt gaa Gln Pro Gln Leu Pro Pro Lys Cys Leu Leu Ser Gly Pro Thr Ser Glu 401 406 411 416	1248
ggg cta atg acc tgg gag cta gac cgg ctg ctc tgg gct cgg tca gtg Gly Leu Met Thr Trp Glu Leu Asp Arg Leu Leu Trp Ala Arg Ser Val 417 422 427 432	1296
gag aac ctg gcc aca gcc acc acc acc ctt acc tcc ctg gcg cag ctt Glu Asn Leu Ala Thr Ala Thr Thr Leu Thr Ser Leu Ala Gln Leu 433 438 443 448	1344
ctg ggc aag atc agc aac att gtc att aag gac gac gtg gca tct gag Leu Gly Lys Ile Ser Asn Ile Val Ile Lys Asp Asp Val Ala Ser Glu 449 454 459 464	1392
gtg tac aag gct gta gct gcc gtc cag aag tcg gca gaa gag ttg gcg Val Tyr Lys Ala Val Ala Ala Val Gln Lys Ser Ala Glu Glu Leu Ala 465 470 475 480	1440
tct ggg cac ctg gca tct gcc ttt gtc gcc agc cag gaa gct gtg aca Ser Gly His Leu Ala Ser Ala Phe Val Ala Ser Gln Glu Ala Val Thr 481 486 491 496	1488
tcc tct gag ctt gcc ttc ttt gac ccg tca ctc ctc cac ctc ctt tat Ser Ser Glu Leu Ala Phe Phe Asp Pro Ser Leu Leu His Leu Leu Tyr 497 502 507 512	1536
ttc cct gat gac cag aag ttt gcc atc tac atc cca ctc ttc ctg cct	1584

Phe	Pro	Asp	Asp	Gln	Lys	Phe	Ala	Ile	Tyr	Ile	Pro	Leu	Phe	Leu	Pro
513						518					523				528
atg	gct	gtg	ccc	atc	ctc	ctg	tcc	ctg	gtc	aag	atc	ttc	ctg	gag	acc
Met	Ala	Val	Pro	Ile	Leu	Leu	Ser	Leu	Val	Lys	Ile	Phe	Leu	Glu	Thr
529						534				539				544	
cgc	aag	tcc	tgg	aga	aag	cct	gag	aag	aca	gac	tga				1632
Arg	Lys	Ser	Trp	Arg	Lys	Pro	Glu	Lys	Thr	Asp	*				1668
545						550				555					

<210> 128
 <211> 3964
 <212> DNA
 <213> Homo sapiens

<220>															
<221>	CDS														
<222>	(174)	..(2540)													
<400>	128														
actgttggag	gtgacctata	gaacaagttt	gtacaaaaaa	gcaggctgg	accggtccgg										60
aattccccggg	atggcgccggg	ggacgtcagc	gctgccagcg	tggaaggagc	tgcggggcgc										120
gggaggagga	agtagagccc	gggaccgcca	ggccaccacc	ggccgcctca	gcc	atg									176
						Met									1
gac	gcg	tcc	ctg	gag	aag	ata	gca	gac	ccc	acg	tta	gct	gaa	atg	gga
Asp	Ala	Ser	Leu	Glu	Lys	Ile	Ala	Asp	Pro	Thr	Leu	Ala	Glu	Met	Gly
2						7					12				17
aaa	aac	ttg	aag	gag	gca	gtg	aag	atg	ctg	gag	gac	agt	cag	aga	aga
Lys	Asn	Leu	Lys	Glu	Ala	Val	Lys	Met	Leu	Glu	Asp	Ser	Gln	Arg	Arg
18						23				28					33
aca	gaa	gag	gaa	aat	gga	aag	aag	ctc	ata	tcc	gga	gat	att	cca	ggc
Thr	Glu	Glu	Asn	Gly	Lys	Lys	Leu	Ile	Ser	Gly	Asp	Ile	Pro	Gly	
34						39				44					49
cca	ctc	cag	ggc	agt	ggg	caa	gat	atg	gtg	agc	atc	ctc	cag	tta	gtt
Pro	Leu	Gln	Gly	Ser	Gly	Gln	Asp	Met	Val	Ser	Ile	Leu	Gln	Leu	Val
50						55				60					65
cag	aat	ctc	atg	cat	gga	gat	gaa	gat	gag	ccc	cag	agc	ccc	aga	
Gln	Asn	Leu	Met	His	Gly	Asp	Glu	Asp	Glu	Glu	Pro	Gln	Ser	Pro	Arg
66						71				76					81
atc	caa	aat	att	gga	gaa	caa	ggt	cat	atg	gct	ttg	ttg	gga	cat	agt
Ile	Gln	Asn	Ile	Gly	Glu	Gln	Gly	His	Met	Ala	Leu	Leu	Gly	His	Ser
82						87				92					97

ctg gga gct tat att tca act ctg gac aaa gag aag ctg aga aaa ctt		512
Leu Gly Ala Tyr Ile Ser Thr Leu Asp Lys Glu Lys Leu Arg Lys Leu		
98	103	108
		113
aca act agg ata ctt tca gat acc acc tta tgg cta tgc aga att ttc		560
Thr Thr Arg Ile Leu Ser Asp Thr Thr Leu Trp Leu Cys Arg Ile Phe		
114	119	124
		129
aga tat gaa aat ggg tgt gct tat ttc cac gaa gag gaa aga gaa gga		608
Arg Tyr Glu Asn Gly Cys Ala Tyr Phe His Glu Glu Glu Arg Glu Gly		
130	135	140
		145
ctt gca aag ata tgt agg ctt gcc att cat tct cga tat gaa gac ttc		656
Leu Ala Lys Ile Cys Arg Leu Ala Ile His Ser Arg Tyr Glu Asp Phe		
146	151	156
		161
gta gtg gat ggc ttc aat gtg tta tat aac aag aag cct gtc ata tat		704
Val Val Asp Gly Phe Asn Val Leu Tyr Asn Lys Lys Pro Val Ile Tyr		
162	167	172
		177
ctt agt gct gct aga cct ggc ctg ggc caa tac ctt tgt aat cag		752
Leu Ser Ala Ala Arg Pro Gly Leu Gly Gln Tyr Leu Cys Asn Gln		
178	183	188
		193
ctc ggc ttg ccc ttc ccc tgc ttg tgc cgt gta ccc tgt aac act gtg		800
Leu Gly Leu Pro Phe Pro Cys Leu Cys Arg Val Pro Cys Asn Thr Val		
194	199	204
		209
ttt gga tcc cag cat cag atg gat gtt gcc ttc ctg gag aaa ctg att		848
Phe Gly Ser Gln His Gln Met Asp Val Ala Phe Leu Glu Lys Leu Ile		
210	215	220
		225
aaa gat gat ata gag cga gga aga ctg ccc ctg ttg ctt gtc gca aat		896
Lys Asp Asp Ile Glu Arg Gly Arg Leu Pro Leu Leu Val Ala Asn		
226	231	236
		241
gca gga acg gca gca gta gga cac aca gac aag att ggg aga ttg aaa		944
Ala Gly Thr Ala Ala Val Gly His Thr Asp Lys Ile Gly Arg Leu Lys		
242	247	252
		257
gaa ctc tgt gag cag tat ggc ata tgg ctt cat gtg gag ggt gtg aat		992
Glu Leu Cys Glu Gln Tyr Gly Ile Trp Leu His Val Glu Gly Val Asn		
258	263	268
		273
ctg gca aca ttg gct ctg ggt tat gtc tcc tca tca gtg ctg gct gca		1040
Leu Ala Thr Leu Ala Leu Gly Tyr Val Ser Ser Val Leu Ala Ala		
274	279	284
		289
gcc aaa tgt gat agc atg acg atg act cct ggc ccg tgg ctg ggt ttg		1088
Ala Lys Cys Asp Ser Met Thr Met Thr Pro Gly Pro Trp Leu Gly Leu		
290	295	300
		305
cca gct gtt cct gcg gtg aca ctg tat aaa cac gat gac cct gcc ttg		1136
Pro Ala Val Pro Ala Val Thr Leu Tyr Lys His Asp Asp Pro Ala Leu		
306	311	316
		321
act tta gtt gct ggt ctt aca tca aat aag ccc aca gac aaa ctc cgt		1184

Thr Leu Val Ala Gly Leu Thr Ser Asn Lys Pro Thr Asp Lys Leu Arg				
322	327	332	337	
gcc ctg cct ctg tgg tta tct tta caa tac ttg gga ctt gat ggg ttt				1232
Ala Leu Pro Leu Trp Leu Ser Leu Gln Tyr Leu Gly Leu Asp Gly Phe				
338	343	348	353	
gtg gag agg atc aag cat gcc tgt caa ctg agt caa cgg ttg cag gaa				1280
Val Glu Arg Ile Lys His Ala Cys Gln Leu Ser Gln Arg Leu Gln Glu				
354	359	364	369	
agt ttg aag aaa gtg aat tac atc aaa atc ttg gtg gaa gat gag ctc				1328
Ser Leu Lys Lys Val Asn Tyr Ile Lys Ile Leu Val Glu Asp Glu Leu				
370	375	380	385	
agc tcc cca gtg gtg ttc aga ttt ttc cag gaa tta cca ggc tca				1376
Ser Ser Pro Val Val Phe Arg Phe Gln Glu Leu Pro Gly Ser				
386	391	396	401	
gat ccg gtg ttt aaa gcc gtc cca gtg ccc aac atg aca cct tca gga				1424
Asp Pro Val Phe Lys Ala Val Pro Val Pro Asn Met Thr Pro Ser Gly				
402	407	412	417	
gtc ggc cgg gag agg cac tcg tgt gac gcg ctg aat cgc tgg ctg gga				1472
Val Gly Arg Glu Arg His Ser Cys Asp Ala Leu Asn Arg Trp Leu Gly				
418	423	428	433	
gaa cag ctg aag cag ctg gtg cct gca agc ggc ctc aca gtc atg gat				1520
Glu Gln Leu Lys Gln Leu Val Pro Ala Ser Gly Leu Thr Val Met Asp				
434	439	444	449	
ctg gaa gct gag ggc acg tgt ttg cgg ttc agc cct ttg atg acc gca				1568
Leu Glu Ala Glu Gly Thr Cys Leu Arg Phe Ser Pro Leu Met Thr Ala				
450	455	460	465	
gca gtt tta gga act cgg gga gag gat gtg gat cag ctc gta gcc tgc				1616
Ala Val Leu Gly Thr Arg Gly Glu Asp Val Asp Gln Leu Val Ala Cys				
466	471	476	481	
ata gaa agc aaa ctg cca gtg ctg tgc tgt acg ctc cag ttg cgt gaa				1664
Ile Glu Ser Lys Leu Pro Val Leu Cys Cys Thr Leu Gln Leu Arg Glu				
482	487	492	497	
gag ttc aag cag gaa gtg gaa gca aca gca ggt ctc cta tat gtt gat				1712
Glu Phe Lys Gln Glu Val Glu Ala Thr Ala Gly Leu Leu Tyr Val Asp				
498	503	508	513	
gac cct aac tgg tct gga ata ggg gtt gtc agg tat gaa cat gct aat				1760
Asp Pro Asn Trp Ser Gly Ile Gly Val Val Arg Tyr Glu His Ala Asn				
514	519	524	529	
gat gat aag agc agt ttg aaa tca gat ccc gaa ggg gaa aac atc cat				1808
Asp Asp Lys Ser Ser Leu Lys Ser Asp Pro Glu Gly Glu Asn Ile His				
530	535	540	545	
gct gga ctc ctg aag aag tta aat gaa ctg gaa tct gac cta acc ttt				1856
Ala Gly Leu Leu Lys Leu Asn Glu Leu Glu Ser Asp Leu Thr Phe				

546	551	556	561	
aaa ata ggc cct gag tat aag agc atg aag agc tgc ctt tat gtc ggc Lys Ile Gly Pro Glu Tyr Lys Ser Met Lys Ser Cys Leu Tyr Val Gly				1904
562	567	572	577	
atg gcg agc gac aac gtc gat gct gct gag ctc gtg gag acc att gcg Met Ala Ser Asp Asn Val Asp Ala Ala Glu Leu Val Glu Thr Ile Ala				1952
578	583	588	593	
gcc aca gcc cg ^g gag ata gag gag aac tcg agg ctt ctg gaa aac atg Ala Thr Ala Arg Glu Ile Glu Glu Asn Ser Arg Leu Leu Glu Asn Met				2000
594	599	604	609	
aca gaa gtg gtt cg ^g aaa ggc att cag gaa gct caa gtg gag ctg cag Thr Glu Val Val Arg Lys Gly Ile Gln Glu Ala Gln Val Glu Leu Gln				2048
610	615	620	625	
aag gca agt gaa gaa cg ^g ctt ctg gaa gag ggg gtg ttg cgg cag atc Lys Ala Ser Glu Glu Arg Leu Leu Glu Glu Gly Val Leu Arg Gln Ile				2096
626	631	636	641	
cct gta gtg ggc tcc gtg ctg aat tgg ttt tct ccg gtc cag gct tta Pro Val Val Gly Ser Val Leu Asn Trp Phe Ser Pro Val Gln Ala Leu				2144
642	647	652	657	
cag aag gga aga act ttt aac ttg aca gca ggc tct ctg gag tcc aca Gln Lys Gly Arg Thr Phe Asn Leu Thr Ala Gly Ser Leu Glu Ser Thr				2192
658	663	668	673	
gaa ccc ata tat gtc tac aaa gca caa ggt gca gga gtc acg ctg cct Glu Pro Ile Tyr Val Tyr Lys Ala Gln Gly Ala Gly Val Thr Leu Pro				2240
674	679	684	689	
cca acg ccc tcg ggc agt cgc acc aag cag agg ctt cca ggc cag aag Pro Thr Pro Ser Gly Ser Arg Thr Lys Gln Arg Leu Pro Gly Gln Lys				2288
690	695	700	705	
cct ttt aaa agg tcc ctg cga ggt tca gat gct ttg agt gag acc agc Pro Phe Lys Arg Ser Leu Arg Gly Ser Asp Ala Leu Ser Glu Thr Ser				2336
706	711	716	721	
tca gtc agt cac att gaa gac tta gaa aag gtg gag cgc cta tcc agt Ser Val Ser His Ile Glu Asp Leu Glu Lys Val Glu Arg Leu Ser Ser				2384
722	727	732	737	
ggg ccg gag cag atc acc ctc gag gcc agc agc act gag gga cac cca Gly Pro Glu Gln Ile Thr Leu Glu Ala Ser Ser Thr Glu Gly His Pro				2432
738	743	748	753	
ggg gct ccc agc cct cag cac acc gac cag acc gag gcc ttc cag aaa Gly Ala Pro Ser Pro Gln His Thr Asp Gln Thr Glu Ala Phe Gln Lys				2480
754	759	764	769	
ggg gtc cca cac cca gaa gat gac cac tca cag gta gaa gga ccg gag Gly Val Pro His Pro Glu Asp Asp His Ser Gln Val Glu Gly Pro Glu				2528
770	775	780	785	

agc tta aga tga gac tcattgtgtg gtttgagact gtactgagta ttgtttcagg 2583
 Ser Leu Arg *
 786

gaagatgaag ttctatttga aatgtgaact gtgcacata ctaatataaa ttactgttgt 2643
 ttgtgcttca ctgggatttt ggcacaaaata tgtgcctgaa agttaggctt tctaggaggg 2703
 gagtcagctt gtctaacttc atgtacatgt agaaccacgt ttgctgtcct actacgactt 2763
 ttccctaagt taccataaac acatTTTATT cacaaaaaac acttcaatt tcaagtgtct 2823
 accagtagca cccttgctct ttctaaacat aagcctaagt atatgaggtt gcccggtggca 2883
 acttttttgtt aaaacagctt ttcatttagca ctctccaggt tctctgcaac acttcacaga 2943
 ggcgagactg gctgtatctt ttgctgtcgg tcttttagtac gatcaagttt caatatacag 3003
 tggttgcctt agacttgaag gagagcagg attgtggat tggaaataag agcatcagaa 3063
 gcccctccccca gctactgctc ttctgggaga cttagtaagg actgtgtctt cttgagctgt 3123
 gccaaggctg ctgtctggga ctgtccctctg ccacaaggcc atttctccca ttatataccg 3183
 ttgttaaaga gaaaactgtaa agtctcctcc tgaccatata tttttaaata ctggcaaagc 3243
 tttttaaattt ggcacacaag tacagactgt gctcatttctt gtttagtac tgaaaacctg 3303
 atagatgcta cccttaagag ctgtctttc ctgtgtctac gtgcacccca cttgtttaaa 3363
 atctgaaaac aagtacccct ttgacctgtc tcccactgaa gcttctactg ccctggcagc 3423
 tcgcctgggc ccaactcaga aacaggagcc agcagagcac tctctcacgc tgatccagcc 3483
 gggcacccctg cttaagtcag tagaagctcg ctggcaactgc ccgttccctac ttttccgaag 3543
 tactgcgtca ctgttcgtta agtaatggcc cctgtgcctt cttaatccag cagtcaagct 3603
 ttggggagac ctgaaaatgg gaaaattcac actgggtttc tggactgttag tattggaaac 3663
 cttagttata gtatattaag cctataatta tactctgatt tgatggatt tttgacattt 3723
 acacttgtca aaatgcaggg ggtttttttt ggtgcagatg attaaacagt ctccctatt 3783
 tgggtcaatg aagtatagca gataaaatgg gggagggta aattatcacc ttcaagaaga 3843
 tgacatgttt ttatatatat ttgaaattgt taaatggtt ttgctgaaac atttcaccct 3903
 ttagatatta ttgttatgtt ggtttcaata aaggtcttg aaattgttaa aaaaaaaaaaa 3963
 a 3964

<211> 2905

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (87)..(2216)

<400> 129

gccacagaga cgggtgcagt ggttagcctag agaggccgct aacagacagg agccgaacgg 60

gggcttcgc tcagcagaga ggcaag atg acg gca ggg ggt ggc tct ggg 113
Met Ala Thr Ala Gly Gly Gly Ser Gly
1 5

gct gac ccg gga agt cgg ggt ctc ctt cgc ctt ctg tct ttc tgc gtc 161
Ala Asp Pro Gly Ser Arg Gly Leu Leu Arg Leu Leu Ser Phe Cys Val
10 15 20 25

cta cta gca ggt ttg tgc agg gga aac tca gtg gag agg aag ata tat 209
Leu Leu Ala Gly Leu Cys Arg Gly Asn Ser Val Glu Arg Lys Ile Tyr
26 31 36 41

atc ccc tta aat aaa aca gct ccc tgt gtt cgc ctg ctc aac gcc act 257
Ile Pro Leu Asn Lys Thr Ala Pro Cys Val Arg Leu Leu Asn Ala Thr
42 47 52 57

cat cag att ggc tgc cag tct tca att agt gga gac aca ggg gtt atc 305
His Gln Ile Gly Cys Gln Ser Ser Ile Ser Gly Asp Thr Gly Val Ile
58 63 68 73

cac gta gta gag aaa gag gag gac cta cag tgg gta ttg act gat ggc 353
His Val Val Glu Lys Glu Asp Leu Gln Trp Val Leu Thr Asp Gly
74 79 84 89

ccc aac ccc cct tac atg gtt ctg ctg gag agc aag cat ttt acc agg 401
Pro Asn Pro Pro Tyr Met Val Leu Leu Glu Ser Lys His Phe Thr Arg
90 95 100 105

gat tta atg gag aag ctg aaa ggg aga acc agc cga att gct ggt ctt 449
Asp Leu Met Glu Lys Leu Lys Gly Arg Thr Ser Arg Ile Ala Gly Leu
106 111 116 121

gca gtg tcc ttg acc aag ccc agt cct gcc tca ggc ttc tct cct agt 497
Ala Val Ser Leu Thr Lys Pro Ser Pro Ala Ser Gly Phe Ser Pro Ser
122 127 132 137

gta cag tgc cca aat gat ggg ttt ggt gtt tac tcc aat tcc tat ggg 545
Val Gln Cys Pro Asn Asp Gly Phe Gly Val Tyr Ser Asn Ser Tyr Gly
138 143 148 153

cca gag ttt gct cac tgc aga gaa ata cag tgg aat tcg ctg ggc aat 593
Pro Glu Phe Ala His Cys Arg Glu Ile Gln Trp Asn Ser Leu Gly Asn
154 159 164 169

ggt ttg gct tat gaa gac ttt agt ttc ccc atc ttt ctt ctt gaa gat 641
Gly Leu Ala Tyr Glu Asp Phe Ser Phe Pro Ile Phe Leu Leu Glu Asp

170	175	180	185	
gaa aat gaa acc aaa gtc atc aag cag tgc tat caa gat cac aac ctg Glu Asn Glu Thr Lys Val Ile Lys Gln Cys Tyr Gln Asp His Asn Leu	186	191	196	689
186	191	196	201	
agt cag aat ggc tca gca cca acc ttc cca cta tgt gcc atg cag ctc Ser Gln Asn Gly Ser Ala Pro Thr Phe Pro Leu Cys Ala Met Gln Leu	202	207	212	737
202	207	212	217	
ttt tca cac atg cat gct gtc atc agc act gcc acc tgc atg cgg cgc Phe Ser His Met His Ala Val Ile Ser Thr Ala Thr Cys Met Arg Arg	218	223	228	785
218	223	228	233	
agc tcc atc caa agc acc ttc agc atc aac cca gaa atc gtc tgt gac Ser Ser Ile Gln Ser Thr Phe Ser Ile Asn Pro Glu Ile Val Cys Asp	234	239	244	833
234	239	244	249	
ccc ctg tct gat tac aat gtg tgg agc atg cta aag cct ata aat aca Pro Leu Ser Asp Tyr Asn Val Trp Ser Met Leu Lys Pro Ile Asn Thr	250	255	260	881
250	255	260	265	
act ggg aca tta aag cct gac gac agg gtt gtg gtt gct gcc acc cgg Thr Gly Thr Leu Lys Pro Asp Asp Arg Val Val Ala Ala Thr Arg	266	271	276	929
266	271	276	281	
ctg gat agt cgt tcc ttt ttc tgg aat gtg gcc cca ggg gct gaa agc Leu Asp Ser Arg Ser Phe Phe Trp Asn Val Ala Pro Gly Ala Glu Ser	282	287	292	977
282	287	292	297	
gca gtg gct tcc ttt gtc acc cag ctg gct gct gct gaa gct ttg caa Ala Val Ala Ser Phe Val Thr Gln Leu Ala Ala Ala Glu Ala Leu Gln	298	303	308	1025
298	303	308	313	
aag gca cct gat gtg acc acc ctg ccc cgc aat gtc atg ttt gtc ttc Lys Ala Pro Asp Val Thr Leu Pro Arg Asn Val Met Phe Val Phe	314	319	324	1073
314	319	324	329	
ttt caa ggg gaa act ttt gac tac att ggc agc tcg agg atg gtc tac Phe Gln Gly Thr Phe Asp Tyr Ile Gly Ser Ser Arg Met Val Tyr	330	335	340	1121
330	335	340	345	
gat atg gag aag ggc aag ttt ccc gtg cag tta gag aat gtt gac tca Asp Met Glu Lys Gly Lys Phe Pro Val Gln Leu Glu Asn Val Asp Ser	346	351	356	1169
346	351	356	361	
ttt gtg gag ctg gga cag gtg gcc tta aga act tca tta gag ctt tgg Phe Val Glu Leu Gly Gln Val Ala Leu Arg Thr Ser Leu Glu Leu Trp	362	367	372	1217
362	367	372	377	
atg cac aca gat cct gtt tct cag aaa aat gag tct gta cgg aac cag Met His Thr Asp Pro Val Ser Gln Lys Asn Glu Ser Val Arg Asn Gln	378	383	388	1265
378	383	388	393	
gtg gag gat ctc ctg gcc aca ttg gag aag agt ggt gct ggt gtc cct Val Glu Asp Leu Leu Ala Thr Leu Glu Lys Ser Gly Ala Gly Val Pro	394	399	404	1313
394	399	404	409	

gct gtc atc ctc agg agg cca aat cag tcc cag cct ctc cca cca tct Ala Val Ile Leu Arg Arg Pro Asn Gln Ser Gln Pro Leu Pro Pro Ser 410 415 420 425	1361
tcc ctg cag cga ttt ctt cga gct cga aac atc tct ggc gtt gtt ctg Ser Leu Gln Arg Phe Leu Arg Ala Arg Asn Ile Ser Gly Val Val Leu 426 431 436 441	1409
gct gac cac tct ggt gcc ttc cat aac aaa tat tac cag agt att tac Ala Asp His Ser Gly Ala Phe His Asn Lys Tyr Tyr Gln Ser Ile Tyr 442 447 452 457	1457
gac act gct gag aac att aat gtg agc tat ccc gaa tgg ctg agc cct Asp Thr Ala Glu Asn Ile Asn Val Ser Tyr Pro Glu Trp Leu Ser Pro 458 463 468 473	1505
gaa gag gac ctg aac ttt gta aca gac act gcc aag gcc ctg gca gat Glu Glu Asp Leu Asn Phe Val Thr Asp Thr Ala Lys Ala Leu Ala Asp 474 479 484 489	1553
gtg gcc acg gtg ctg gga cgt gct ctg tat gag ctt gca gga gga acc Val Ala Thr Val Leu Gly Arg Ala Leu Tyr Glu Leu Ala Gly Gly Thr 490 495 500 505	1601
aac ttc agc gac aca gtt cag gct gat ccc caa acg gtt acc cgc ctg Asn Phe Ser Asp Thr Val Gln Ala Asp Pro Gln Thr Val Thr Arg Leu 506 511 516 521	1649
ctc tat ggg ttc ctg att aaa gcc aac aac tca tgg ttc cag tct atc Leu Tyr Gly Phe Leu Ile Lys Ala Asn Asn Ser Trp Phe Gln Ser Ile 522 527 532 537	1697
ctc agg cag gac cta agg tcc tac ttg ggt gac ggg cct ctt caa cat Leu Arg Gln Asp Leu Arg Ser Tyr Leu Gly Asp Gly Pro Leu Gln His 538 543 548 553	1745
tac atc gct gtc tcc agc ccc acc aac acc act tat gtt gta cag tat Tyr Ile Ala Val Ser Ser Pro Thr Asn Thr Tyr Val Val Gln Tyr 554 559 564 569	1793
gcc ttg gca aat ttg act ggc aca gtg gtc aac ctc acc cga gag cag Ala Leu Ala Asn Leu Thr Gly Thr Val Val Asn Leu Thr Arg Glu Gln 570 575 580 585	1841
tgc cag gat cca agt aaa gtc cca agt gaa aac aag gat ctg tat gag Cys Gln Asp Pro Ser Lys Val Pro Ser Glu Asn Lys Asp Leu Tyr Glu 586 591 596 601	1889
tac tca tgg gtc cag ggc cct ttg cat tct aat gag acg gac cga ctc Tyr Ser Trp Val Gln Gly Pro Leu His Ser Asn Glu Thr Asp Arg Leu 602 607 612 617	1937
ccc cgg tgt gtg cgt tct act gca cga tta gcc agg gcc ttg tct cct Pro Arg Cys Val Arg Ser Thr Ala Arg Leu Ala Arg Ala Leu Ser Pro 618 623 628 633	1985

gcc ttt gaa ctg agt cag tgg agc tct act gaa tac tct aca tgg act		2033
Ala Phe Glu Leu Ser Gln Trp Ser Ser Thr Glu Tyr Ser Thr Trp Thr		
634 639 644 649		
 gag agc cgc tgg aaa gat atc cgt gcc cg ^g ata ttt ctc atc gcc agc		2081
Glu Ser Arg Trp Lys Asp Ile Arg Ala Arg Ile Phe Leu Ile Ala Ser		
650 655 660 665		
 aaa gag ctt gag ttg atc acc ctg aca gtg ggc ttc ggc atc ctc atc		2129
Lys Glu Leu Glu Leu Ile Thr Leu Thr Val Gly Phe Gly Ile Leu Ile		
666 671 676 681		
 ttc tcc ctc atc gtc acc tac tgc atc aat gcc aaa gct gat gtc ctt		2177
Phe Ser Leu Ile Val Thr Tyr Cys Ile Asn Ala Lys Ala Asp Val Leu		
682 687 692 697		
 ttc att gct ccc cg ^g gag cca gga gct gtg tca tac tga ggaggacccc		2226
Phe Ile Ala Pro Arg Glu Pro Gly Ala Val Ser Tyr *		
698 703 708		
 agcttttctt gccagctcag cagttcactt cctagagcat ctgtcccact gggacacaac		2286
cactaatttg tcactggaac ctccctggc ctgtctcaga ttgggattaa cataaaagag		2346
tggaactatc caaaaagagac agggagaaat aaataaaatg cctcccttcc tccgctcccc		2406
tttcccatca ccccttcccc a ^t ttcctctt cttctctac tcatgccaga ttttggatt		2466
acaaatagaa gcttcttgct cctgttaac tcccttagtta cccaccctaa tttgcccttc		2526
aggacccttc tacttttcc ttctgtccct gtacctctct ctgtccctca ccccccacccc		2586
tgtacccagc caccttcctg actgggaagg acataaaagg ttatgtca gggtcaaact		2646
acattgagcc cctgaggaca gggcatctc tggctgagc ctactgtctc cttccactg		2706
tcctttctcc aggcctcag atggcacatt agggtggcg tgctgcgggt gggtatccca		2766
cctccagccc acagtgtca gttgtacttt ttatagct gtaatatcta ttttgtttt		2826
tgtcttttcc ctttattctt ttgtaaata tatataat gagttcatt aaaatagatt		2886
atcccacaaa aaaaaaaaaa		2905

<210> 130
 <211> 8503
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (91)..(8082)

<400> 130

taaatttaaa ggccggggcgg cctgtgagcc ctgaagtgcc ggccgcggag ggtcctggcc		60
attttggtgg gaccagttca gcctgatagg	atg gcg gag gaa gga gcc gtg Met Ala Glu Glu Gly Ala Val 1 5	111
gcc gtc tgc gtg cga gtg cggtcg aac agc aga gaa gaa tca ctt Ala Val Cys Val Arg Val Arg Pro Leu Asn Ser Arg Glu Glu Ser Leu 8 13 18 23		159
gga gaa act gcc caa gtt tac tgg aaa act gac aat aat gtc att tat Gly Glu Thr Ala Gln Val Tyr Trp Lys Thr Asp Asn Asn Val Ile Tyr 24 29 34 39		207
caa gtt gat gga agt aaa tcc ttc aat ttt gat cgt gtc ttt cat ggt Gln Val Asp Gly Ser Lys Ser Phe Asn Phe Asp Arg Val Phe His Gly 40 45 50 55		255
aat gaa act acc aaa aat gtg tat gaa gaa ata gca gca cca atc atc Asn Glu Thr Thr Lys Asn Val Tyr Glu Glu Ile Ala Ala Pro Ile Ile 56 61 66 71		303
gat tct gcc ata caa ggc tac aat ggt act ata ttt gcc tat gga cag Asp Ser Ala Ile Gln Gly Tyr Asn Gly Thr Ile Phe Ala Tyr Gly Gln 72 77 82 87		351
act gct tca gga aaa aca tat acc atg atg ggt tca gaa gat cat ttg Thr Ala Ser Gly Lys Thr Tyr Thr Met Met Gly Ser Glu Asp His Leu 88 93 98 103		399
gga gtt ata ccc agg gca att cat gac att ttc caa aaa att aag aag Gly Val Ile Pro Arg Ala Ile His Asp Ile Phe Gln Lys Ile Lys Lys 104 109 114 119		447
ttt cct gat agg gaa ttt ctc tta cgt gta tct tac atg gaa ata tac Phe Pro Asp Arg Glu Phe Leu Leu Arg Val Ser Tyr Met Glu Ile Tyr 120 125 130 135		495
aat gaa acc att aca gat tta ctc tgt ggc act caa aaa atg aaa cct Asn Glu Thr Ile Thr Asp Leu Leu Cys Gly Thr Gln Lys Met Lys Pro 136 141 146 151		543
tta att att cga gaa gat gtc aat agg aat gtg tat gtt gct gat ctc Leu Ile Ile Arg Glu Asp Val Asn Arg Asn Val Tyr Val Ala Asp Leu 152 157 162 167		591
aca gaa gaa gtt gta tat aca tca gaa atg gct ttg aaa tgg att aca Thr Glu Glu Val Val Tyr Thr Ser Glu Met Ala Leu Lys Trp Ile Thr 168 173 178 183		639
aag gga gaa aag agc agg cat tat gga gaa aca aaa atg aat caa aga Lys Gly Glu Lys Ser Arg His Tyr Gly Glu Thr Lys Met Asn Gln Arg 184 189 194 199		687
agc agt cgt tct cat acc atc ttt agg atg att ttg gaa agc aga gag Ser Ser Arg Ser His Thr Ile Phe Arg Met Ile Leu Glu Ser Arg Glu 200 205 210 215		735

aag ggt gaa cct tct aat tgt gaa gga tct gtt aag gta tcc cat ttg		783	
Lys Gly Glu Pro Ser Asn Cys Glu Gly Ser Val Lys Val Ser His Leu			
216	221	226	231
aat ttg gtt gat ctt gca ggc agt gaa aga gct gct caa aca ggc gct		831	
Asn Leu Val Asp Leu Ala Gly Ser Glu Arg Ala Ala Gln Thr Gly Ala			
232	237	242	247
gca ggt gtg cgg ctc aag gaa ggc tgt aat ata aat cga agc tta ttt		879	
Ala Gly Val Arg Leu Lys Glu Gly Cys Asn Ile Asn Arg Ser Leu Phe			
248	253	258	263
att ttg gga caa gtg atc aag aaa ctt agt gat gga caa gtt ggt ggt		927	
Ile Leu Gly Gln Val Ile Lys Lys Leu Ser Asp Gly Gln Val Gly Gly			
264	269	274	279
tcc ata aat tat cga gat agc aag tta aca cga att ctt cag aat tcc		975	
Phe Ile Asn Tyr Arg Asp Ser Lys Leu Thr Arg Ile Leu Gln Asn Ser			
280	285	290	295
ttg gga gga aat cca aag aca cgt att atc tgc aca att act cca gta		1023	
Leu Gly Gly Asn Pro Lys Thr Arg Ile Ile Cys Thr Ile Thr Pro Val			
296	301	306	311
tct ttt gat gaa act ctt act gct ctc cag ttt gcc agt act gct aaa		1071	
Ser Phe Asp Glu Thr Leu Thr Ala Leu Gln Phe Ala Ser Thr Ala Lys			
312	317	322	327
tat atg aag aat act cct tat gtt aat gag gta tca act gat gaa gct		1119	
Tyr Met Lys Asn Thr Pro Tyr Val Asn Glu Val Ser Thr Asp Glu Ala			
328	333	338	343
ctc ctg aaa agg tat aga aaa gaa ata atg gat ctt aaa aaa caa tta		1167	
Leu Leu Lys Arg Tyr Arg Lys Glu Ile Met Asp Leu Lys Lys Gln Leu			
344	349	354	359
gag gag gtt tct tta gag acg cgg gct cag gca atg gaa aaa gac caa		1215	
Glu Glu Val Ser Leu Glu Thr Arg Ala Gln Ala Met Glu Lys Asp Gln			
360	365	370	375
ttg gcc caa ctt ttg gaa gaa aaa gat ttg ctt cag aaa gta cag aat		1263	
Leu Ala Gln Leu Leu Glu Glu Lys Asp Leu Leu Gln Lys Val Gln Asn			
376	381	386	391
gag aaa att gaa aac tta aca cgg atg ctg gtg acc tct tct tcc ctc		1311	
Glu Lys Ile Glu Asn Leu Thr Arg Met Leu Val Thr Ser Ser Ser Leu			
392	397	402	407
acg ttg caa cag gaa tta aag gct aaa aga aaa cga aga gtt act tgg		1359	
Thr Leu Gln Gln Glu Leu Lys Ala Lys Arg Lys Arg Arg Val Thr Trp			
408	413	418	423
tgc ctt ggc aaa att aac aaa atg aag aac tca aac tat gca gat caa		1407	
Cys Leu Gly Lys Ile Asn Lys Met Lys Asn Ser Asn Tyr Ala Asp Gln			
424	429	434	439

ttt aat ata cca aca aat ata aca aca aaa aca cat aag ctt tct ata Phe Asn Ile Pro Thr Asn Ile Thr Thr Lys Thr His Lys Leu Ser Ile 440 445 450 455	1455
aat tta tta cga gaa att gat gaa tct gtc tgt tca gag tct gat gtt Asn Leu Leu Arg Glu Ile Asp Glu Ser Val Cys Ser Glu Ser Asp Val 456 461 466 471	1503
ttc agt aac act ctt gat aca tta agt gag ata gaa tgg aat cca gca Phe Ser Asn Thr Leu Asp Thr Leu Ser Glu Ile Glu Trp Asn Pro Ala 472 477 482 487	1551
aca aag cta cta aat cag gag aat ata gaa agt gag ttg aac tca ctt Thr Lys Leu Leu Asn Gln Glu Asn Ile Glu Ser Glu Leu Asn Ser Leu 488 493 498 503	1599
cgt gct gac tat gat aat ctg gta tta gac tat gaa caa cta cga aca Arg Ala Asp Tyr Asp Asn Leu Val Leu Asp Tyr Glu Gln Leu Arg Thr 504 509 514 519	1647
gaa aaa_aaa_aaa atg_gaa_ttg_aaa tta .aaa_gaa_aag_aat_gat_ttg_gat Glu Lys Lys Lys Met Glu Leu Lys Leu Lys Glu Lys Asn Asp Leu Asp 520 525 530 535	1695
gaa ttt gag gct cta gaa aga aaa act aaa aaa gat caa gag atg caa Glu Phe Glu Ala Leu Glu Arg Lys Thr Lys Lys Asp Gln Glu Met Gln 536 541 546 551	1743
cta att cat gaa att tcg aac tta aag aat tta gtt aag cat cga gaa Leu Ile His Glu Ile Ser Asn Leu Lys Asn Leu Val Lys His Arg Glu 552 557 562 567	1791
gta tat aat caa gat ctt gag aat gaa ctc agt tca aaa gta gag ctg Val Tyr Asn Gln Asp Leu Glu Asn Glu Leu Ser Ser Lys Val Glu Leu 568 573 578 583	1839
ctt aga gaa aag gaa gac cag att aag aag cta cag gaa tac ata gac Leu Arg Glu Lys Glu Asp Gln Ile Lys Lys Leu Gln Glu Tyr Ile Asp 584 589 594 599	1887
tct caa aag cta gaa aat ata aaa atg gac ttg tca tac tca ttg gaa Ser Gln Lys Leu Glu Asn Ile Lys Met Asp Leu Ser Tyr Ser Leu Glu 600 605 610 615	1935
agc att gaa gac cca aaa caa atg aag cag act ctg ttt gat gct gaa Ser Ile Glu Asp Pro Lys Gln Met Lys Gln Thr Leu Phe Asp Ala Glu 616 621 626 631	1983
act gta gcc ctt gat gcc aag aga gaa tca gcc ttt ctt aga agt gaa Thr Val Ala Leu Asp Ala Lys Arg Glu Ser Ala Phe Leu Arg Ser Glu 632 637 642 647	2031
aat ctg gag ttg aag gag aaa atg aaa gaa ctt gca act aca tac aag Asn Leu Glu Leu Lys Glu Lys Met Lys Glu Leu Ala Thr Thr Tyr Lys 648 653 658 663	2079
caa atg gaa aat gat att cag tta tat caa agc caa ttg gag gca aaa	2127

Gln	Met	Glu	Asn	Asp	Ile	Gln	Leu	Tyr	Gln	Ser	Gln	Leu	Glu	Ala	Lys	
664		669			674				674		679					
aag	aaa	atg	caa	gtt	gat	ctg	gag	aaa	gaa	tta	caa	tct	gct	ttt	aat	2175
Lys	Lys	Met	Gln	Val	Asp	Leu	Glu	Lys	Glu	Leu	Gln	Ser	Ala	Phe	Asn	
680		685			690				690		695					
gag	ata	aca	aaa	ctc	acc	tcc	ctt	ata	gat	ggc	aaa	gtt	cca	aaa	gat	2223
Glu	Ile	Thr	Lys	Leu	Thr	Ser	Leu	Ile	Asp	Gly	Lys	Val	Pro	Lys	Asp	
696		701			706			706		711						
ttg	ctc	tgt	aat	ttg	gaa	ttg	gaa	gga	aag	att	act	gat	ctt	cag	aaa	2271
Leu	Leu	Cys	Asn	Leu	Glu	Leu	Glu	Gly	Lys	Ile	Thr	Asp	Leu	Gln	Lys	
712		717			722			722		727						
gaa	cta	aat	aaa	gaa	gtt	gaa	gaa	aat	gaa	gct	ttg	cgg	gaa	gaa	gtc	2319
Glu	Leu	Asn	Lys	Glu	Val	Glu	Glu	Asn	Glu	Ala	Leu	Arg	Glu	Glu	Val	
728		733			738			738		743						
att	ttg	ctt	tca	gaa	ttg	aaa	tct	tta	cct	tct	gaa	gta	gaa	agg	ctg	2367
Ile	Leu	Leu	Ser	Glu	Leu	Lys	Ser	Leu	Pro	Ser	Glu	Val	Glu	Arg	Leu	
744		749			754			754		759						
agg	aaa	gag	ata	caa	gac	aaa	tct	gaa	gag	ctc	cat	ata	ata	aca	tca	2415
Arg	Lys	Glu	Ile	Gln	Asp	Lys	Ser	Glu	Glu	Leu	His	Ile	Ile	Thr	Ser	
760		765			770			770		775						
gaa	aaa	gat	aaa	ttg	ttt	tct	gaa	gta	gtt	cat	aag	gag	agt	aga	gtt	2463
Glu	Lys	Asp	Lys	Leu	Phe	Ser	Glu	Val	Val	His	Lys	Glu	Ser	Arg	Val	
776		781			786			786		791						
caa	ggt	tta	ctt	gaa	gaa	att	ggg	aaa	aca	aaa	gat	gac	cta	gca	act	2511
Gln	Gly	Leu	Leu	Glu	Ile	Gly	Lys	Thr	Lys	Asp	Asp	Asp	Leu	Ala	Thr	
792		797			802			802		807						
aca	cag	tcg	aat	tat	aaa	agc	act	gat	caa	gaa	ttc	caa	aat	ttc	aaa	2559
Thr	Gln	Ser	Asn	Tyr	Lys	Ser	Thr	Asp	Gln	Glu	Phe	Gln	Asn	Phe	Lys	
808		813			818			818		823						
acc	ctt	cat	atg	gac	ttt	gag	caa	aag	tat	aag	atg	gtc	ctt	gag	gag	2607
Thr	Leu	His	Met	Asp	Phe	Glu	Gln	Lys	Tyr	Lys	Met	Val	Leu	Glu	Glu	
824		829			834			834		839						
aat	gag	aga	atg	aat	cag	gaa	ata	gtt	aat	ctc	tct	aaa	gaa	gcc	caa	2655
Asn	Glu	Arg	Met	Asn	Gln	Glu	Ile	Val	Asn	Leu	Ser	Lys	Glu	Ala	Gln	
840		845			850			850		855						
aaa	ttt	gat	tcg	agt	ttg	ggt	gct	ttg	aag	acc	gag	ctt	tct	tac	aag	2703
Lys	Phe	Asp	Ser	Ser	Leu	Gly	Ala	Leu	Lys	Thr	Glu	Leu	Ser	Tyr	Lys	
856		861			866			866		871						
acc	caa	gaa	ctt	cag	gag	aaa	aca	cgt	gag	gtt	caa	gaa	aga	cta	aat	2751
Thr	Gln	Glu	Leu	Gln	Glu	Lys	Thr	Arg	Glu	Val	Gln	Glu	Arg	Leu	Asn	
872		877			882			882		887						
gag	atg	gaa	cag	ctg	aag	gaa	caa	tta	gaa	aat	aga	gat	tct	ccg	ctg	2799
Glu	Met	Glu	Gln	Leu	Lys	Glu	Gln	Leu	Glu	Asn	Arg	Asp	Ser	Pro	Leu	

888	893	898	903	
caa act gta gaa agg gag aaa aca ctg att act gag aaa ctg cag caa Gln Thr Val Glu Arg Glu Lys Thr Leu Ile Thr Glu Lys Leu Gln Gln 904 909 914 919				2847
act tta gaa gaa gta aaa act tta act caa gaa aaa gat gat cta aaa Thr Leu Glu Glu Val Lys Thr Leu Thr Gln Glu Lys Asp Asp Leu Lys 920 925 930 935				2895
caa ctc caa gaa agc ttg caa att gag agg gac caa ctc aaa agt gat Gln Leu Gln Glu Ser Leu Gln Ile Glu Arg Asp Gln Leu Lys Ser Asp 936 941 946 951				2943
att cac gat act gtt aac atg aat ata gat act caa gaa caa tta cga Ile His Asp Thr Val Asn Met Asn Ile Asp Thr Gln Glu Gln Leu Arg 952 957 962 967				2991
aat gct ctt gag tct ctg aaa caa cat caa gaa aca att aat aca cta Asn Ala Leu Glu Ser Leu Lys Gln His Gln Glu Thr Ile Asn Thr Leu 968 973 978 983				3039
aaa tcg aaa att tct gag gaa gtt tcc agg aat ttg cat atg gag gaa Lys Ser Lys Ile Ser Glu Glu Val Ser Arg Asn Leu His Met Glu Glu 984 989 994 999				3087
aat aca gga gaa act aaa gat gaa ttt cag caa aag atg gtt ggc ata Asn Thr Gly Glu Thr Lys Asp Glu Phe Gln Gln Lys Met Val Gly Ile 1000 1005 1010 1015				3135
gat aaa aaa cag gat ttg gaa gct aaa aat acc caa aca cta act gca Asp Lys Lys Gln Asp Leu Glu Ala Lys Asn Thr Gln Thr Leu Thr Ala 1016 1021 1026 1031				3183
gat gtt aag gat aat gag ata att gag caa caa agg aag ata ttt tct Asp Val Lys Asp Asn Glu Ile Ile Glu Gln Gln Arg Lys Ile Phe Ser 1032 1037 1042 1047				3231
tta ata cag gag aaa aat gaa ctc caa caa atg tta gag agt gtt ata Leu Ile Gln Glu Lys Asn Glu Leu Gln Gln Met Leu Glu Ser Val Ile 1048 1053 1058 1063				3279
gca gaa aag gaa caa ttg aag act gac cta aag gaa aat att gaa atg Ala Glu Lys Glu Gln Leu Lys Thr Asp Leu Lys Glu Asn Ile Glu Met 1064 1069 1074 1079				3327
acc att gaa aac cag gaa gaa tta aga ctt ctt ggg gat gaa ctt aaa Thr Ile Glu Asn Gln Glu Glu Leu Arg Leu Leu Gly Asp Glu Leu Lys 1080 1085 1090 1095				3375
aag caa caa gag ata gtt gca caa gaa aag aac cat gcc ata aag aaa Lys Gln Gln Glu Ile Val Ala Gln Glu Lys Asn His Ala Ile Lys Lys 1096 1101 1106 1111				3423
gaa gga gag ctt tct agg acc tgt gac aga ctg gca gaa gtt gaa gaa Glu Gly Glu Leu Ser Arg Thr Cys Asp Arg Leu Ala Glu Val Glu Glu 1112 1117 1122 1127				3471

aaa cta aag gaa aag agc cag caa ctc caa gaa aaa cag caa caa ctt				3519
Lys Leu Lys Glu Lys Ser Gln Gln Leu Gln Glu Lys Gln Gln Gln Leu				
1128	1133	1138	1143	
ctt aat gta caa gaa gag atg agt gag atg cag aaa aag att aat gaa				3567
Leu Asn Val Gln Glu Glu Met Ser Glu Met Gln Lys Lys Ile Asn Glu				
1144	1149	1154	1159	
ata gag aat tta aag aat gaa tta aag aac aaa gaa ttg aca ttg gaa				3615
Ile Glu Asn Leu Lys Asn Glu Leu Lys Asn Lys Glu Leu Thr Leu Glu				
1160	1165	1170	1175	
cat atg gaa aca gag agg ctt gag ttg gct cag aaa ctt aat gaa aat				3663
His Met Glu Thr Glu Arg Leu Glu Leu Ala Gln Lys Leu Asn Glu Asn				
1176	1181	1186	1191	
tat gag gaa gtg aaa tct ata acc aaa gaa aga aaa gtt cta aag gaa				3711
Tyr Glu Glu Val Lys Ser Ile Thr Lys Glu Arg Lys Val Leu Lys Glu				
1192	1197	1202	1207	
tta cag aag tca ttt gaa aca gag aga gac cac ctt aga gga tat ata				3759
Leu Gln Lys Ser Phe Glu Thr Glu Arg Asp His Leu Arg Gly Tyr Ile				
1208	1213	1218	1223	
aga gaa att gaa gct aca ggc cta caa acc aaa gaa gaa cta aaa att				3807
Arg Glu Ile Glu Ala Thr Gly Leu Gln Thr Lys Glu Glu Leu Lys Ile				
1224	1229	1234	1239	
gct cat att cac cta aaa gaa cac caa gaa act att gat gaa cta aga				3855
Ala His Ile His Leu Lys Glu His Gln Glu Thr Ile Asp Glu Leu Arg				
1240	1245	1250	1255	
aga agc gta tct gag aag aca gct caa ata ata aat act cag gac tta				3903
Arg Ser Val Ser Glu Lys Thr Ala Gln Ile Ile Asn Thr Gln Asp Leu				
1256	1261	1266	1271	
gaa aaa tcc cat acc aaa tta caa gaa gag atc cca gtg ctt cat gag				3951
Glu Lys Ser His Thr Lys Leu Gln Glu Glu Ile Pro Val Leu His Glu				
1272	1277	1282	1287	
gaa caa gag tta ctg cct aat gtg aaa aaa gtc agt gag act cag gaa				3999
Glu Gln Glu Leu Leu Pro Asn Val Lys Lys Val Ser Glu Thr Gln Glu				
1288	1293	1298	1303	
aca atg aat gaa ctg gag tta tta aca gaa cag tcc aca acc aag gac				4047
Thr Met Asn Glu Leu Glu Leu Leu Thr Glu Gln Ser Thr Thr Lys Asp				
1304	1309	1314	1319	
tca aca aca ctg gca aga ata gaa atg gaa agg ctc agg ttg aat gaa				4095
Ser Thr Thr Leu Ala Arg Ile Glu Met Glu Arg Leu Arg Leu Asn Glu				
1320	1325	1330	1335	
aaa ttt caa gaa agt cag gaa gag ata aaa tct cta acc aag gaa aga				4143
Lys Phe Gln/Glu Ser Gln Glu Glu Ile Lys Ser Leu Thr Lys Glu Arg				
1336	1341	1346	1351	

gac aac ctt aaa acg ata aaa gaa gcc ctt gaa gtt aaa cat gac cag			4191
Asp Asn Leu Lys Thr Ile Lys Glu Ala Leu Glu Val Lys His Asp Gln			
1352	1357	1362	1367
ctg aaa gaa cat att aga gaa act ttg gct aaa atc cag gag tct caa			4239
Leu Lys Glu His Ile Arg Glu Thr Leu Ala Lys Ile Gln Glu Ser Gln			
1368	1373	1378	1383
agc aaa caa gaa cag tcc tta aat atg aaa gaa aaa gac aat gaa act			4287
Ser Lys Gln Glu Gln Ser Leu Asn Met Lys Glu Lys Asp Asn Glu Thr			
1384	1389	1394	1399
acc aaa atc gtg agt gag atg gag caa ttc aaa ccc aaa gat tca gca			4335
Thr Lys Ile Val Ser Glu Met Glu Gln Phe Lys Pro Lys Asp Ser Ala			
1400	1405	1410	1415
cta cta agg ata gaa ata gaa atg ctc gga ttg tcc aaa aga ctt caa			4383
Leu Leu Arg Ile Glu Ile Glu Met Leu Gly Leu Ser Lys Arg Leu Gln			
1416	1421	1426	1431
gaa agt cat gat gaa atg aaa tct gta gct aag gag aaa gat gac cta			4431
Glu Ser His Asp Glu Met Lys Ser Val Ala Lys Glu Lys Asp Asp Leu			
1432	1437	1442	1447
cag agg ctg caa gaa gtt ctt caa tct gaa agt gac cag ctc aaa gaa			4479
Gln Arg Leu Gln Glu Val Leu Gln Ser Glu Ser Asp Gln Leu Lys Glu			
1448	1453	1458	1463
aac ata aaa gaa att gta gct aaa cac ctg gaa act gaa gag gaa ctt			4527
Asn Ile Lys Glu Ile Val Ala Lys His Leu Glu Thr Glu Glu Glu Leu			
1464	1469	1474	1479
aaa gtt gct cat tgt tgc ctg aaa gaa caa gag gaa act att aat gag			4575
Lys Val Ala His Cys Cys Leu Lys Glu Gln Glu Glu Thr Ile Asn Glu			
1480	1485	1490	1495
tta aga gtg aat ctt tca gag aag gaa act gaa ata tca acc att caa			4623
Leu Arg Val Asn Leu Ser Glu Lys Glu Thr Glu Ile Ser Thr Ile Gln			
1496	1501	1506	1511
aag cag tta gaa gca atc aat gat aaa tta cag aac aag atc caa gag			4671
Lys Gln Leu Glu Ala Ile Asn Asp Lys Leu Gln Asn Lys Ile Gln Glu			
1512	1517	1522	1527
att tat gag aaa gag gaa caa ctt aat ata aaa caa att agt gag gtt			4719
Ile Tyr Glu Lys Glu Glu Gln Leu Asn Ile Lys Gln Ile Ser Glu Val			
1528	1533	1538	1543
cag gaa aaa gtg aat gaa ctg aaa caa ttc aag gag cat cgc aaa gcc			4767
Gln Glu Lys Val Asn Glu Leu Lys Gln Phe Lys Glu His Arg Lys Ala			
1544	1549	1554	1559
aag gat tca gca cta caa agt ata gaa agt aag atg ctc gag ttg acc			4815
Lys Asp Ser Ala Leu Gln Ser Ile Glu Ser Lys Met Leu Glu Leu Thr			
1560	1565	1570	1575
aac aga ctt caa gaa agt caa gaa ata caa att atg att aag gaa			4863

Asn Arg Leu Gln Glu Ser Gln Glu Glu Ile Gln Ile Met Ile Lys Glu				
1576	1581	1586	1591	
aaa gag gaa atg aaa aga gta cag gag gcc ctt cag ata gag aga gac				4911
Lys Glu Glu Met Lys Arg Val Gln Glu Ala Leu Gln Ile Glu Arg Asp				
1592	1597	1602	1607	
caa ctg aaa gaa aac act aaa gaa att gta gct aaa atg aaa gaa tct				4959
Gln Leu Lys Glu Asn Thr Lys Glu Ile Val Ala Lys Met Lys Glu Ser				
1608	1613	1618	1623	
caa gaa aaa gaa tat cag ttt ctt aag atg aca gct gtc aat gag act				5007
Gln Glu Lys Glu Tyr Gin Phe Leu Lys Met Thr Ala Val Asn Glu Thr				
1624	1629	1634	1639	
cag gag aaa atg tgt gaa ata gaa cac ttg aag gag caa ttt gag acc				5055
Gln Glu Lys Met Cys Glu Ile Glu His Leu Lys Glu Gln Phe Glu Thr				
1640	1645	1650	1655	
cag aag tta aac ctg gaa aac ata gaa acg gag aat ata agg ttg act				5103
Gln Lys Leu Asn Leu Asn Ile Glu Thr Glu Asn Ile Arg Leu Thr				
1656	1661	1666	1671	
cag ata cta cat gaa aac ctt gaa gaa atg aga tct gta aca aaa gaa				5151
Gln Ile Leu His Glu Asn Leu Glu Glu Met Arg Ser Val Thr Lys Glu				
1672	1677	1682	1687	
aga gat gac ctt agg agt gtg gag gag act ctc aaa gta gag aga gac				5199
Arg Asp Asp Leu Arg Ser Val Glu Glu Thr Leu Lys Val Glu Arg Asp				
1688	1693	1698	1703	
cag ctc aag gaa aac ctt aga gaa act ata act aga gac cta gaa aaa				5247
Gln Leu Lys Glu Asn Leu Arg Glu Thr Ile Thr Arg Asp Leu Glu Lys				
1704	1709	1714	1719	
caa gag gag cta aaa att gtt cac atg cat ctg aag gag cac caa gaa				5295
Gln Glu Glu Leu Lys Ile Val His Met His Leu Lys Glu His Gln Glu				
1720	1725	1730	1735	
act att gat aaa cta aga ggg att gtt tca gag aaa aca aat gaa ata				5343
Thr Ile Asp Lys Leu Arg Gly Ile Val Ser Glu Lys Thr Asn Glu Ile				
1736	1741	1746	1751	
tca aat atg caa aag gac tta gaa cac tca aat gat gcc tta aaa gca				5391
Ser Asn Met Gln Lys Asp Leu Glu His Ser Asn Asp Ala Leu Lys Ala				
1752	1757	1762	1767	
cag gat ctg aaa ata caa gag gaa cta aga att gct cac atg cat ctg				5439
Gln Asp Leu Lys Ile Gln Glu Glu Leu Arg Ile Ala His Met His Leu				
1768	1773	1778	1783	
aaa gag cag cag gaa act att gac aaa ctc aga gga att gtt tct gag				5487
Lys Glu Gln Gln Glu Thr Ile Asp Lys Leu Arg Gly Ile Val Ser Glu				
1784	1789	1794	1799	
aag aca gat aaa cta tca aat atg caa aaa gat tta gaa aat tca aat				5535
Lys Thr Asp Lys Leu Ser Asn Met Gln Lys Asp Leu Glu Asn Ser Asn				

1800	1805	1810	1815	
gct aaa tta caa gaa aag att caa gaa ctt aag gca aat gaa cat caa Ala Lys Leu Gln Glu Lys Ile Gln Glu Leu Lys Ala Asn Glu His Gln 1816 1821 1826 1831				5583
ctt att acg tta aaa aaa gat gtc aat gag aca cag aaa aaa gtg tct Leu Ile Thr Leu Lys Lys Asp Val Asn Glu Thr Gln Lys Lys Val Ser 1832 1837 1842 1847				5631
gaa atg gag caa cta aag aaa caa ata aaa gac caa agc tta act ctg Glu Met Glu Gln Leu Lys Lys Gln Ile Lys Asp Gln Ser Leu Thr Leu 1848 1853 1858 1863				5679
agt aaa tta gaa ata gag aat tta aat ttg gct caa gaa ctt cat gaa Ser Lys Leu Glu Ile Glu Asn Leu Asn Leu Ala Gln Glu Leu His Glu 1864 1869 1874 1879				5727
aac ctt gaa gaa atg aaa tct gta atg aaa gaa aga gat aat cta aga Asn Leu Glu Glu Met Lys Ser Val Met Lys Glu Arg Asp Asn Leu Arg 1880 1885 1890 1895				5775
aga gta gag gag aca ctc aaa ctg gag aga gac caa ctc aag gaa agc Arg Val Glu Glu Thr Leu Lys Leu Glu Arg Asp Gln Leu Lys Glu Ser 1896 1901 1906 1911				5823
ctg caa gaa acc aaa gct aga gat ctg gaa ata caa cag gaa cta aaa Leu Gln Glu Thr Lys Ala Arg Asp Leu Glu Ile Gln Gln Glu Leu Lys 1912 1917 1922 1927				5871
act gct cgt atg cta tca aaa gaa cac aaa gaa act gtt gat aaa ctt Thr Ala Arg Met Leu Ser Lys Glu His Lys Glu Thr Val Asp Lys Leu 1928 1933 1938 1943				5919
aga gaa aaa att tca gaa aag aca att caa att tca gac att caa aag Arg Glu Lys Ile Ser Glu Lys Thr Ile Gln Ile Ser Asp Ile Gln Lys 1944 1949 1954 1959				5967
gat tta gat aaa tca aaa gat gaa tta cag aaa aag atc caa gaa ctt Asp Leu Asp Lys Ser Lys Asp Glu Leu Gln Lys Lys Ile Gln Glu Leu 1960 1965 1970 1975				6015
cag aaa aaa gaa ctt caa ctg ctt aga gtg aaa gaa gat gtc aat atg Gln Lys Lys Glu Leu Gln Leu Leu Arg Val Lys Glu Asp Val Asn Met 1976 1981 1986 1991				6063
agt cat aaa aaa att aat gaa atg gaa cag ttg aag aag caa ttt gag Ser His Lys Lys Ile Asn Glu Met Glu Gln Leu Lys Lys Gln Phe Glu 1992 1997 2002 2007				6111
cca aac tat cta tgc aag tgt gag atg gat aac ttc cag ttg act aag Pro Asn Tyr Leu Cys Lys Cys Glu Met Asp Asn Phe Gln Leu Thr Lys 2008 2013 2018 2023				6159
aaa ctt cat gaa agc ctt gaa gaa ata aga att gta gct aaa gaa aga Lys Leu His Glu Ser Leu Glu Glu Ile Arg Ile Val Ala Lys Glu Arg 2024 2029 2034 2039				6207

gat gag cta agg agg ata aaa gaa tct ctc aaa atg gaa agg gac caa			6255
Asp Glu Leu Arg Arg Ile Lys Glu Ser Leu Lys Met Glu Arg Asp Gln			
2040 2045 2050 2055			
ttc ata gca acc tta agg gaa atg ata gct aga gac cga cag aac cac			6303
Phe Ile Ala Thr Leu Arg Glu Met Ile Ala Arg Asp Arg Gln Asn His			
2056 2061 2066 2071			
caa gta aaa cct gaa aaa agg tta cta agt gat gga caa cag cac ctt			6351
Gln Val Lys Pro Glu Lys Arg Leu Leu Ser Asp Gly Gln Gln His Leu			
2072 2077 2082 2087			
atg gaa agc ctg aga gaa aag tgc tct aga ata aaa gag ctt ttg aag			6399
Met Glu Ser Leu Arg Glu Lys Cys Ser Arg Ile Lys Glu Leu Leu Lys			
2088 2093 2098 2103			
aga tac tca gag atg gat cat tat gag tgc ttg aat aga ttg tct			6447
Arg Tyr Ser Glu Met Asp Asp His Tyr Glu Cys Leu Asn Arg Leu Ser			
2104 2109 2114 2119			
ctt gac ttg gag aag gaa att gaa ttc cac aga atc atg aag aaa ctg			6495
Leu Asp Leu Glu Lys Glu Ile Glu Phe His Arg Ile Met Lys Lys Leu			
2120 2125 2130 2135			
aag tat gtg tta agc tat gtt aca aaa ata aaa gaa gaa caa cat gaa			6543
Lys Tyr Val Leu Ser Tyr Val Thr Lys Ile Lys Glu Glu Gln His Glu			
2136 2141 2146 2151			
tcc atc aat aaa ttt gaa atg gat ttt att gat gaa gtg gaa aag caa			6591
Ser Ile Asn Lys Phe Glu Met Asp Phe Ile Asp Glu Val Glu Lys Gln			
2152 2157 2162 2167			
aag gaa ttg cta att aaa ata cag cac ctt caa caa gat tgt gat gta			6639
Lys Glu Leu Leu Ile Lys Ile Gln His Leu Gln Gln Asp Cys Asp Val			
2168 2173 2178 2183			
cca tcc aga gaa tta agg gat ctc aaa ttg aac cag aat atg gat cta			6687
Pro Ser Arg Glu Leu Arg Asp Leu Lys Leu Asn Gln Asn Met Asp Leu			
2184 2189 2194 2199			
cat att gag gaa att ctc aaa gat ttc tca gaa agt gag ttc cct agc			6735
His Ile Glu Glu Ile Leu Lys Asp Phe Ser Glu Ser Glu Phe Pro Ser			
2200 2205 2210 2215			
ata aag act gaa ttt caa caa gta cta agt aat agg aaa gaa atg aca			6783
Ile Lys Thr Glu Phe Gln Gln Val Leu Ser Asn Arg Lys Glu Met Thr			
2216 2221 2226 2231			
cag ttt ttg gaa gag tgg tta aat act cgt ttt gat ata gaa aag ctt			6831
Gln Phe Leu Glu Glu Trp Leu Asn Thr Arg Phe Asp Ile Glu Lys Leu			
2232 2237 2242 2247			
aaa aat ggc atc cag aaa gaa aat gat agg att tgt caa gtg aat aac			6879
Lys Asn Gly Ile Gln Lys Glu Asn Asp Arg Ile Cys Gln Val Asn Asn			
2248 2253 2258 2263			

ttc ttt aat aac aga ata att gcc ata atg aat gaa tca aca gag ttt			6927
Phe Phe Asn Asn Arg Ile Ile Ala Ile Met Asn Glu Ser Thr Glu Phe			
2264	2269	2274	2279
 gag gaa aga agt gct acc ata tcc aaa gag tgg gaa cag gac ctg aaa			6975
Glu Glu Arg Ser Ala Thr Ile Ser Lys Glu Trp Glu Gln Asp Leu Lys			
2280	2285	2290	2295
 tca ctg aaa gag aaa aat gaa aaa cta ttt aaa aac tac caa aca ttg			7023
Ser Leu Lys Glu Lys Asn Glu Lys Leu Phe Lys Asn Tyr Gln Thr Leu			
2296	2301	2306	2311
 aag act tcc ttg gca tct ggt gcc cag gtt aat cct acc aca caa gac			7071
Lys Thr Ser Leu Ala Ser Gly Ala Gln Val Asn Pro Thr Thr Gln Asp			
2312	2317	2322	2327
 aat aag aat cct cat gtt aca tca aga gct aca cag tta acc aca gag			7119
Asn Lys Asn Pro His Val Thr Ser Arg Ala Thr Gln Leu Thr Thr Glu			
2328	2333	2338	2343
 aaa att cga gag ctg gaa aat tca ctg cat gaa gct aaa gaa agt gct			7167
Lys Ile Arg Glu Leu Glu Asn Ser Leu His Glu Ala Lys Glu Ser Ala			
2344	2349	2354	2359
 atg cat aag gaa agc aag att ata aag atg cag aaa gaa ctt gag gtg			7215
Met His Lys Glu Ser Lys Ile Ile Lys Met Gln Lys Glu Leu Glu Val			
2360	2365	2370	2375
 act aat gac ata ata gca aaa ctt caa gcc aaa gtt cat gaa tca aat			7263
Thr Asn Asp Ile Ile Ala Lys Leu Gln Ala Lys Val His Glu Ser Asn			
2376	2381	2386	2391
 aaa tgc ctt gaa aaa aca aaa gag aca att caa gta ctt cag gac aaa			7311
Lys Cys Leu Glu Lys Thr Lys Glu Thr Ile Gln Val Leu Gln Asp Lys			
2392	2397	2402	2407
 gtt gct tta gga gct aag cca tat aaa gaa gaa att gaa gat ctc aaa			7359
Val Ala Leu Gly Ala Lys Pro Tyr Lys Glu Glu Ile Glu Asp Leu Lys			
2408	2413	2418	2423
 atg aag ctt gtg aaa ata gac cta gag aaa atg aaa aat gcc aaa gaa			7407
Met Lys Leu Val Lys Ile Asp Leu Glu Lys Met Lys Asn Ala Lys Glu			
2424	2429	2434	2439
 ttt gaa aag gaa atc agt gct aca aaa gcc act gta gaa tat caa aag			7455
Phe Glu Lys Glu Ile Ser Ala Thr Lys Ala Thr Val Glu Tyr Gln Lys			
2440	2445	2450	2455
 gaa gtt ata agg cta ttg aga gaa aat ctc aga aga agt caa cag gcc			7503
Glu Val Ile Arg Leu Leu Arg Glu Asn Leu Arg Arg Ser Gln Gln Ala			
2456	2461	2466	2471
 caa gat acc tca gtg ata tca gaa cat act gat cct cag cct tca aat			7551
Gln Asp Thr Ser Val Ile Ser Glu His Thr Asp Pro Gln Pro Ser Asn			
2472	2477	2482	2487
 aaa ccc tta act tgt gga ggt ggc agc ggc att gta caa aac aca aaa			7599

Lys Pro Leu Thr Cys Gly Gly Ser Gly Ile Val Gln Asn Thr Lys				
2488	2493	2498	2503	
gct ctt att ttg aaa agt gaa cat ata agg cta gaa aaa gaa att tct				7647
Ala Leu Ile Leu Lys Ser Glu His Ile Arg Leu Glu Lys Glu Ile Ser				
2504	2509	2514	2519	
aag tta aag cag caa aat gaa cag cta ata aaa caa aag aat gaa ttg				7695
Lys Leu Lys Gln Gln Asn Glu Gln Leu Ile Lys Gln Lys Asn Glu Leu				
2520	2525	2530	2535	
tta agc aat aat cag cat ctt tcc aat gag gtc aaa act tgg aag gaa				7743
Leu Ser Asn Asn Gln His Leu Ser Asn Glu Val Lys Thr Trp Lys Glu				
2536	2541	2546	2551	
aga acc ctt aaa aga gag gct cac aaa caa gta act tgt gag aat tct				7791
Arg Thr Leu Lys Arg Glu Ala His Lys Gln Val Thr Cys Glu Asn Ser				
2552	2557	2562	2567	
cca aag tct cct aaa gtg act gga aca gct tct aaa aag aaa caa att				7839
Pro Lys Ser Pro Lys Val Thr Gly Thr Ala Ser Lys Lys Lys Gln Ile				
2568	2573	2578	2583	
aca ccc tct caa tgc aag gaa cgg aat tta caa gat cct gtg cca aag				7887
Thr Pro Ser Gln Cys Lys Glu Arg Asn Leu Gln Asp Pro Val Pro Lys				
2584	2589	2594	2599	
gaa tca cca aaa tct tgt ttt ttt gat agc cga tca aag tct tta cca				7935
Glu Ser Pro Lys Ser Cys Phe Phe Asp Ser Arg Ser Lys Ser Leu Pro				
2600	2605	2610	2615	
tca cct cat cca gtt cgc tat ttt gat aac tca agt tta ggc ctt tgt				7983
Ser Pro His Pro Val Arg Tyr Phe Asp Asn Ser Ser Leu Gly Leu Cys				
2616	2621	2626	2631	
cca gag gtg caa aat gca gga gca gag agt gtg gat tct cag cca ggt				8031
Pro Glu Val Gln Asn Ala Gly Ala Glu Ser Val Asp Ser Gln Pro Gly				
2632	2637	2642	2647	
cct tgg cac gcc tcc tca ggc aag gat gtg cct gag tgc aaa act cag				8079
Pro Trp His Ala Ser Ser Gly Lys Asp Val Pro Glu Cys Lys Thr Gln				
2648	2653	2658	2663	
tag actc ctctttgtca cttctctgga gatccagcat tccttatttg gaaatgactt				8136
*				
2664				
tgttatgtg tctatccctg gtaatgatgt tgttagtgcag cttatattca attcagtctt				8196
tactttgcca ctagagttga aagataaggg aacaggaaat gaatgcattg tggtaattta				
gaatggtgat agcaataacct tcttcttgca tatggtaata cttttaaaag ttgaattgtt				
ttatattttt gtatattttg taaaagaataa agttattgaa agaaatgtaa agttatctac				
atgacttagc atattccaaa gcataataca tacattaata taaaacatca ttttattaaa				
				8316
				8376
				8436

aaaattgtaa atgttttaa taccttacac attcaataaa tgtagtag ttctgaaaaa 8496

aaaaaaaaa 8503

<210> 131
<211> 1693
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (88)..(1512)

<400> 131

atggAACgc ttgaggtccc ggtccggaat tcccggtcg acccacgcgt ccgcggacgc 60

gtgggattct tttaatcaga gttagta atg tgg aca gta caa aat cga gag 111
Met Trp Thr Val Gln Asn Arg Glu
1 5

agt ctg ggg ctt ctc tct ttc cct gtg atg att acc atg gtc tgt tgt 159
Ser Leu Gly Leu Leu Ser Phe Pro Val Met Ile Thr Met Val Cys Cys
9 14 19 24

gca cac agc acc aat gaa ccc agc aac atg tca tac gtg aaa gag aca 207
Ala His Ser Thr Asn Glu Pro Ser Asn Met Ser Tyr Val Lys Glu Thr
25 30 35 40

gtg gac aga ttg ctc aaa gga tat gac att cgc ttg cggtccg gac ttc 255
Val Asp Arg Leu Leu Lys Gly Tyr Asp Ile Arg Leu Arg Pro Asp Phe
41 46 51 56

gga ggg ccc ccc gtc gac gtt ggg atg cggtccg gac ttc 303
Gly Gly Pro Pro Val Asp Val Gly Met Arg Ile Asp Val Ala Ser Ile
57 62 67 72

gac atg gtc tcc gaa gtg aat atg gat tat aca ctc acc atg tat ttc 351
Asp Met Val Ser Glu Val Asn Met Asp Tyr Thr Leu Thr Met Tyr Phe
73 78 83 88

cag cag tct tgg aaa gac aaa agg ctt tct tat tct gga atc cca ctg 399
Gln Gln Ser Trp Lys Asp Lys Arg Leu Ser Tyr Ser Gly Ile Pro Leu
89 94 99 104

aac ctc acc cta gac aat agg gta gct gac caa ctc tgg gta cca gac 447
Asn Leu Thr Leu Asp Asn Arg Val Ala Asp Gln Leu Trp Val Pro Asp
105 110 115 120

acc tac ttt ctg aat gac aag aaa tca ttt gtg cat ggg gtc aca gtg 495
Thr Tyr Phe Leu Asn Asp Lys Lys Ser Phe Val His Gly Val Thr Val
121 126 131 136

aaa aat cga atg att cga ctg cat cct gat gga aca gtt ctc tat gga 543
Lys Asn Arg Met Ile Arg Leu His Pro Asp Gly Thr Val Leu Tyr Gly

137	142	147	152	
ctc cga atc aca acc aca gct gca tgt atg atg gat ctt cga aga tat Leu Arg Ile Thr Thr Ala Ala Cys Met Met Asp Leu Arg Arg Tyr				591
153	158	163	168	
cca ctg gat gag cag aac tgc acc ctg gag atc gaa agt tat ggc tat Pro Leu Asp Glu Gln Asn Cys Thr Leu Glu Ile Glu Ser Tyr Gly Tyr				639
169	174	179	184	
acc act gat gac att gaa ttt tac tgg aat gga gga gaa ggg gca gtc Thr Thr Asp Asp Ile Glu Phe Tyr Trp Asn Gly Gly Glu Gly Ala Val				687
185	190	195	196	200
act ggt gtt aat aaa atc gaa ctt cct caa ttt tca att gtt gac tac Thr Gly Val Asn Lys Ile Glu Leu Pro Gln Phe Ser Ile Val Asp Tyr				735
201	206	211	216	
aag atg gtg tct aag aag gtg gag ttc aca aca gga gcg tat cca cga Lys Met Val Ser Lys Lys Val Glu Phe Thr Thr Gly Ala Tyr Pro Arg				783
217	222	227	232	
ctg tca cta agt ttt cgt cta aag aga aac att ggt tac ttc att ttg Leu Ser Leu Ser Phe Arg Leu Lys Arg Asn Ile Gly Tyr Phe Ile Leu				831
233	238	243	248	
caa acc tac atg cct tct aca ctg att aca att ctg tcc tgg gtg tct Gln Thr Tyr Met Pro Ser Thr Leu Ile Thr Ile Leu Ser Trp Val Ser				879
249	254	259	264	
ttt tgg atc aac tat gat gca tct gca gcc aga gtc gca cta gga atc Phe Trp Ile Asn Tyr Asp Ala Ser Ala Ala Arg Val Ala Leu Gly Ile				927
265	270	275	280	
acg acg gtg ctt aca atg aca acc atc agc acc cac ctc agg gag acc Thr Thr Val Leu Thr Met Thr Thr Ile Ser Thr His Leu Arg Glu Thr				975
281	286	291	296	
ctg cca aag atc cct tat gtc aaa gcg att gat att tat ctg atg ggt Leu Pro Lys Ile Pro Tyr Val Lys Ala Ile Asp Ile Tyr Leu Met Gly				1023
297	302	307	312	
tgc ttt gtg ttt gtg ttc ctg gct ctg ctg gag tat gcc ttt gta aat Cys Phe Val Phe Val Phe Leu Ala Leu Leu Glu Tyr Ala Phe Val Asn				1071
313	318	323	328	
tac atc ttc ttt ggg aaa ggc cct cag aaa aag gga gct agc aaa caa Tyr Ile Phe Phe Gly Lys Gly Pro Gln Lys Lys Gly Ala Ser Lys Gln				1119
329	334	339	344	
gac cag agt gcc aat gag aag aat aaa ctg gag atg aat aaa gtc cag Asp Gln Ser Ala Asn Glu Lys Asn Lys Leu Glu Met Asn Lys Val Gln				1167
345	350	355	360	
'gtc gac gcc cac ggt aac att ctc ctc agc acc ctg gaa atc cg aat Val Asp Ala His Gly Asn Ile Leu Leu Ser Thr Leu Glu Ile Arg Asn				1215
361	366	371	376	

gag acg agt ggc tcg gaa gtg ctc acg agc gtg agc gac ccc aag gcc		1263
Glu Thr Ser Gly Ser Glu Val Leu Thr Ser Val Ser Asp Pro Lys Ala		
377	382	387
		392
acc atg tac tcc tat gac agc gcc agc atc cag tac cgc aag ccc ctg		1311
Thr Met Tyr Ser Tyr Asp Ser Ala Ser Ile Gln Tyr Arg Lys Pro Leu		
393	398	403
		408
agc agc cgc gag gcc tac ggg cgc gcc ctg gac cgg cac ggg gta ccc		1359
Ser Ser Arg Glu Ala Tyr Gly Arg Ala Leu Asp Arg His Gly Val Pro		
409	414	419
		424
agc aag ggg cgc atc cgc agg cgt gcc tcc cag ctc aaa gtc aag atc		1407
Ser Lys Gly Arg Ile Arg Arg Ala Ser Gln Leu Lys Val Lys Ile		
425	430	435
		440
ccc gac ttg act gat gtg aat tcc ata gac aag tgg tcc cga atg ttt		1455
Pro Asp Leu Thr Asp Val Asn Ser Ile Asp Lys Trp Ser Arg Met Phe		
441	446	451
		456
ttc ccc atc acc ttt tct ctt ttt aat gtc gtc tat tgg ctt tac tat		1503
Phe Pro Ile Thr Phe Ser Leu Phe Asn Val Val Tyr Trp Leu Tyr Tyr		
457	462	467
		472
gta cac tga ggtctgt tctaattgggtt ccatttagac tactttcctc ttctattgtt		1559
Val His *		
473		
tttaacctt acaggcccc aacagcgata ctgctgtttc tcgaggtaag agattcagcc		1619
atccaattgg ttttaggtct tgcataatcag ttttattact gcaccatgtt tacttcaaaa		1679
agacaaaaaa aaaa		1693

<210> 132
 <211> 920
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (171)...(737)

<400> 132		
ttagttatgt gattggagac catggaacgc ctgcggtaacc ggtccggaat tcccggtcg		60
acccacgcgt ccggactagt tctagatcgc gagccgccgc ccaggaaggg gatgcggaaa		120
ccctggctc ggtggagcgg agaggcaggc gggcaggagc cgaggacggc	atg tcc	176
	Met Ser	
	1	
cag gcc ccg gga gca cag ccg agc cca ccc acc gtg tac cac gaa cgg		224

Gln	Ala	Pro	Gly	Ala	Gln	Pro	Ser	Pro	Pro	Thr	Val	Tyr	His	Glu	Arg	
3					8					13				18		
cag	cgc	ctg	gag	ctg	tgt	gct	gtc	cac	gcc	ctc	aac	aac	gtt	ctg	cag	272
Gln	Arg	Leu	Glu	Leu	Cys	Ala	Val	His	Ala	Leu	Asn	Asn	Val	Leu	Gln	
19					24					29				34		
cag	cag	ctc	ttt	agc	cag	gag	gct	gcc	gat	gag	atc	tgc	aag	agg	ttg	320
Gln	Gln	Leu	Phe	Ser	Gln	Glu	Ala	Ala	Asp	Glu	Ile	Cys	Lys	Arg	Leu	
35					40					45				50		
gcc	cca	gac	tcc	cg	ctg	aac	cct	cat	cgc	agc	ctc	ctg	ggc	acc	ggc	368
Ala	Pro	Asp	Ser	Arg	Leu	Asn	Pro	His	Arg	Ser	Leu	Leu	Gly	Thr	Gly	
51					56					61				66		
aac	tat	gat	gtc	aat	gtg	atc	atg	gcc	gct	ctg	cag	ggg	ctg	ggc	ctg	416
Asn	Tyr	Asp	Val	Asn	Val	Ile	Met	Ala	Ala	Leu	Gln	Gly	Leu	Gly	Leu	
67					72					77				82		
gcc	gcc	gtg	tgg	tgg	gac	agg	agg	ccc	ctg	tcc	cag	ctg	gcc	ctg	464	
Ala	Ala	Val	Trp	Trp	Asp	Arg	Arg	Arg	Pro	Leu	Ser	Gln	Leu	Ala	Leu	
83					88					93				98		
ccc	cag	gta	ctg	ggg	ctg	atc	ctg	aac	ctg	ccc	tcg	ccc	gtg	tcg	ctg	512
Pro	Gln	Val	Leu	Gly	Leu	Ile	Leu	Asn	Leu	Pro	Ser	Pro	Val	Ser	Leu	
99					104					109				114		
ggg	ctg	ctg	tca	ctg	ccg	ctg	cgc	cg	cac	tgg	gtg	gcc	ctg	cgc	560	
Gly	Leu	Leu	Ser	Leu	Pro	Leu	Arg	Arg	Arg	His	Trp	Val	Ala	Leu	Arg	
115					120					125				130		
cag	gtg	gac	ggt	gtc	tac	tac	aac	ctg	gac	tcc	aag	ctg	cg	g	ccc	608
Gln	Val	Asp	Gly	Val	Tyr	Tyr	Asn	Leu	Asp	Ser	Lys	Leu	Arg	Ala	Pro	
131					136					141				146		
gag	gcc	ctg	ggg	gat	gag	gac	gga	gtc	agg	gcc	ttc	ctg	g	cg	656	
Glu	Ala	Leu	Gly	Asp	Glu	Asp	Gly	Val	Arg	Ala	Phe	Leu	Ala	Ala	Ala	
147					152					157				162		
ctg	gcc	cag	ggc	ctg	tgc	gag	gtg	ctg	gt	acc	aag	gag	gt	gt	704	
Leu	Ala	Gln	Gly	Leu	Cys	Glu	Val	Leu	Leu	Val	Val	Thr	Lys	Glu	Val	
163					168					173				178		
gag	gag	aag	ggc	agc	tgg	ctg	cg	aca	gac	tga	ccatggct	gaccatggc	*		755	
Glu	Glu	Lys	Gly	Ser	Trp	Leu	Arg	Thr	Asp							
179					184					189						
gccccacagcg	cagtccctgc	acatccccct	ccggctgcgc	acactgcatg	cctggaaag										815	
gcccagcatt	catggaccct	ggggaggccc	cgccccctcc	ccacacccct	gctccccact										875	
gcccgtgctg	cctcaataaa	tctgctgatt	tgcaaaaaaa	aaaaaa											920	
															/	
															/	

<211> 1005

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (276) .. (584)

<400> 133

ttcggtaccg	ctccggaaatt	cccggtcga	cccacgcgtc	cgcagaaaatc	tccaggccac	60
cggctttccg	ctaccggatt	ggctgcgtcc	gggtgctgag	gcccgccccca	tttccccggg	120
tcctttgatc	acgcgcctga	cggctttcc	ggggccccggg	agccaaccga	gggcgttcct	180
gtcggggctg	cagcggcggg	agggagccca	gtggaggcgc	cctccgaag	cgccactgccc	240
catgctgacc	acccagccct	ccggctgctg	atgtc	atg agt aac acc act	gtg	293
				Met Ser Asn Thr Thr	Val	
				1		
ccc	aat gcc ccc	cag gcc aac	agc gac tcc	atg gtg ggc	tat gtg ttg	341
Pro	Asn Ala Pro	Gln Ala Asn	Ser Asp Ser	Met Val Gly	Tyr Val Leu	
7		12	.	17	.	22
ggg	ccc ttc ttc	ctc atc acc	ctg gtc	ggg gtg gtg	gtg gct gtg gta	389
Gly	Pro Phe Phe	Leu Ile	Thr Leu Val	Gly Val Val	Ala Val Val	
23		28	.	33	.	38
atg	tat gta cag	aaa aaa aag	cggttg	gac cggttg	cgccatcac	437
Met	Tyr Val Gln Lys	Lys Arg Val	Asp Arg	Leu Arg His	His His Leu	
39		44	.	49	.	54
ctc	ccc atg tac	agc tat gac	ccaa	gttgaa	ctgtcatgag	485
Leu	Pro Met Tyr Ser	Tyr Asp	Pro Ala Glu	Glu Leu His	Glu Ala Glu	
55		60	.	65	.	70
cag	gag ctg ctc tct	gac atg gga	gac ccc	aag gtgt	gtacatgg	533
Gln	Glu Leu Leu Ser	Asp Met Gly	Asp Pro	Lys Val Val	His Gly Trp	
71		76	.	81	.	86
cag	agt ggc tac	cag cac aag	cggttg	atg ccac	ctgtgtat	581
Gln	Ser Gly Tyr Gln	His Lys Arg	Met Pro	Leu Leu Asp	Val Lys Thr	
87		92	.	97	.	102
tga	cctg acccccttc	cccacccttc	agagcctggg	gtcctggact	gcctggggcc	638
*						
103						
ctgccccatttgc	cttccccctgc	tgtcacctgg	ctccccctgc	tgggtgctgg	gtttccattt	698
ttccctccac	ccaccctcaa	cagcatttgc	tttccatgcc	ctcaccatca	cctcactgccc	758
ccccaggcctt	ttgcccccttg	tgggtgttga	gctccccgccc	ccccccagg	cactcatagg	818
aaaaaggcttt	ccttttggga	tggcggcggc	tggtaaaccc	ctttgccttt	tctagccctc	878

ctgggctggg cttgggcccc aatccccagg caggcttgg agttgttcc atggtgatgg	938
ggccagatgt atagtattca gtatatatTT tgtaaataaa atgtttgtg gctaggaaaa	998
aaaaaaaa	1005

<210> 134
 <211> 4323
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (81)...(3920)

<400> 134	
tccaggctct gcgtgataag ctgtggatct tcctggttca gtctttctat gctgttcgtc	60
acacagaaaag ctggaagctg atg agc aca gat gat caa cag aaa atc caa	110
Met Ser Thr Asp Asp Gln Gln Lys Ile Gln	
1 5	
gca gct gca ttt gac aaa ggt gat gat cga aga ctt ggc aaa aag cct	158
Ala Ala Ala Phe Asp Lys Gly Asp Asp Arg Arg Leu Gly Lys Lys Pro	
11 16 21 26	
ata ttc agt agc tcg cag caa agg aaa caa gtt tct gac tct ggt gat	206
Ile Phe Ser Ser Gln Gln Arg Lys Gln Val Ser Asp Ser Gly Asp	
27 32 37 42	
ata aaa atc aaa tct tgg agg gga aat aac aag aaa gag tgt tgg agt	254
Ile Lys Ile Lys Ser Trp Arg Gly Asn Asn Lys Lys Glu Cys Trp Ser	
43 48 53 58	
tat ctc tct act aat aaa aag atg aaa tct gat gga tta gga gca tct	302
Tyr Leu Ser Thr Asn Lys Lys Met Lys Ser Asp Gly Leu Gly Ala Ser	
59 64 69 74	
gga cat tcg tca agt acc aat aga aat agt ata aat aaa act ctg aag	350
Gly His Ser Ser Ser Thr Asn Arg Asn Ser Ile Asn Lys Thr Leu Lys	
75 80 85 90	
caa gat gat gta aag gaa aaa gat ggt aca aaa ata gca tct aag att	398
Gln Asp Asp Val Lys Glu Lys Asp Gly Thr Lys Ile Ala Ser Lys Ile	
91 96 101 106	
aca aaa gaa cta aaa act ggg gga aaa aat gtt tct gga aag ccc aaa	446
Thr Lys Glu Leu Lys Thr Gly Gly Lys Asn Val Ser Gly Lys Pro Lys	
107 112 117 122	
act gta aca aaa tcc aaa aca gaa aat ggt gat aag gca cgg ttg gaa	494
Thr Val Thr Lys Ser Lys Thr Glu Asn Gly Asp Lys Ala Arg Leu Glu	
123 128 133 138	

aac atg tca cct aga caa gtt gta gaa aga tca gca aca gca gca Asn Met Ser Pro Arg Gln Val Val Glu Arg Ser Ala Thr Ala Ala Ala 139 144 149 154	542
gca gca act gga cag aag aat tta cta aat gga aaa gga gtg aga aat Ala Ala Thr Gly Gln Lys Asn Leu Leu Asn Gly Lys Gly Val Arg Asn 155 160 165 170	590
cag gaa ggg caa att tca ggt gcc aga ccc aag gta ctc aca gga aac Gln Glu Gly Gln Ile Ser Gly Ala Arg Pro Lys Val Leu Thr Gly Asn 171 176 181 186	638
tta aat gtg caa gcc aaa gca aag cct ttg aag aaa gct aca ggg aag Leu Asn Val Gln Ala Lys Ala Lys Pro Leu Lys Ala Thr Gly Lys 187 192 197 202	686
gat tca cca tgc ctc agc atc gca gga ccc tcc agc aga tcc aca gat Asp Ser Pro Cys Leu Ser Ile Ala Gly Pro Ser Ser Arg Ser Thr Asp 203 208 213 218	734
tca agt atg gaa ttc tca att tcc act gaa tgt ctg gat gaa ccg aaa Ser Ser Met Glu Phe Ser Ile Ser Thr Glu Cys Leu Asp Glu Pro Lys 219 224 229 234	782
gaa aat gga tca aca gaa gaa aag cct tct gga cat aaa cta tcc Glu Asn Gly Ser Thr Glu Glu Lys Pro Ser Gly His Lys Leu Ser 235 240 245 250	830
ttt tgt gat tct cca gga cag atg atg aaa aac agt gta gat agt gtc Phe Cys Asp Ser Pro Gly Gln Met Met Lys Asn Ser Val Asp Ser Val 251 256 261 266	878
aaa aat tcc act gta gcc ata aaa tct cga cct gtt tca aga gtt acc Lys Asn Ser Thr Val Ala Ile Lys Ser Arg Pro Val Ser Arg Val Thr 267 272 277 282	926
aat gga act tcc aat aaa aaa agt att cat gaa caa gac act aat gta Asn Gly Thr Ser Asn Lys Ser Ile His Glu Gln Asp Thr Asn Val 283 288 293 298	974
aat aac agt gta cta aag aaa gtc agt ggc aaa gga tgt agt gag cca Asn Asn Ser Val Leu Lys Lys Val Ser Gly Lys Gly Cys Ser Glu Pro 299 304 309 314	1022
gta cca cag gca att ttg aag aaa aga gga act agc aat gga tgt act Val Pro Gln Ala Ile Leu Lys Lys Arg Gly Thr Ser Asn Gly Cys Thr 315 320 325 330	1070
gca gct cag cag agg aca aag agt acc cca tct aat ctt act aaa act Ala Ala Gln Gln Arg Thr Lys Ser Thr Pro Ser Asn Leu Thr Lys Thr 331 336 341 346	1118
caa gga tcc caa gga gag tca cca aac tca gta aaa tct tca gtc tct Gln Gly Ser Gln Gly Glu Ser Pro Asn Ser Val Lys Ser Ser Val Ser 347 352 357 362	1166
tca agg cag tct gat gaa aat gtg gca aag ttg gac cac aat aca act	1214

Ser Arg Gln Ser Asp Glu Asn Val Ala Lys Leu Asp His Asn Thr Thr			
363	368	373	378
aca gag aaa caa gca cct aag aga aaa atg gtc aag caa gta cac aca			1262
Thr Glu Lys Gln Ala Pro Lys Arg Lys Met Val Lys Gln Val His Thr			
379	384	389	394
gct ttg cct aag gtt aat gca aaa ata gtg gca atg cct aaa aat cta			1310
Ala Leu Pro Lys Val Asn Ala Lys Ile Val Ala Met Pro Lys Asn Leu			
395	400	405	410
aat cag tca aaa aaa ggt gaa act ttg aat aat aaa gat tca aaa cag			1358
Asn Gln Ser Lys Lys Gly Glu Thr Leu Asn Asn Lys Asp Ser Lys Gln			
411	416	421	426
aaa atg cct cct gga cag gtt ata tca aaa act cag cct tcc tcc caa			1406
Lys Met Pro Pro Gly Gln Val Ile Ser Lys Thr Gln Pro Ser Ser Gln			
427	432	437	442
aga cct tta aaa cat gaa aca tct act gtc caa aaa agt atg ttt cat			1454
Arg Pro Leu Lys His Glu Thr Ser Thr Val Gln Lys Ser Met Phe His			
443	448	453	458
gat gtg cgt gat aat aac aac aag gac agt gtt tct gaa cag aag cct			1502
Asp Val Arg Asp Asn Asn Lys Asp Ser Val Ser Glu Gln Lys Pro			
459	464	469	474
cac aaa cct ctc att aat ctt gca tct gaa ata agt gat gca gaa gca			1550
His Lys Pro Leu Ile Asn Leu Ala Ser Glu Ile Ser Asp Ala Glu Ala			
475	480	485	490
ctc cag tca tcc tgc agg cct gac cca caa aag cca tta aac gat caa			1598
Leu Gln Ser Ser Cys Arg Pro Asp Pro Gln Lys Pro Leu Asn Asp Gln			
491	496	501	506
gaa aaa gag aag ttg gcg tta gaa tgc caa aat att tca aag ctg gat			1646
Glu Lys Glu Lys Leu Ala Leu Glu Cys Gln Asn Ile Ser Lys Leu Asp			
507	512	517	522
aaa tca tta aaa cac gaa ctg gaa tca aaa cag att tgt tta gat aaa			1694
Lys Ser Leu Lys His Glu Leu Glu Ser Lys Gln Ile Cys Leu Asp Lys			
523	528	533	538
agt gaa aca aaa ttt ccc aat cac aaa gaa aca gat gat tgc gat gca			1742
Ser Glu Thr Lys Phe Pro Asn His Lys Glu Thr Asp Asp Cys Asp Ala			
539	544	549	554
gct aac ata tgt tgt cat tct gtt ggg agt gat aat gta aat tca aaa			1790
Ala Asn Ile Cys Cys His Ser Val Gly Ser Asp Asn Val Asn Ser Lys			
555	560	565	570
ttt tat agc acc aca gcc cta aaa tac atg gtt tca aat cca aat gaa			1838
Phe Tyr Ser Thr Thr Ala Leu Lys Tyr Met Val Ser Asn Pro Asn Glu			
571	576	581	586
aac tcc ttg aac tct aat cca gtt tgt gat tta gac tca aca agt gca			1886
Asn Ser Leu Asn Ser Asn Pro Val Cys Asp Leu Asp Ser Thr Ser Ala			

587	592	597	602	
ggg caa atc cat ttg ata tca gat agg gag aac caa gta ggg aga aaa Gly Gln Ile His Leu Ile Ser Asp Arg Glu Asn Gln Val Gly Arg Lys 603 608 613 618				1934
gat aca aac aaa caa tca agt att aaa tgt gtg gaa gat gtt tca ctg Asp Thr Asn Lys Gln Ser Ser Ile Lys Cys Val Glu Asp Val Ser Leu 619 624 629 634				1982
tgt aat cct gaa agg aca aat ggt acc tta aat tct gct caa gaa gac Cys Asn Pro Glu Arg Thr Asn Gly Thr Leu Asn Ser Ala Gln Glu Asp 635 640 645 650				2030
aaa aaa tcg aaa gtt cct gtg gaa gga ctg aca att cct agt aag ttg Lys Lys Ser Lys Val Pro Val Glu Gly Leu Thr Ile Pro Ser Lys Leu 651 656 661 666				2078
tca gat gaa tct gct atg gat gaa gac aaa cat gct aca gca gac tca Ser Asp Glu Ser Ala Met Asp Glu Asp Lys His Ala Thr Ala Asp Ser 667 672 677 682				2126
gat gta tct tcc aag tgt ttt tcg gga cag cta tca gaa aaa aat tct Asp Val Ser Ser Lys Cys Phe Ser Gly Gln Leu Ser Glu Lys Asn Ser 683 688 693 698				2174
cct aaa aat atg gaa aca tca gaa tct cca gag agc cat gaa act cca Pro Lys Asn Met Glu Thr Ser Glu Ser Pro Glu Ser His Glu Thr Pro 699 704 709 714				2222
gaa act cca ttt gtg ggt cac tgg aat ttg agt act ggt gtt ctg cat Glu Thr Pro Phe Val Gly His Trp Asn Leu Ser Thr Gly Val Leu His 715 720 725 730				2270
cag cga gag agt cct gaa tct gac act ggc agt gct acc acc tcc tcc Gln Arg Glu Ser Pro Glu Ser Asp Thr Gly Ser Ala Thr Thr Ser Ser 731 736 741 746				2318
gat gac ata aag ccc aga tct gaa gac tat gat gct gga ggg tct cag Asp Asp Ile Lys Pro Arg Ser Glu Asp Tyr Asp Ala Gly Gly Ser Gln 747 752 757 762				2366
gat gat gat ggg tca aat gac aga ggt atc tct aaa tgt ggc act atg Asp Asp Asp Gly Ser Asn Asp Arg Gly Ile Ser Lys Cys Gly Thr Met 763 768 773 778				2414
ctg tgc cat gat ttt ctt gga aga agt agc agt gat acc agt act cct Leu Cys His Asp Phe Leu Gly Arg Ser Ser Asp Thr Ser Thr Pro 779 784 789 794				2462
gaa gaa tta aaa att tat gat agt aat tta aga att gaa gta aaa atg Glu Glu Leu Lys Ile Tyr Asp Ser Asn Leu Arg Ile Glu Val Lys Met 795 800 805 810				2510
aaa aag caa agt agt aat gat ctt ttc caa gtt aat tca acg agt gat Lys Lys Gln Ser Ser Asn Asp Leu Phe Gln Val Asn Ser Thr Ser Asp 811 816 821 826				2558

gat gaa atc cct agg aaa agg cca gaa att tgg tct cga tct gca ata Asp Glu Ile Pro Arg Lys Arg Pro Glu Ile Trp Ser Arg Ser Ala Ile 827 832 837 842	2606
gtt cac tct agg gaa aga gaa aat att cca cga ggc agt gtc cag ttt Val His Ser Arg Glu Arg Asn Ile Pro Arg Gly Ser Val Gln Phe 843 848 853 858	2654
gct cag gaa ata gat cag gta tct tct tca gca gat gaa aca gaa gat Ala Gln Glu Ile Asp Gln Val Ser Ser Ala Asp Glu Thr Glu Asp 859 864 869 874	2702
gaa aga tct gaa gct gaa aac gtt gca gaa aat ttc tct ata tct aac Glu Arg Ser Glu Ala Glu Asn Val Ala Glu Asn Phe Ser Ile Ser Asn 875 880 885 890	2750
cca gct cct cag cag ttt cag gga ata att aat tta gct ttt gaa gat Pro Ala Pro Gln Gln Phe Gln Gly Ile Ile Asn Leu Ala Phe Glu Asp 891 896 901 906	2798
gca act gaa aat gaa tgt cgt gaa ttt tct gca aat aaa aag ttt aaa Ala Thr Glu Asn Glu Cys Arg Glu Phe Ser Ala Asn Lys Lys Phe Lys 907 912 917 922	2846
agg tca gtt tta ctt tca gtc gat gaa tgt gaa gag ctg gga tca gat Arg Ser Val Leu Leu Ser Val Asp Glu Cys Glu Glu Leu Gly Ser Asp 923 928 933 938	2894
gaa gga gaa gtc cat act ccc ttt cag gct tct gta gat tct ttt tca Glu Gly Glu Val His Thr Pro Phe Gln Ala Ser Val Asp Ser Phe Ser 939 944 949 954	2942
cct tct gat gtt ttt gat ggc att tct cat gaa cat cat gga agg acc Pro Ser Asp Val Phe Asp Gly Ile Ser His Glu His His Gly Arg Thr 955 960 965 970	2990
tgc tat tcc aga ttc tca cga gaa agt gaa gat aat att tta gaa tgt Cys Tyr Ser Arg Phe Ser Arg Glu Ser Glu Asp Asn Ile Leu Glu Cys 971 976 981 986	3038
aaa caa aat aaa ggc aat agt gta tgt aaa aat gaa agc act gtc ttg Lys Gln Asn Lys Gly Asn Ser Val Cys Lys Asn Glu Ser Thr Val Leu 987 992 997 1002	3086
gat ctt agt agc att gac tct tca aga aaa aat aaa cag agt gtt tca Asp Leu Ser Ser Ile Asp Ser Ser Arg Lys Asn Lys Gln Ser Val Ser 1003 1008 1013 1018	3134
gcc aca gaa aaa aag aac aca ata gac gtc cta tcc agt aga agc aga Ala Thr Glu Lys Lys Asn Thr Ile Asp Val Leu Ser Ser Arg Ser Arg 1019 1024 1029 1034	3182
cag ctt ctt cga gaa gat aaa aaa gta aac aat gga agc aat gtg gaa Gln Leu Leu Arg Glu Asp Lys Lys Val Asn Asn Gly Ser Asn Val Glu 1035 1040 1045 1050	3230

aat gac att cag caa cgc agc aaa ttc ttg gat agt gat gta aaa tct Asn Asp Ile Gln Gln Arg Ser Lys Phe Leu Asp Ser Asp Val Lys Ser 1051 1056 1061 1066	3278
caa gaa aga cca tgt cac ttg gat ctt cat caa aga gaa ccc aat tct Gln Glu Arg Pro Cys His Leu Asp Leu His Gln Arg Glu Pro Asn Ser 1067 1072 1077 1082	3326
gac ata cca aag aac agc tct aca aaa tct cta gac tcc ttt cgg agt Asp Ile Pro Lys Asn Ser Ser Thr Lys Ser Leu Asp Ser Phe Arg Ser 1083 1088 1093 1098	3374
caa gtt ctg cct cag gaa ggt cca gtg aaa gag agc cat tct aca act Gln Val Leu Pro Gln Glu Gly Pro Val Lys Glu Ser His Ser Thr Thr 1099 1104 1109 1114	3422
act gaa aaa gct aat att gct tta tct gca gga gac ata gat gat tgt Thr Glu Lys Ala Asn Ile Ala Leu Ser Ala Gly Asp Ile Asp Asp Cys 1115 1120 1125 1130	3470
gac aca ctg gca caa acc cgc atg tat gac cat cgg cct tca aaa acc Asp Thr Leu Ala Gln Thr Arg Met Tyr Asp His Arg Pro Ser Lys Thr 1131 1136 1141 1146	3518
ctg tct cca ata tat gag atg gat gta ata gaa gca ttt gag cag aaa Leu Ser Pro Ile Tyr Glu Met Asp Val Ile Glu Ala Phe Glu Gln Lys 1147 1152 1157 1162	3566
gtg gaa tca gaa aca cat gtt aca gat atg gat ttt gaa gat gac caa Val Glu Ser Glu Thr His Val Thr Asp Met Asp Phe Glu Asp Asp Gln 1163 1168 1173 1178	3614
cat ttt gca aaa caa gat tgg aca cta cta aag caa ctg ctc tct gaa His Phe Ala Lys Gln Asp Trp Thr Leu Leu Lys Gln Leu Leu Ser Glu 1179 1184 1189 1194	3662
cag gat tca aac tta gat gtt aca aat tcc gtt cct gaa gac tta agt Gln Asp Ser Asn Leu Asp Val Thr Asn Ser Val Pro Glu Asp Leu Ser 1195 1200 1205 1210	3710
tta gca cag tat cta atc aat cag aca cta ctt tta gca cga gat agc Leu Ala Gln Tyr Leu Ile Asn Gln Thr Leu Leu Leu Ala Arg Asp Ser 1211 1216 1221 1226	3758
tca aaa cct cag ggt ata aca cat att gac act ttg aac aga tgg agt Ser Lys Pro Gln Gly Ile Thr His Ile Asp Thr Leu Asn Arg Trp Ser 1227 1232 1237 1242	3806
gaa cta aca tct cca ctt gat tcc tca gcg agc atc acc atg gct agt Glu Leu Thr Ser Pro Leu Asp Ser Ser Ala Ser Ile Thr Met Ala Ser 1243 1248 1253 1258	3854
ttt tcc tct gaa gat tgt tcg cct caa ggc gag tgg aca att ctg gaa Phe Ser Ser Glu Asp Cys Ser Pro Gln Gly Glu Trp Thr Ile Leu Glu 1259 1264 / 1269 1274	3902
ctg gaa act cag cat taa gtgtta acatTTTgga aaaatttatg ccactcctt	3956

Leu Glu Thr Gln His *

1275 1280

atttttgat gccttatatta tatccaaatg ataattgcat tagccggata taaaacttct 4016
ttaatattga gtcttccaa tttaatgagg taaacatagt ttatattatta atatatcaca 4076
tatagaaaaaa tgttttcta aagttttga gcatgtttc tctaattatt agagaaaatta 4136
gaagacttat aaggaaaccc tagcttcagt tttccttcc tagctgatga tttgttcact 4196
taatcattat tcaagaattt aaaatgtcaa tgcagaagta gatcagtccc tttactttt 4256
gctctgcata gggtaacata gtaatttaac aataaaaact taaccgtgctt gtgtccaaaa 4316
aaaaaaaaa 4323

<210> 135
<211> 6320
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (237)..(5549)

<400> 135
taagcttgcg gccgcggcc tcctaggagc gctgcacctg gtgatgaccc tcgttagtggc 60
tgcggcgcg cgccgagaag gaagcattcg ttcaagtca gaggataata gaagtactgc 120
gttttgatga tggagggcta ctacagaccc agacaacact tggactcagt tcatatcagc 180
agaaaaagtat atctctctac cggggaaatt gcaggccat acgatttgag ccacca 236
atg ctg gat ttc cat gaa caa cca gtt gga atg cca aaa atg gaa aaa 284
Met Leu Asp Phe His Glu Gln Pro Val Gly Met Pro Lys Met Glu Lys
1 5 10 15
gtc tac tta cat aat cct agt tct gaa gaa acg att act tta gta tca 332
Val Tyr Leu His Asn Pro Ser Ser Glu Glu Thr Ile Thr Leu Val Ser
17 22 27 32
ata tct gct aca aca tca cat ttt cat gca tca ttt ttt caa aat agg 380
Ile Ser Ala Thr Thr Ser His Phe His Ala Ser Phe Phe Gln Asn Arg
33 38 43 48
aaa att ctt cca gga gga aat aca tca ttt gat gta gtt ttt ctt gca 428
Lys Ile Leu Pro Gly Gly Asn Thr Ser Phe Asp Val Val Phe Leu Ala
49 54 59 64
aga gta gta gga aat gta gaa aat act tta ttt att aat aca tct aat 476
Arg Val Val Gly Asn Val Glu Asn Thr Leu Phe Ile Asn Thr Ser Asn
65 70 75 80

cat ggg gta ttt act tac cag gta ttt ggt gtt gga gtt cca aat cca	524
His Gly Val Phe Thr Tyr Gln Val Phe Gly Val Gly Val Pro Asn Pro	
81 86 91 96	
tat cga ttg agg ccg ttc ctt ggg gcc aga gtc cct gtg aat agc agt	572
Tyr Arg Leu Arg Pro Phe Leu Gly Ala Arg Val Pro Val Asn Ser Ser	
97 102 107 112	
ttc tca cct ata ata aac atc cac aat cct cac agt gag cct tta cag	620
Phe Ser Pro Ile Ile Asn Ile His Asn Pro His Ser Glu Pro Leu Gln	
113 118 123 128	
gtt gta gaa atg tac tct agt gga gga gac ctt cac cta gaa ctc cca	668
Val Val Glu Met Tyr Ser Ser Gly Gly Asp Leu His Leu Glu Leu Pro	
129 134 139 144	
acg ggt caa caa gga ggt acc aga aaa ctg tgg gaa att cct cct tat	716
Thr Gly Gln Gln Gly Gly Thr Arg Lys Leu Trp Glu Ile Pro Pro Tyr	
145 150 155 160	
-gaa -acc -aag gga -gtg -atg -aga -gcc -agt -ttt -tca -tct -aga -gaa -gca -gat	764
Glu Thr Lys Gly Val Met Arg Ala Ser Phe Ser Ser Arg Glu Ala Asp	
161 166 171 176	
aat cac aca gcc ttc ata aga ata aag act aat gct tca gac agc aca	812
Asn His Thr Ala Phe Ile Arg Ile Lys Thr Asn Ala Ser Asp Ser Thr	
177 182 187 192	
gag ttt atc att ctt cct gtt gag gtt gaa gtt aca aca gct cct gga	860
Glu Phe Ile Ile Leu Pro Val Glu Val Glu Val Thr Thr Ala Pro Gly	
193 198 203 208	
att tat tcc tca act gaa atg tta gat ttt ggt aca cta aga aca caa	908
Ile Tyr Ser Ser Thr Glu Met Leu Asp Phe Gly Thr Leu Arg Thr Gln	
209 214 219 224	
gat cta cca aaa gtt tta aac ctt cat tta aat tca gga aca aaa	956
Asp Leu Pro Lys Val Leu Asn Leu His Leu Leu Asn Ser Gly Thr Lys	
225 230 235 240	
gat gta cca ata aca agt gtt cga cct aca cca caa aat gat gct ata	1004
Asp Val Pro Ile Thr Ser Val Arg Pro Thr Pro Gln Asn Asp Ala Ile	
241 246 251 256	
acg gta cac ttt aaa cca att aca tta aaa gca tca gaa agt aaa tac	1052
Thr Val His Phe Lys Pro Ile Thr Leu Lys Ala Ser Glu Ser Lys Tyr	
257 262 267 272	
acc aag gtt gca agc att agt ttt gat gca tcg aag gca aaa aag cca	1100
Thr Lys Val Ala Ser Ile Ser Phe Asp Ala Ser Lys Ala Lys Lys Pro	
273 278 283 288	
tct cag ttt tct ggg aaa ata aca gtt aaa gca aag gaa aag agt tat	1148
Ser Gln Phe Ser Gly Lys Ile Thr Val Lys Ala Lys Glu Lys Ser Tyr	
289 294 299 304	
tct aaa ctt gaa ata cca tat caa gca gaa gtt tta gat ggt tat ttg	1196

Ser Lys Leu Glu Ile Pro Tyr Gln Ala Glu Val Leu Asp Gly Tyr Leu			
305	310	315	320
gga ttt gat cat gct gca aca tta ttt cac atc cga gac agc cct gct			1244
Gly Phe Asp His Ala Ala Thr Leu Phe His Ile Arg Asp Ser Pro Ala			
321	326	331	336
gat cct gtg gaa agg cca att tac ctt act aac act ttc agt ttt gcg			1292
Asp Pro Val Glu Arg Pro Ile Tyr Leu Thr Asn Thr Phe Ser Phe Ala			
337	342	347	352
atc ctc att cac gat gtg ttg cta cca gaa gaa gcc aaa aca atg ttt			1340
Ile Leu Ile His Asp Val Leu Leu Pro Glu Glu Ala Lys Thr Met Phe			
353	358	363	368
aaa gtt cac aac ttc agc aaa cca gtc tta att ctt cct aat gaa tca			1388
Lys Val His Asn Phe Ser Lys Pro Val Leu Ile Leu Pro Asn Glu Ser			
369	374	379	384
gga tac att ttt acc ctg ctt ttt atg cct tcc aca tca tcc atg cac			1436
Gly Tyr Ile Phe Thr Leu Leu Phe Met Pro Ser Thr Ser Ser Met His			
385	390	395	400
att gat aac aac att tta ctt att acc aat gct tct aaa ttt cat tta			1484
Ile Asp Asn Asn Ile Leu Leu Ile Thr Asn Ala Ser Lys Phe His Leu			
401	406	411	416
ccc gtg cggt gta tac aca ggc ttt tta gat tac ttt gta ttg ccc ccc			1532
Pro Val Arg Val Tyr Thr Gly Phe Leu Asp Tyr Phe Val Leu Pro Pro			
417	422	427	432
aaa ata gag gaa cgt ttc ata gat ttt gga gta ctg agt gct aca gaa			1580
Lys Ile Glu Glu Arg Phe Ile Asp Phe Gly Val Leu Ser Ala Thr Glu			
433	438	443	448
gca agt aat att tta ttt gca att ata aac agc aat cca att gag ttg			1628
Ala Ser Asn Ile Leu Phe Ala Ile Ile Asn Ser Asn Pro Ile Glu Leu			
449	454	459	464
gct ata aaa agt tgg cat atc ata gga gac ggt tta tca ata gaa ctt			1676
Ala Ile Lys Ser Trp His Ile Ile Gly Asp Gly Leu Ser Ile Glu Leu			
465	470	475	480
gta gct gtg gaa aga ggc aat aga act aca ata att tca agc ctg cca			1724
Val Ala Val Glu Arg Gly Asn Arg Thr Thr Ile Ile Ser Ser Leu Pro			
481	486	491	496
gag ttt gaa aaa tcc tct tta tca gat caa tca tcg gta aca tta gct			1772
Glu Phe Glu Lys Ser Ser Leu Ser Asp Gln Ser Ser Val Thr Leu Ala			
497	502	507	512
tca ggc tat ttt gca gtc ttc aga gtc aaa ctt act gca aaa aaa tta			1820
Ser Gly Tyr Phe Ala Val Phe Arg Val Lys Leu Thr Ala Lys Lys Leu			
513	518	523	528
gag ggg att cat gat gga gcc atc cag atc aca aca gac tat gag atc			1868
Glu Gly Ile His Asp Gly Ala Ile Gln Ile Thr Thr Asp Tyr Glu Ile			

529	534	539	544		
ctg aca atc cct gtg aag gct gtg att gca gta ggc tca ctg acc tgc Leu Thr Ile Pro Val Lys Ala Val Ile Ala Val Gly Ser Leu Thr Cys				1916	
545	550	555	560		
ttc cct aag cac gtg gtt ctt cca cct tcc ttt cca ggg aaa ata gtt Phe Pro Lys His Val Val Leu Pro Pro Ser Phe Pro Gly Lys Ile Val				1964	
561	566	571	576		
cat caa agt tta aat att atg aat tcc ttc tca cag aag gta aaa ata His Gln Ser Leu Asn Ile Met Asn Ser Phe Ser Gln Lys Val Lys Ile				2012	
577	582	587	592		
cag caa ata cga tct ttg tca gaa gat gtg cga ttt tac tat aaa cga Gln Gln Ile Arg Ser Leu Ser Glu Asp Val Arg Phe Tyr Tyr Lys Arg				2060	
593	598	603	608		
tta cggtt ggc aat aag gaa gac ttg gag cca gga aaa aaa tca aag att Leu Arg Gly Asn Lys Glu Asp Leu Glu Pro Gly Lys Ser Lys Ile				2108	
609	614	619	624		
gca aac att tat ttt gat cct gga cta cag tgt ggg gat cat tgc tat Ala Asn Ile Tyr Phe Asp Pro Gly Leu Gln Cys Gly Asp His Cys Tyr				2156	
625	630	635	640		
gtt ggc ttg cct ttt cta tcc aaa tct gaa ccc aaa gtg cag cct ggt Val Gly Leu Pro Phe Leu Ser Lys Ser Glu Pro Lys Val Gln Pro Gly				2204	
641	646	651	656		
gta gcc atg cag gaa gat atg tgg gat gct gac tgg gat ttg cat caa Val Ala Met Gln Glu Asp Met Trp Asp Ala Asp Trp Asp Leu His Gln				2252	
657	662	667	672		
agc ctg ttc aag gga tgg aca gga ata aag gaa aat tca ggt cat aga Ser Leu Phe Lys Gly Trp Thr Gly Ile Lys Glu Asn Ser Gly His Arg				2300	
673	678	683	688		
ttg agt gct ata ttt gaa gta aat aca gac ctt caa aaa aat ata ata Leu Ser Ala Ile Phe Glu Val Asn Thr Asp Leu Gln Lys Asn Ile Ile				2348	
689	694	699	704		
tca aaa atc act gct gag ctc tcc tgg cct tcc ata ctt agc tca ccc Ser Lys Ile Thr Ala Glu Leu Ser Trp Pro Ser Ile Leu Ser Ser Pro				2396	
705	710	715	720		
cgg cac ttg aaa ttt cca ctt act aat aca aac tgc tcc tca gaa gaa Arg His Leu Lys Phe Pro Leu Thr Asn Thr Asn Cys Ser Ser Glu Glu				2444	
721	726	731	736		
gag att act tta gaa aat cct gca gat gtt cct gtc tat gtt cag ttt Glu Ile Thr Leu Glu Asn Pro Ala Asp Val Pro Val Tyr Val Gln Phe				2492	
737		742	747	752	
att cct ctg gct tta tat tcc aac cct tca gtg ttt gta gat aag tta Ile Pro Leu Ala Leu Tyr Ser Asn Pro Ser Val Phe Val Asp Lys Leu				2540	
753	758	763	768		

gta tca agg ttt aac ttg agt aag gtg gca aag ata gat ttg aga aca			2588
Val Ser Arg Phe Asn Leu Ser Lys Val Ala Lys Ile Asp Leu Arg Thr			
769	774	779	784
ctc gaa ttt caa gtc ttc aga aac agt gct cat cca ctg cag agt tca			2636
Leu Glu Phe Gln Val Phe Arg Asn Ser Ala His Pro Leu Gln Ser Ser			
785	790	795	800
aca gga ttt atg gag ggc ctc tct cga cat tta att tta aac cta att			2684
Thr Gly Phe Met Glu Gly Leu Ser Arg His Leu Ile Leu Asn Leu Ile			
801	806	811	816
tta aaa cct gga gaa aag aaa tct gtc aaa gta aag ttt act cca gtt			2732
Leu Lys Pro Gly Glu Lys Lys Ser Val Lys Val Lys Phe Thr Pro Val			
817	822	827	832
cac aac aga act gtt tct tca ctt atc ata gtc aga aat aac ctg act			2780
His Asn Arg Thr Val Ser Ser Leu Ile Ile Val Arg Asn Asn Leu Thr			
833	838	843	848
gtg atg gat gct gtg atg gtc caa gga caa gga aca act gag aac ttg			2828
Val Met Asp Ala Val Met Val Gln Gly Gln Gly Thr Thr Glu Asn Leu			
849	854	859	864
agg gtg gca ggc aag ctt cca ggt cca gga agc tcc tta cgc ttt aaa			2876
Arg Val Ala Gly Lys Leu Pro Gly Pro Gly Ser Ser Leu Arg Phe Lys			
865	870	875	880
atc acg gaa gca ttg tta aaa gat tgt aca gat agt tta aaa cta aga			2924
Ile Thr Glu Ala Leu Leu Lys Asp Cys Thr Asp Ser Leu Lys Leu Arg			
881	886	891	896
gaa cca aat ttc aca ttg aaa aga aca ttt aag gta gag aat aca gga			2972
Glu Pro Asn Phe Thr Leu Lys Arg Thr Phe Lys Val Glu Asn Thr Gly			
897	902	907	912
caa ctt caa att cac ata gaa acc att gaa atc agt gga tac tca tgt			3020
Gln Leu Gln Ile His Ile Glu Thr Ile Glu Ile Ser Gly Tyr Ser Cys			
913	918	923	928
gaa gga tat ggc ttt aaa gtt gtt aat tgt caa gag ttt act cta agt			3068
Glu Gly Tyr Gly Phe Lys Val Val Asn Cys Gln Glu Phe Thr Leu Ser			
929	934	939	944
gcc aat gct tct aga gat ata atc ata ttg ttt act cct gat ttt aca			3116
Ala Asn Ala Ser Arg Asp Ile Ile Ile Leu Phe Thr Pro Asp Phe Thr			
945	950	955	960
gct tct aga gtt att cgg gaa ctg aag ttt ata aca acc agt ggc tct			3164
Ala Ser Arg Val Ile Arg Glu Leu Lys Phe Ile Thr Thr Ser Gly Ser			
961	966	971	976
gag ttt gta ttt ata ttg aat gca tcc ctt cct tac cat atg tta gca			3212
Glu Phe Val Phe Ile Leu Asn Ala Ser Leu Pro Tyr His Met Leu Ala			
977	982	987	992

acc tgt gca gaa gcc cta ccc aga cct aac tgg gaa ctg gct ctg tat			3260
Thr Cys Ala Glu Ala Leu Pro Arg Pro Asn Trp Glu Leu Ala Leu Tyr			
993	998	1003	1008
atc atc atc tca gga ata atg agt gca ctg ttt ctt ttg gtc att gga			3308
Ile Ile Ile Ser Gly Ile Met Ser Ala Leu Phe Leu Leu Val Ile Gly			
1009	1014	1019	1024
aca gcc tat ttg gaa gct caa gga ata tgg gag cca ttt cga agg cg			3356
Thr Ala Tyr Leu Glu Ala Gln Gly Ile Trp Glu Pro Phe Arg Arg Arg			
1025	1030	1035	1040
cta tcc ttt gag gcc tcg aac ccg ccc ttc gat gtg gga agg cca ttt			3404
Leu Ser Phe Glu Ala Ser Asn Pro Pro Phe Asp Val Gly Arg Pro Phe			
1041	1046	1051	1056
gat ctc agg aga atc gtt ggt att tca tct gaa gga aac ttg aac aca			3452
Asp Leu Arg Arg Ile Val Gly Ile Ser Ser Glu Gly Asn Leu Asn Thr			
1057	1062	1067	1072
ctc agc tgt gac ccc ggt cac agt agg ggg ttc tgt gga gca ggc ggt			3500
Leu Ser Cys Asp Pro Gly His Ser Arg Gly Phe Cys Gly Ala Gly Gly			
1073	1078	1083	1088
tca tca tcc cga ccc agt gcc ggg agt cat aag cag tgt ggc cca tcg			3548
Ser Ser Ser Arg Pro Ser Ala Gly Ser His Lys Gln Cys Gly Pro Ser			
1089	1094	1099	1104
gtc cac cca cac agc agt cac agc aat aga aac tca gct gac gtg gaa			3596
Val His Pro His Ser Ser His Ser Asn Arg Asn Ser Ala Asp Val Glu			
1105	1110	1115	1120
aac gtc aga gcc aaa aac agt tca agt acc tct agt agg act tct gct			3644
Asn Val Arg Ala Lys Asn Ser Ser Ser Thr Ser Ser Arg Thr Ser Ala			
1121	1126	1131	1136
caa gca gct tct tca cag tct gct aac aaa aca agc ccc ctt gtc tta			3692
Gln Ala Ala Ser Ser Gln Ser Ala Asn Lys Thr Ser Pro Leu Val Leu			
1137	1142	1147	1152
gat tcg aac aca gtg act caa ggt cat aca gcg ggc aga aag tcc aaa			3740
Asp Ser Asn Thr Val Thr Gln Gly His Thr Ala Gly Arg Lys Ser Lys			
1153	1158	1163	1168
ggg gca aag cag agc cag cac ggc agc cag cac cat gcc cac agc ccg			3788
Gly Ala Lys Gln Ser Gln His Gly Ser Gln His His Ala His Ser Pro			
1169	1174	1179	1184
ctg gag cag cac cct cag cct ctg cca ccg cca gtg cct cag ccc			3836
Leu Glu Gln His Pro Gln Pro Pro Leu Pro Pro Pro Val Pro Gln Pro			
1185	1190	1195	1200
cag gag ccg cag cct gaa agg ctg tct ccc gcc ccc ctc gca cac cct			3884
Gln Glu Pro Gln Pro Glu Arg Leu Ser Pro Ala Pro Leu Ala His Pro			
1201	1206	1211	1216
tcc cac cca gaa cgt gcc agc agc gcg agg cac agt tcc gag gac tcg			3932

Ser His Pro Glu Arg Ala Ser Ser Ala Arg His Ser Ser Glu Asp Ser				
1217	1222	1227	1232	
gac atc acc agt ctc ata gaa gcc atg gac aaa gac ttc gac cac cat				3980
Asp Ile Thr Ser Leu Ile Glu Ala Met Asp Lys Asp Phe Asp His His				
1233	1238	1243	1248	
gac tcc cca gcc cta gaa gtg ttt aca gag cag cct cca tcg cca ttg				4028
Asp Ser Pro Ala Leu Glu Val Phe Thr Glu Gln Pro Pro Ser Pro Leu				
1249	1254	1259	1264	
cca aaa agc aaa ggg aaa gga aaa cct ctt cag cgc aag gtg aaa cca				4076
Pro Lys Ser Lys Gly Lys Pro Leu Gln Arg Lys Val Lys Pro				
1265	1270	1275	1280	
cct aag aag caa gag gaa aag gag aag gga aag gga aag cca cag				4124
Pro Lys Lys Gln Glu Lys Glu Lys Lys Gly Lys Pro Gln				
1281	1286	1291	1296	
gaa gat gag ctg aag gac tct ttg gct gat gat gat agc tcc tcc acc				4172
Glü Asp Glü Leu Lys Asp Ser Leu Ala Asp Asp Asp Ser Ser Ser Thr				
1297	1302	1307	1312	
acc aca gag acc tcc aac cct gac aca gaa ccg ctc ctc aag gag gat				4220
Thr Thr Glu Thr Ser Asn Pro Asp Thr Glu Pro Leu Leu Lys Glu Asp				
1313	1318	1323	1328	
aca gaa aag caa aag gga aaa caa gcc atg cct gaa aaa cat gaa agt				4268
Thr Glu Lys Gln Lys Gly Gln Ala Met Pro Glu Lys His Glu Ser				
1329	1334	1339	1344	
gaa atg tct caa gtg aag caa aaa agc aaa aaa ctc tta aat att aag				4316
Glu Met Ser Gln Val Lys Gln Lys Ser Lys Lys Leu Leu Asn Ile Lys				
1345	1350	1355	1360	
aaa gaa atc cca aca gat gtg aaa ccc agt tca tta gaa cta cca tat				4364
Lys Glu Ile Pro Thr Asp Val Lys Pro Ser Ser Leu Glu Leu Pro Tyr				
1361	1366	1371	1376	
act ccc cct ttg gaa agt aag caa cgt aga aat ctc cca agc aag att				4412
Thr Pro Pro Leu Glu Ser Lys Gln Arg Arg Asn Leu Pro Ser Lys Ile				
1377	1382	1387	1392	
cct ctt cca act gca atg aca agt gga tcc aaa tca cga aat gcc cag				4460
Pro Leu Pro Thr Ala Met Thr Ser Gly Ser Lys Ser Arg Asn Ala Gln				
1393	1398	1403	1408	
aaa aca aaa ggt aca agt aag tta gtg gat aac aga cca cct gcc cta				4508
Lys Thr Lys Gly Thr Ser Lys Leu Val Asp Asn Arg Pro Pro Ala Leu				
1409	1414	1419	1424	
gca aaa ttc ctc ccg aat agt caa gaa tta ggc aac acc agt agc tca				4556
Ala Lys Phe Leu Pro Asn Ser Gln Glu Leu Gly Asn Thr Ser Ser Ser				
1425	1430	1435	1440	
gag ggt gaa aaa gac tct cct cca ccg gag tgg gat tcc gtt cca gtt				4604
Glu Gly Glu Lys Asp Ser Pro Pro Glu Trp Asp Ser Val Pro Val				

1441	1446	1451	1456	
cac aaa cct ggc agc tct act gat agt ctt tat aaa ctt tct ctg caa His Lys Pro Gly Ser Ser Thr Asp Ser Leu Tyr Lys Leu Ser Leu Gln				4652
1457	1462	1467	1472	
acc ctc aac gca gac att ttc tta aaa caa cgcc cag acc tca ccg aca Thr Leu Asn Ala Asp Ile Phe Leu Lys Gln Arg Gln Thr Ser Pro Thr				4700
1473	1478	1483	1488	
cct gct tcc ccg tct ccc cca gct gcc ccc tgc ccc ttt gtg gtc cgg Pro Ala Ser Pro Ser Pro Ala Ala Pro Cys Pro Phe Val Val Arg				4748
1489	1494	1499	1504	
ggc agc tac agc agc atc gtc aac agc agc tcc agc agt gac cct aaa Gly Ser Tyr Ser Ser Ile Val Asn Ser Ser Ser Ser Asp Pro Lys				4796
1505	1510	1515	1520	
ata aaa cag cca aat gga agc aaa cac aag ttg aca aag gca gcc tcg Ile Lys Gln Pro Asn Gly Ser Lys His Lys Leu Thr Lys Ala Ala Ser				4844
1521	1526	1531	1536	
ctc ccg ggc aag aac ggc aac ccc act ttt gct gca gtc acg gct ggc Leu Pro Gly Lys Asn Gly Asn Pro Thr Phe Ala Ala Val Thr Ala Gly				4892
1537	1542	1547	1552	
tac gac aag agc cca ggt ggg aat ggc ttt gct aaa gtt tct tca aac Tyr Asp Lys Ser Pro Gly Gly Asn Phe Ala Lys Val Ser Ser Asn				4940
1553	1558	1563	1568	
aaa aca ggt ttc tcc agc agc ctt ggc att tca cac gct cct gtt gac Lys Thr Gly Phe Ser Ser Leu Gly Ile Ser His Ala Pro Val Asp				4988
1569	1574	1579	1584	
agc gat ggc tca gac agc tcg ggt ttg agt ccc gtc agc aac cca Ser Asp Gly Ser Asp Ser Gly Leu Trp Ser Pro Val Ser Asn Pro				5036
1585	1590	1595	1600	
agc agc cct gac ttc act ccc ctc aat tcg ttc tcc gcc ttt gga aac Ser Ser Pro Asp Phe Thr Pro Leu Asn Ser Phe Ser Ala Phe Gly Asn				5084
1601	1606	1611	1616	
tct ttt aat cta act ggt gaa gtt ttc agc aaa ctc gga tta tct cga Ser Phe Asn Leu Thr Gly Glu Val Phe Ser Lys Leu Gly Leu Ser Arg				5132
1617	1622	1627	1632	
tcg tgc aat cag gcc tca cag agg agc tgg aac gag ttt aat agt ggc Ser Cys Asn Gln Ala Ser Gln Arg Ser Trp Asn Glu Phe Asn Ser Gly				5180
1633	1638	1643	1648	
cct tca tac ctt tgg gag tcg cca gcg aca gat ccc agt cct tcc tgg Pro Ser Tyr Leu Trp Glu Ser Pro Ala Thr Asp Pro Ser Pro Ser Trp				5228
1649	1654	1659	1664	
cca gcc agt tcc ggc tcc ccg acc cac aca gcc aca tcg gtc ctc ggt Pro Ala Ser Ser Gly Ser Pro Thr His Thr Ala Thr Ser Val Leu Gly				5276
1665	1670	1675	1680	

aac acc agc ggc ctg tgg tcc acc act cca ttc agc agc tcc att tgg		5324
Asn Thr Ser Gly Leu Trp Ser Thr Thr Pro Phe Ser Ser Ser Ile Trp		
1681 1686 1691 1696		
tcc agc aac ctt agc agc gcc ctt ccc ttc acc act cca gca aac acg		5372
Ser Ser Asn Leu Ser Ser Ala Leu Pro Phe Thr Thr Pro Ala Asn Thr		
1697 1702 1707 1712		
ctg gca agc atc ggc ctc atg ggc aca gaa aac tcc cct gct cct cac		5420
Leu Ala Ser Ile Gly Leu Met Gly Thr Glu Asn Ser Pro Ala Pro His		
1713 1718 1723 1728		
gct ccc tcc acc tcc agt cca gct gac ttg gga cag acc tac aac		5468
Ala Pro Ser Thr Ser Ser Pro Ala Asp Asp Leu Gly Gln Thr Tyr Asn		
1729 1734 1739 1744		
ccg tgg cggtata tgg agc ccc acg att gga aga aga agc tcg gac cct		5516
Pro Trp Arg Ile Trp Ser Pro Thr Ile Gly Arg Arg Ser Ser Asp Pro		
1745 1750 1755 1760		
tgg tct aat tcg cac ttt cct cac gag aat taa attaagca aaaaacaaac		5567
Trp Ser Asn Ser His Phe Pro His Glu Asn *		
1761 1766 1771		
aaacatagtggccctcgtagatcatgatgtgccagtttctgagacatcttttaagg		5627
ctcttactgcagctccctcccacccacctccatcttttgcaaaacagacc caagcaggc		5687
aggctcagac cactcgcttc ttccagatct ttcttgcaat tatgataaca tgagatttgc		5747
tgttgtgcttttagaaaaaa gtctggactc agccacaaac tctaataaga cctgtacatc		5807
tgagaacctt tcccgttact gcgtttcac cacctgtctt cccatgctt tatttatctg		5867
tatgaacaca gatttgacat tacagctaag gaaataattt gagttgattc agaaatcctg		5927
gcatgtgaca attttgttaa attaccaagt ttgggtttta ataatttctc aatattatgc		5987
gccaagatct aattttaaaa ctgtatgagg actttgtgct gaaaatagag tatttttta		6047
aagtaaggct gtcttggtt aaaagcagat tacagaaatg taagtcaact taagaacgg		6107
gaatgaatgt aaaaacattc agttgagacc atatgcattt tctgtgctgt ttgtacttga		6167
ggtatgtaac atttgatac ctgaacttat tttaaagatg aactgaaatg cacatagcca		6227
agtcttgaga tacaagattt aatgtgtatt tcttaaaaat acaactttgt gttgtacttt		6287
gaaataaaatg atgctttttt caaaaaaaaaaaa aaa		6320

<210> 136
<211> 1085
<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (250)..(1059)

<400> 136

cccggtgatg tatatatcta tctattcgat gatgaagata ccccaccaaa cccaaaaaaaa	60
gagatctctc gaggatccga attcgccggcc gcgtcgacct ttatctgaat ctattgaatt	120
gagacgatca tgtgattttt ggccttcatt ctattgatgt aacgtataac gtttagtaat	180
ttgcataatt tgaactatct ttgcattcct gggataaaatc ccacttgact gtggatatt	240
atgatttg atg tgt tgc tgg att tgg ttt gca ggc att ttg tgc aaa	288
Met Cys Cys Trp Ile Trp Phe Ala Gly Ile Leu Cys Lys	
1 5 10	
aat ttt gcg agg cgg cat gag gac ctg cgg cag gcc ctc ttc ggc agt	336
Asn Phe Ala Arg Arg His Glu Asp Leu Arg Gln Ala Leu Phe Gly Ser	
14 19 24 29	
ctc tct ggc ccg ggt tcc ctc ggc gtg cta ctg tgc gct cga tcc agc	384
Leu Ser Gly Pro Gly Ser Leu Gly Val Leu Leu Cys Ala Arg Ser Ser	
30 35 40 45	
acc atg ggg aag cgg gac aat cgg gtg gcc tat atg aac cca ata gca	432
Thr Met Gly Lys Arg Asp Asn Arg Val Ala Tyr Met Asn Pro Ile Ala	
46 51 56 61	
atg gcg aga tca agg ggt cca atc cag tct tca ggg cca aca ata cag	480
Met Ala Arg Ser Arg Gly Pro Ile Gln Ser Ser Gly Pro Thr Ile Gln	
62 67 72 77	
gat tat ctg aat cga cca agg cct acc tgg gaa gaa gta aaa gag caa	528
Asp Tyr Leu Asn Arg Pro Arg Pro Thr Trp Glu Glu Val Lys Glu Gln	
78 83 88 93	
cta gaa aag aaa aag aaa ggc tcc aag gct ttg gct gaa ttt gaa gaa	576
Leu Glu Lys Lys Lys Gly Ser Lys Ala Leu Ala Glu Phe Glu Glu	
94 99 104 109	
aaa atg aat gag aac tgg aag aaa gaa ctg gaa aaa cac agg gag aaa	624
Lys Met Asn Glu Asn Trp Lys Glu Leu Glu Lys His Arg Glu Lys	
110 115 120 125	
ttg tta agt gga agt gag agc tca tcc aaa aaa aga cag aga aag aaa	672
Leu Leu Ser Gly Ser Glu Ser Ser Lys Lys Arg Gln Arg Lys Lys	
126 131 136 141	
aaa gaa aag aag aaa tct ggt agg tat tca tct tct tca tca agc	720
Lys Glu Lys Lys Ser Gly Arg Tyr Ser Ser Ser Ser Ser Ser	
142 147 152 157	
tct gat tct tcc agc agt tct tct gat tct gaa gat gag gat aag aaa	768
Ser Asp Ser Ser Ser Ser Asp Ser Glu Asp Glu Asp Lys Lys	

158	163	168	173	
caa gga aaa cg	aga aag aaa aag aac cgt tca cat aaa tct tct			816
Gln Gly Lys Arg	Arg Lys Lys Lys Asn Arg Ser His Lys Ser Ser			
174	179	184	189	
gaa agc tcc atg tca gaa act gaa tca gac agt aag gat agt tta aaa				864
Glu Ser Ser Met Ser	Glu Thr Glu Ser Asp Ser Lys Asp Ser Leu Lys			
190	195	200	205	
aag aaa aag aag tca aaa gat gga act gag aaa gaa aag gat att aaa				912
Lys Lys Lys Ser Lys Asp Gly Thr Glu Lys Glu Lys Asp Ile Lys				
206	211	216	221	
gga ctc agc aaa aag aga aag atg tat tct gaa gat aaa cct tta tca				960
Gly Leu Ser Lys Lys Arg Lys Met Tyr Ser Glu Asp Lys Pro Leu Ser				
222	227	232	237	
tct gag tcc ttg tca gaa tca gag tat att gag gag gtg cga gca aaa				1008
Ser Glu Ser Leu Ser Glu Ser Glu Tyr Ile Glu Glu Val Arg Ala Lys				
238	243	248	253	
aag aag aaa agc agt gaa gaa cga gaa aaa gca aca gca agt atc tct				1056
Lys Lys Lys Ser Ser Glu Glu Arg Glu Lys Ala Thr Ala Ser Ile Ser				
254	259	264	269	
taa cgaaaaataca gacaatagaa tagtg				1085
*				
270				

<210> 137
 <211> 809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (252)..(809)

<400> 137				
atttggccct cgaggccaag aattcgac gaggcacgtt ccaggctgga cacaacaaa				60
ggcggaggac ccgtggccca cgaagctcat ctggactg tccccgcctt ctcggccctt				120
gacttgcac cctaggccct ttggggcgcc tctgaccagg ctagccagat cccggaccctt				180
aaccatgttc cctgtgaagg tgaaagtggaa gaaatcagag ctggagatgg ccaaagcccg				240
gaaccaactg g atg ctg tct tgc agt gtc tgc tgg aga aga gtc aca tgg				290
Met Leu Ser Cys Ser Val Cys Trp Arg Arg Val Thr Trp				
1	5	10		
aca ggg agc gtc tgg atg agg aag ctg gga aaa cac cct cag aca ccc				338

Thr	Gly	Ser	Val	Trp	Met	Arg	Lys	Leu	Gly	Lys	His	Pro	Gln	Thr	Pro	
14					19				24				29			
aca	ata	aac	aca	tat	gtg	atc	aag	ctg	ttc	gac	cgg	agc	gtg	gac	ttg	386
Thr	Ile	Asn	Thr	Tyr	Val	Ile	Lys	Leu	Phe	Asp	Arg	Ser	Val	Asp	Leu	
30						35				40				45		
gcc	cag	ttc	agc	gag	aac	acg	cca	ctg	tac	cca	atc	tgc	cgc	gcc	tgg	434
Ala	Gln	Phe	Ser	Glu	Asn	Thr	Pro	Leu	Tyr	Pro	Ile	Cys	Arg	Ala	Trp	
46							51			56				61		
atg	cgc	aac	agc	ccc	tct	gtg	cgc	gag	cgt	gaa	tgc	tct	ccc	agc	tca	482
Met	Arg	Asn	Ser	Pro	Ser	Val	Arg	Glu	Arg	Glu	Cys	Ser	Pro	Ser	Ser	
62						67				72		77				
ccc	ctg	ccc	ccg	ctg	cct	gag	gat	gag	gag	ggc	tca	gag	gta	acc	aac	530
Pro	Leu	Pro	Pro	Leu	Pro	Glu	Asp	Glu	Glu	Gly	Ser	Glu	Val	Thr	Asn	
78						83			88					93		
agc	aag	agt	cgt	gat	gtg	tac	aag	ctg	ccg	cca	ccc	aca	ccc	ccg	ggg	578
Ser	Lys	Ser	Arg	Asp	Val	Tyr	Lys	Leu	Pro	Pro	Pro	Pro	Thr	Pro	Pro	Gly
94						99				104				109		
cca	ccc	gga	gat	gcc	tgc	aga	tcc	ccg	atc	cca	tct	cca	ctg	cag	cct	626
Pro	Pro	Gly	Asp	Ala	Cys	Arg	Ser	Arg	Ile	Pro	Ser	Pro	Leu	Gln	Pro	
110						115				120				125		
gag	atg	cag	ggc	acc	cct	gac	gat	gag	ccc	tct	gag	ccc	gag	ccc	tca	674
Glu	Met	Gln	Gly	Thr	Pro	Asp	Asp	Glu	Pro	Ser	Glu	Pro	Glu	Pro	Ser	
126						131				136				141		
ccc	tcc	aca	ctc	atc	tat	cgc	aac	atg	cag	cgc	tgg	aaa	cgc	atc	cgc	722
Pro	Ser	Thr	Leu	Ile	Tyr	Arg	Asn	Met	Gln	Arg	Trp	Lys	Arg	Ile	Arg	
142						147				152				157		
cag	agg	tgg	aag	gag	gcc	tct	cat	cgg	aac	cag	ctt	cgt	tac	tca	gaa	770
Gln	Arg	Trp	Lys	Glu	Ala	Ser	His	Arg	Asn	Gln	Leu	Arg	Tyr	Ser	Glu	
158						163				168				173		
agc	atg	aag	atc	cta	cga	gag	atg	tac	gaa	cga	cag	tga				809
Ser	Met	Lys	Ile	Leu	Arg	Glu	Met	Tyr	Glu	Arg	Gln	*				
174						179				184						

<210> 138
<211> 5314
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (531)..(4376)

<400> 138

aattttgaag ccggtcgcct gccttacccgg tccggaattc cgggtcgac gatttcgtgg	60
ttgttgttagt aaccggggaa gcagccgtcg gcggctgccc tgagccttcc tggggaaagga	120
ggagggaggt aggccagag cgccgtccac gcctgctcg cccgaaccat ggaaagatga	180
gacaggtaaa cgcctgcgcc cgccgcgttc cctaccctag ggaggagcat tcccgggtcc	240
gggctggcgc ctgcagcagg acttcccgtc cagagccgg gagtagctgt tggcttccgg	300
gcgcgcgcgc ttgaatcgcg gctgcggggt cgtccgtcc ttccggggg gagcatctgc	360
ggacctacgt gggattgggg tgagctgggg gtggggctga gaagcaaatt ccttcggga	420
gaggagtctc ctaggaatc tgtgccatcc aaattgcttg atccagtgaa tctgcttagga	480
aaggctctg aggccccgt ctgctgactg catgacaaac cctaaaggaa atg cca Met Pro 1	536
atc gtg atg gcc cgg gac ctg gag gaa aca gca tca tcc tca gag gat Ile Val Met Ala Arg Asp Leu Glu Glu Thr Ala Ser Ser Ser Glu Asp	584
3 8 13 18	
gag gag gtc ata agt caa gag gat cat cca tgc atc atg tgg act gga Glu Glu Val Ile Ser Gln Glu Asp His Pro Cys Ile Met Trp Thr Gly	632
19 24 29 34	
ggc tgc agg aga att cca gtt ttg gta ttc cat gcc gac gct att ctt Gly Cys Arg Arg Ile Pro Val Leu Val Phe His Ala Asp Ala Ile Leu	680
35 40 45 50	
aca aag gac aac aat att aga gta att gga gaa cgt tat cat ttg tct Thr Lys Asp Asn Asn Ile Arg Val Ile Gly Glu Arg Tyr His Leu Ser	728
51 56 61 66	
tat aag att gta cga acg gac agt cgc cta gta cgc agc att ctg aca Tyr Lys Ile Val Arg Thr Asp Ser Arg Leu Val Arg Ser Ile Leu Thr	776
67 72 77 82	
gcc cat gga ttt cat gaa gtt cac cca agc agc act gac tat aac cta Ala His Gly Phe His Glu Val His Pro Ser Ser Thr Asp Tyr Asn Leu	824
83 88 93 98	
atg tgg aca gga tcc cac ctg aag ccc ttc tta ctg cgc acc ctc tct Met Trp Thr Gly Ser His Leu Lys Pro Phe Leu Leu Arg Thr Leu Ser	872
99 104 109 114	
gaa gca caa aaa gtt aat cac ttt ccc agg tct tat gaa ctt acc cgg Glu Ala Gln Lys Val Asn His Phe Pro Arg Ser Tyr Glu Leu Thr Arg	920
115 120 125 130	
aag gac cga ctg tac aaa aac att att cga atg cag cat aca cat gga Lys Asp Arg Leu Tyr Lys Asn Ile Ile Arg Met Gln His Thr His Gly	968
131 136 141 146	
ttc aag gtt ttt cac atc ctc ccc cag acc ttc ctc ctg cca gct gag	1016

Phe Lys Val Phe His Ile Leu Pro Gln Thr Phe Leu Leu Pro Ala Glu			
147	152	157	162
tac gcg gaa ttt tgt aat tca tat tcg aag gac cgg gga cct tgg ata			1064
Tyr Ala Glu Phe Cys Asn Ser Tyr Ser Lys Asp Arg Gly Pro Trp Ile			
163	168	173	178
gta aaa cca gtg gca tct tca agg ggg cgg ggc gtc tac ctg atc aac			1112
Val Lys Pro Val Ala Ser Ser Arg Gly Arg Gly Val Tyr Leu Ile Asn			
179	184	189	194
aat cca aac cag atc tcc ctg gaa gag aac att ttg gtc tcc cgt tac			1160
Asn Pro Asn Gln Ile Ser Leu Glu Glu Asn Ile Leu Val Ser Arg Tyr			
195	200	205	210
att aac aac ccc ctg ctc ata gat gat ttc aag ttt gac gtg cgc ctc			1208
Ile Asn Asn Pro Leu Leu Ile Asp Asp Phe Lys Phe Asp Val Arg Leu			
211	216	221	226
tat gtg ctc gtg act tcc tat gat cct ctt gtc atc tat ctc tat gaa			1256
Tyr Val Leu Val Thr Ser Tyr Asp Pro Leu Val Ile Tyr Leu Tyr Glu			
227	232	237	242
gaa gga ttg gct agg ttt gca act gtg cga tat gat caa gga gcc aag			1304
Glu Gly Leu Ala Arg Phe Ala Thr Val Arg Tyr Asp Gln Gly Ala Lys			
243	248	253	258
aac att cgg aac cag ttc atg cat ctg aca aac tac agt gtc aac aag			1352
Asn Ile Arg Asn Gln Phe Met His Leu Thr Asn Tyr Ser Val Asn Lys			
259	264	269	274
aaa agt gga gat tac gtc agt tgt gac gat cca gaa gtg gag gat tat			1400
Lys Ser Gly Asp Tyr Val Ser Cys Asp Asp Pro Glu Val Glu Asp Tyr			
275	280	285	290
gga aac aaa tgg agc atg agt gct atg ctt agg tac ctg aaa caa gaa			1448
Gly Asn Lys Trp Ser Met Ser Ala Met Leu Arg Tyr Leu Lys Gln Glu			
291	296	301	306
ggc aga gat aca acc gca ttg atg gcc cat gta gaa gac ctg atc att			1496
Gly Arg Asp Thr Thr Ala Leu Met Ala His Val Glu Asp Leu Ile Ile			
307	312	317	322
aag act ata atc tct gct gaa cta gct att gct act gcc tgt aaa acc			1544
Lys Thr Ile Ile Ser Ala Glu Leu Ala Ile Ala Thr Ala Cys Lys Thr			
323	328	333	338
ttt gtt cct cat cgc agc agt tgt ttt gaa ctc tat ggc ttt gac gtg			1592
Phe Val Pro His Arg Ser Ser Cys Phe Glu Leu Tyr Gly Phe Asp Val			
339	344	349	354
ctc ata gat tct act ctg aag cca tgg ttg ttg gaa gtg aat ctc tct			1640
Leu Ile Asp Ser Thr Leu Lys Pro Trp Leu Leu Glu Val Asn Leu Ser			
355	360	365	370
cct tct ttg gcc tgt gat gcg cct ctg gac cta aag att aaa gcc agt			1688
Pro Ser Leu Ala Cys Asp Ala Pro Leu Asp Leu Lys Ile Lys Ala Ser			

371	376	381	386	
atg att tca gat atg ttc act gtt gta gga ttt gtg tgc caa gat cct Met Ile Ser Asp Met Phe Thr Val Val Gly Phe Val Cys Gln Asp Pro 387 392 397 402				1736
gcc cag cgg gca tca act cgg cca att tat ccc acc ttc gag tct tcc Ala Gln Arg Ala Ser Thr Arg Pro Ile Tyr Pro Thr Phe Glu Ser Ser 403 408 413 418				1784
agg cga aac cct ttc cag aaa cct cag cgt tgc cgt cca ctc tct gcc Arg Arg Asn Pro Phe Gln Lys Pro Gln Arg Cys Arg Pro Leu Ser Ala 419 424 429 434				1832
agt gat gcg gaa atg aaa aac ctc gtg ggc tca gcc cgg gag aaa ggg Ser Asp Ala Glu Met Lys Asn Leu Val Gly Ser Ala Arg Glu Lys Gly 435 440 445 450				1880
cca ggg aag ttg ggt ggt tct gtg ctt ggt ctg tca atg gag gag atc Pro Gly Lys Leu Gly Ser Val Leu Gly Leu Ser Met Glu Glu Ile 451 456 461 466				1928
aaa gtt tta cga agg gtg aag gag gag aat gat cgg cga ggt gga ttt Lys Val Leu Arg Arg Val Lys Glu Glu Asn Asp Arg Arg Gly Gly Phe 467 472 477 482				1976
att cgc ata ttt cct aca tct gag aca tgg gaa ata tat ggg tcc tac Ile Arg Ile Phe Pro Thr Ser Glu Thr Trp Glu Ile Tyr Gly Ser Tyr 483 488 493 498				2024
ctc gag cat aag acc tca atg aac tat atg ctg gca aca cgc ctc ttc Leu Glu His Lys Thr Ser Met Asn Tyr Met Leu Ala Thr Arg Leu Phe 499 504 509 514				2072
cag gac aga atg act gct gat gga gcg cca gaa ttg aag ata gag agt Gln Asp Arg Met Thr Ala Asp Gly Ala Pro Glu Leu Lys Ile Glu Ser 515 520 525 530				2120
ctg aat tca aag gcc aag ctg cat gct gca ctt tac gag agg aag ctc Leu Asn Ser Lys Ala Lys Leu His Ala Ala Leu Tyr Glu Arg Lys Leu 531 536 541 546				2168
ctg tct ctg gag gtg cga aaa cgt aga cga cgg agt agc aga ttg agg Leu Ser Leu Glu Val Arg Lys Arg Arg Arg Ser Ser Arg Leu Arg 547 552 557 562				2216
gca atg agg cca aaa tac cca gtg att acc caa cca gct gaa atg aat Ala Met Arg Pro Lys Tyr Pro Val Ile Thr Gln Pro Ala Glu Met Asn 563 568 573 578				2264
gtt aaa act gag aca gag agt gaa gag gag gaa gaa gtc gca tta gat Val Lys Thr Glu Thr Glu Ser Glu Glu Glu Glu Val Ala Leu Asp 579 584 589 594				2312
aat gaa gat gaa gaa cag gag gct tcc cag gag gag tct gca gga ttt Asn Glu Asp Glu Glu Gln Glu Ala Ser Gln Glu Glu Ser Ala Gly Phe 595 600 605 610				2360

ctt aga gaa aat caa gcc aaa tat aca ccc tca ttg aca gct ttg gta Leu Arg Glu Asn Gln Ala Lys Tyr Thr Pro Ser Leu Thr Ala Leu Val	611	616	621	626	2408
gaa aat aca ccc aaa gaa aat tcc atg aaa gtt cgt gaa tgg aat aat Glu Asn Thr Pro Lys Glu Asn Ser Met Lys Val Arg Glu Trp Asn Asn	627	632	637	642	2456
aaa ggt gga cac tgc tgc aaa ctt gag act cag gag cta gag cct aaa Lys Gly Gly His Cys Cys Lys Leu Glu Thr Gln Glu Leu Glu Pro Lys	643	648	653	658	2504
ttt aac ctg atg cag att ctt caa gat aat ggc aat ctt agc aaa atg Phe Asn Leu Met Gln Ile Leu Gln Asp Asn Gly Asn Leu Ser Lys Met	659	664	669	674	2552
cag gcc cga ata gca ttc tct gcc tat ctc cag cat gtt caa att cgc Gln Ala Arg Ile Ala Phe Ser Ala Tyr Leu Gln His Val Gln Ile Arg	675	680	685	690	2600
ctg atg aaa gac agt ggc ggt cag acg ttc agt gcc agt tgg gct gcc Leu Met Lys Asp Ser Gly Gly Gln Thr Phe Ser Ala Ser Trp Ala Ala	691	696	701	706	2648
aaa gag gat gaa cag atg gag ctg gtt cgt ttc ctc aag cga gca Lys Glu Asp Glu Gln Met Glu Leu Val Val Arg Phe Leu Lys Arg Ala	707	712	717	722	2696
tca aat aac ctc cag cat tca ctg agg atg gta tta ccc agt cga cga Ser Asn Asn Leu Gln His Ser Leu Arg Met Val Leu Pro Ser Arg Arg	723	728	733	738	2744
ttg gca ctt ctg gaa cgc aga aga atc ctg gcc cac cag ctg ggt gac Leu Ala Leu Leu Glu Arg Arg Ile Leu Ala His Gln Leu Gly Asp	739	744	749	754	2792
ttt atc att gta tac aac aag gaa aca gaa caa atg gct gaa aag aaa Phe Ile Ile Val Tyr Asn Lys Glu Thr Glu Gln Met Ala Glu Lys Lys	755	760	765	770	2840
tca aag aag aaa gtt gag gaa gaa gag gaa gat ggg gtg aat atg gaa Ser Lys Lys Val Glu Glu Glu Glu Asp Gly Val Asn Met Glu	771	776	781	786	2888
aac ttt cag gag ttc atc aga caa gca agt gag gct gaa ctg gag gag Asn Phe Gln Glu Phe Ile Arg Gln Ala Ser Glu Ala Glu Leu Glu Glu	787	792	797	802	2936
gtg ttg act ttt tat acc caa aag aac aag tct gct agt gtc ttc ctg Val Leu Thr Phe Tyr Thr Gln Lys Asn Lys Ser Ala Ser Val Phe Leu	803	808	813	818	2984
ggg act cac tct aaa att tct aag aac aac aat tat tct gat agt Gly Thr His Ser Lys Ile Ser Lys Asn Asn Asn Asn Tyr Ser Asp Ser	819	824	829	834	3032

ggg gca aaa ggt gat cac cct gag act ata atg gaa gaa gtg aaa ata Gly Ala Lys Gly Asp His Pro Glu Thr Ile Met Glu Glu Val Lys Ile 835 840 845 850	3080
aag cca cct aaa cag caa cag acg aca gaa att cat tct gat aaa tta Lys Pro Pro Lys Gln Gln Thr Thr Glu Ile His Ser Asp Lys Leu 851 856 861 866	3128
tct cga ttt acc act tca gca gaa aaa gag gca aaa tta gtt tat agc Ser Arg Phe Thr Thr Ser Ala Glu Lys Glu Ala Lys Leu Val Tyr Ser 867 872 877 882	3176
aat tcc tcc tct ggt cct act gct act ctg cag aaa att ccc aac acc Asn Ser Ser Ser Gly Pro Thr Ala Thr Leu Gln Lys Ile Pro Asn Thr 883 888 893 898	3224
cat ttg tca tct gtt aca acc tct gac ctc tct cca ggg cct tgc cac His Leu Ser Ser Val Thr Thr Ser Asp Leu Ser Pro Gly Pro Cys His 899 904 909 914	3272
cat tct tct <u>tta</u> tct caa att cct tca gct atc ccc agc atg cct cac His Ser Ser Leu Ser Gln Ile Pro Ser Ala Ile Pro Ser Met Pro His 915 920 925 930	3320
cag cca aca att tta ctg aac aca gtc tct gcc agt gct tct ccc tgc Gln Pro Thr Ile Leu Asn Thr Val Ser Ala Ser Ala Ser Pro Cys 931 936 941 946	3368
cta cat ccc ggg gca cag aac atc cca agc cct act ggc ctg cca cgc Leu His Pro Gly Ala Gln Asn Ile Pro Ser Pro Thr Gly Leu Pro Arg 947 952 957 962	3416
tgt cga tca gga agt cac acc att ggt ccc ttt tct tcc ttc caa agt Cys Arg Ser Gly Ser His Thr Ile Gly Pro Phe Ser Ser Phe Gln Ser 963 968 973 978	3464
gct gca cac atc tat agc cag aaa ctg tct cgt ccc tct tca gca aag Ala Ala His Ile Tyr Ser Gln Lys Leu Ser Arg Pro Ser Ser Ala Lys 979 984 989 994	3512
gca gga tcg tgc tat cta aac aag cat cat tca gga ata gcc aaa aca Ala Gly Ser Cys Tyr Leu Asn Lys His Ser Gly Ile Ala Lys Thr 995 1000 1005 1010	3560
caa aaa gag gga gaa gat gct tct tta tat agc aaa cggt tac aac caa Gln Lys Glu Gly Glu Asp Ala Ser Leu Tyr Ser Lys Arg Tyr Asn Gln 1011 1016 1021 1026	3608
agt atg gtt aca gct gaa ctt cag cgg cta gct gag aag cag gca gcg Ser Met Val Thr Ala Glu Leu Gln Arg Leu Ala Glu Lys Gln Ala Ala 1027 1032 1037 1042	3656
aga cag tat tct cca tcc agc cac atc aac ctc ctc acc caa cag gta Arg Gln Tyr Ser Pro Ser Ser His Ile Asn Leu Leu Thr Gln Gln Val 1043 1048 1053 1058	3704
aca aac ctg aat ttg gca act ggc atc ata aac aga agc agt gct tca	3752

Thr Asn Leu Asn Leu Ala Thr Gly Ile Ile Asn Arg Ser Ser Ala Ser				
1059	1064	1069	1074	
gct ccc cca acc ctc cga ccc atc atc agt cct agt ggc ccg aca tgg				3800
Ala Pro Pro Thr Leu Arg Pro Ile Ile Ser Pro Ser Gly Pro Thr Trp				
1075	1080	1085	1090	
tct aca cag tca gac ccc caa gct ccc gag aat cac tcc agc tct cct				3848
Ser Thr Gln Ser Asp Pro Gln Ala Pro Glu Asn His Ser Ser Ser Pro				
1091	1096	1101	1106	
gga agc agg agc ctg cag aca ggg gga ttt gcc tgg gaa gga gaa gta				3896
Gly Ser Arg Ser Leu Gln Thr Gly Gly Phe Ala Trp Glu Gly Glu Val				
1107	1112	1117	1122	
gaa aac aac gtg tac agc cag gct aca ggg gtg gtc ccc cag cac aag				3944
Glu Asn Asn Val Tyr Ser Gln Ala Thr Gly Val Val Pro Gln His Lys				
1123	1128	1133	1138	
tat cac ccc aca gca ggc agc tat cag ctt caa ttt gcc ctg cag caa				3992
Tyr His Pro Thr Ala Gly Ser Tyr Gln Leu Gln Phe Ala Leu Gln Gln				
1139	1144	1149	1154	
ctt gaa caa caa aaa ctt cag tcc cgg cag ctc ctg gac cag agt cga				4040
Leu Glu Gln Gln Lys Leu Gln Ser Arg Gln Leu Leu Asp Gln Ser Arg				
1155	1160	1165	1170	
gcc cggtcac cag gca atc ttt ggc agc cag aca cta cct aac tcc aat				4088
Ala Arg His Gln Ala Ile Phe Gly Ser Gln Thr Leu Pro Asn Ser Asn				
1171	1176	1181	1186	
tta tgg aca atg aat aat ggt gca ggt tgt aga att tcc agt gcc aca				4136
Leu Trp Thr Met Asn Asn Gly Ala Gly Cys Arg Ile Ser Ser Ala Thr				
1187	1192	1197	1202	
gct agt ggc cag aag cca acc act ctg cca caa aaa gtg gta cca cct				4184
Ala Ser Gly Gln Lys Pro Thr Thr Leu Pro Gln Lys Val Val Pro Pro				
1203	1208	1213	1218	
cca agt tct tgc gcc tcc ctg gtt ccc aaa ccc cca ccc aac cac gaa				4232
Pro Ser Ser Cys Ala Ser Leu Val Pro Lys Pro Pro Pro Asn His Glu				
1219	1224	1229	1234	
caa gtg ctc aga agg gca aca tcc cag aaa gct tcc aaa ggg tcc tcc				4280
Gln Val Leu Arg Arg Ala Thr Ser Gln Lys Ala Ser Lys Gly Ser Ser				
1235	1240	1245	1250	
gcg gaa ggg cag ctg aat gga ctc cag agc agc ctt aac cct gca gcc				4328
Ala Glu Gly Gln Leu Asn Gly Leu Gln Ser Ser Leu Asn Pro Ala Ala				
1251	1256	1261	1266	
ttt gtg ccc atc acc agc tct aca gat cct gct cac act aaa ata tga				4376
Phe Val Pro Ile Thr Ser Ser Thr Asp Pro Ala His Thr Lys Ile *				
1267	1272	1277	1282	
accacaaaaca cacagagaaa caacctgttc accactcctg ggtgcatgat tgagggtgaa				4436

gcatccacca gcacttcaag gggtccatag tattttttt tttgctgcct caaagtcccc	4496
aaaggccttcg agcagaagtg gcagtagatg gttgccaatc agccaatgca gactttcact	4556
gggacaacaa gaaagcagat cttctgggtt ttgatggaac ttggcagttgg ggacattcag	4616
ctgatgcatt atatacccg tcagagcaca cttgtatctt ttaccttccc tttgccccat	4676
gcccccaaac tgcttaggtc ttctctgtcc cttaactgct gctgcacaga gatgatataa	4736
aagaggctct ttggctattt gcattttgct tcctcttctt ttccagattha cagtatgaag	4796
ctttatTTTC tttgtacaag cttaaaattt caacatcatc atecgc当地 gttttccctc	4856
cctttcggg gatatctagg ggaaagagga gcattcatca caagtttccctt agagagagga	4916
gacaaatcgg tgtgccattt acaacatgag ccaggtaaa ggcacccttt ggaattactg	4976
atttcaaaga ttaataaaagt aattctattt ttatTTTCTT tttttccctt ttactaattt	5036
cccaacaatc -aatattcaca-aacaggactg-aagttagaacc-agttttttat_tttactttgt	5096
ggctgtgcaa ttttttaaac atttttagaaa tgtgagctgt aaagagatgt tttatTTTAA	5156
catttcattt cagcagatgg tgggtccagg ctattcccaa aggcagctcc tgcacctggg	5216
gagcgggcat gtgcagatgt ctccgttatac agccotcgac aggcaggctc actcacagcg	5276
tgggcctcca gtggcttgag ccctgtatcc agttgcat	5314

<210> 139
 <211> 3262
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60) .. (2279)

<400> 139

agcgggattc gatagcatac tcagtgtggt ggaattcgta acttctgaca gctctctcc	59
atg gaa gga ggc ggc ggc cgc gat gag cct tca gcc tgc cgg gca ggg	107
Met Glu Gly Gly Gly Arg Asp Glu Pro Ser Ala Cys Arg Ala Gly	
1 5 10 15	

gac gtg aac atg gat gac cct aag aag gaa gac att ctt ctt ttg gcc	155
Asp Val Asn Met Asp Asp Pro Lys Lys Glu Asp Ile Leu Leu Leu Ala	
17 22 27 32	

gat gaa aaa ttt gac ttc gat ctt tca ttg tct tct tcg agt gca aat	203
Asp Glu Lys Phe Asp Phe Asp Leu Ser Leu Ser Ser Ser Ala Asn	
33 38 43 48	

gaa gat gat gaa gtc ttc gga ccc ttt gga cat aaa gaa aga tgt	251
---	-----

Glu	Asp	Asp	Glu	Val	Phe	Phe	Gly	Pro	Phe	Gly	His	Lys	Glu	Arg	Cys	
49				54					59				64			
att	gct	gcc	agc	ttg	gaa	tta	aat	aat	ccg	gtt	ccc	gaa	cag	cct	ccg	299
Ile	Ala	Ala	Ser	Leu	Glu	Leu	Asn	Asn	Pro	Val	Pro	Glu	Gln	Pro	Pro	
65				70					75				80			
ttg	ccc	aca	tct	gag	agt	ccc	ttt	gcc	tgg	agc	cct	ctg	gcc	ggg	gag	347
Leu	Pro	Thr	Ser	Glu	Ser	Pro	Phe	Ala	Trp	Ser	Pro	Leu	Ala	Gly	Glu	
81				86					91				96			
aag	ttc	gtg	gag	gtg	tac	aaa	gaa	gct	cac	tta	ctg	gct	tta	cac	att	395
Lys	Phe	Val	Glu	Val	Tyr	Lys	Glu	Ala	His	Leu	Leu	Ala	Leu	His	Ile	
97				102					107				112			
gag	agc	agc	agc	cg	aa	cag	gca	gcc	caa	gct	gcc	aag	cct	gaa	gac	443
Glu	Ser	Ser	Ser	Arg	Asn	Gln	Ala	Ala	Gln	Ala	Ala	Lys	Pro	Glu	Asp	
113				118					123				128			
cct	cg	agc	cag	ggc	gtg	gaa	aga	ttc	ata	cag	gag	tca	aaa	tta	aaa	491
Pro	-Arg	Ser	-Gln	Gly	-Val	Glu	Arg	Phe	Ile	Gln	Glu	Ser	Lys	Leu	Lys	
129				134					139				144			
ata	aa	ctc	ttt	gag	aaa	gaa	aag	gaa	atg	aag	aaa	agc	ccc	acg	tct	539
Ile	Asn	Leu	Phe	Glu	Lys	Glu	Lys	Glu	Met	Lys	Lys	Ser	Pro	Thr	Ser	
145				150					155				160			
ctt	aaa	agg	gag	aca	ta	ta	ctg	tca	gac	agc	ccc	ttg	ctg	ggg	ccc	587
Leu	Lys	Arg	Glu	Thr	Tyr	Tyr	Leu	Ser	Asp	Ser	Pro	Leu	Leu	Gly	Pro	
161				166					171				176			
cct	gtg	gg	gag	cct	cg	ctc	ttg	gcc	tcc	tcc	ccg	gcc	ctg	ccc	agc	635
Pro	Val	Gly	Glu	Pro	Arg	Leu	Leu	Ala	Ser	Ser	Pro	Ala	Leu	Pro	Ser	
177				182					187				192			
tct	gg	g	ca	g	cc	ctc	acc	cg	gc	ccg	ggg	cct	ccg	cac	tct	683
Ser	Gly	Ala	Gln	Ala	Arg	Leu	Thr	Arg	Ala	Pro	Gly	Pro	Pro	His	Ser	
193				198					203				208			
gct	cat	gct	ttg	ccc	agg	gaa	tca	tgc	act	gct	cat	gct	gca	agt	cag	731
Ala	His	Ala	Leu	Pro	Arg	Glu	Ser	Cys	Thr	Ala	His	Ala	Ala	Ser	Gln	
209				214					219				224			
gca	g	cg	act	cag	agg	aag	ccc	ggg	acc	aaa	ttg	ctg	ctg	cct	cga	779
Ala	Ala	Thr	Gln	Arg	Lys	Pro	Gly	Thr	Lys	Leu	Leu	Leu	Pro	Arg	Ala	
225				230					235				240			
gcc	tct	gtt	aga	gga	aga	agc	atc	cct	ggg	gct	g	g	ag	aag	ccc	827
Ala	Ser	Val	Arg	Gly	Arg	Ser	Ile	Pro	Gly	Ala	Ala	Glu	Lys	Pro	Lys	
241				246					251				256			
aaa	gag	att	cca	gct	agt	cct	tcc	agg	aca	aaa	atc	cca	gct	gag	aag	875
Lys	Glu	Ile	Pro	Ala	Ser	Pro	Ser	Arg	Thr	Lys	Ile	Pro	Ala	Glu	Lys	
257				262					267				272			
gaa	tcc	cac	cg	gat	gtt	ctc	cct	gac	aaa	cct	gcc	ccg	gg	gt	gtc	923
Glu	Ser	His	Arg	Asp	Val	Leu	Pro	Asp	Lys	Pro	Ala	Pro	Gly	Ala	Val	

273	278	283	288	
aat gtg ccg gcc gcc gga agc cac ttg ggc cag ggc aag cgg gcg atc Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln Gly Lys Arg Ala Ile 289	294	299	304	971
cct gtt cca aac aag ttg ggg ctg aag aag acc ctg tta aaa gca ccc Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr Leu Leu Lys Ala Pro 305	310	315	320	1019
ggc tct acc agc aat ctc gca agg aag tcc tcc tcg ggg cct gtt tgg Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser Ser Gly Pro Val Trp 321	326	331	336	1067
agc ggg gca tcc agt gcg tgc aca tcc cca gca gtg ggc aaa gct aaa Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala Val Gly Lys Ala Lys 337	342	347	352	1115
tca agt gaa ttt gca agt att cct gca aat agc tcc cgg cct ctg tca Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser Ser Arg Pro Leu Ser 353	358	363	368	1163
aac atc agc aag tca ggc aga atg gga ccc gcc atg ctg cgg cca gct Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala Met Leu Arg Pro Ala 369	374	379	384	1211
ctg cct gca ggc cct gtg'ggg gca tcc tcc tgg cag gcc aag cgg gtc Leu Pro Ala Gly Pro Val Gly Ala Ser Ser Trp Gln Ala Lys Arg Val 385	390	395	400	1259
gat gtt tct gag ctg gca gcg gag cag ctc acg gca ccc ccc tca gca Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr Ala Pro Pro Ser Ala 401	406	411	416	1307
tcc ccc acc caa ccc cag act ccg gaa ggt ggc ggc cag tgg ctg aac Ser Pro Thr Gln Pro Gln Thr Pro Glu Gly Gly Gln Trp Leu Asn 417	422	427	432	1355
tcc agt tgc gct tgg tca gaa tct tct caa ttg aat aag act aga agt Ser Ser Cys Ala Trp Ser Glu Ser Ser Gln Leu Asn Lys Thr Arg Ser 433	438	443	448	1403
atc aga cgg cga gat tcc tgt cta aat tcc aag aca aag gtt atg cct Ile Arg Arg Arg Asp Ser Cys Leu Asn Ser Lys Thr Lys Val Met Pro 449	454	459	464	1451
act cct aca aat caa ttt aaa att cct aag ttt tct att ggt gac tcc Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe Ser Ile Gly Asp Ser 465	470	475	480	1499
ccg gac agc tca aca cca aag ctt tcg cgg gca cag cgg ccg cag tcg Pro Asp Ser Ser Thr Pro Lys Leu Ser Arg Ala Gln Arg Pro Gln Ser 481	486	491	496	1547
tgc acg tca gtt ggc agg gtc act gtc cac agc acc ccg gtt aga cgc Cys Thr Ser Val Gly Arg Val Thr Val His Ser Thr Pro Val Arg Arg 497	502	507	512	1595

tca tct ggg cca gca cca caa agc ctg ctg agc gca cg ^g cgt gtg tca Ser Ser Gly Pro Ala Pro Gln Ser Leu Leu Ser Ala Arg Arg Val Ser 513 518 523 528	1643
gcc ttg ccc aca ccc gcc agc cg ^g cgc tgc tct ggc ctt cca ccg atg Ala Leu Pro Thr Pro Ala Ser Arg Arg Cys Ser Gly Leu Pro Pro Met 529 534 539 544	1691
acc ccc aaa acg atg ccc agg gcc gtg ggc tct ccc ctg tgt gtg cca Thr Pro Lys Thr Met Pro Arg Ala Val Gly Ser Pro Leu Cys Val Pro 545 550 555 560	1739
gct cg ^g aga cgt tcc tct gag ccc cgc aag aac tct gca atg aga act Ala Arg Arg Arg Ser Ser Glu Pro Arg Lys Asn Ser Ala Met Arg Thr 561 566 571 576	1787
gaa cca aca agg gag agc aac aga aag aca gat tcc agg ctg gtg gat Glu Pro Thr Arg Glu Ser Asn Arg Lys Thr Asp Ser Arg Leu Val Asp 577 582 587 592	1835
gtg tcc cct gac agg ggt tct cct tcc cgt gtg cct cag gca ctt Val Ser Pro Asp Arg Gly Ser Pro Pro Ser Arg Val Pro Gln Ala Leu 593 598 603 608	1883
aac ttt tct cca gag gaa agc gat tct act ttc tcc aaa agt act gcc Asn Phe Ser Pro Glu Glu Ser Asp Ser Thr Phe Ser Lys Ser Thr Ala 609 614 619 624	1931
aca gaa gta gct cg ^g gag gaa gcc aag ccg ggt gga gat gca gcc cct Thr Glu Val Ala Arg Glu Ala Lys Pro Gly Gly Asp Ala Ala Pro 625 630 635 640	1979
agt gag gct ctt gta gat atc aaa ctg gaa cca ctc gc ^g gtc act Ser Glu Ala Leu Leu Val Asp Ile Lys Leu Glu Pro Leu Ala Val Thr 641 646 651 656	2027
cca gat gct gca agc cag ccc ctc att gac ctt cct ctc atc gac ttc Pro Asp Ala Ala Ser Gln Pro Leu Ile Asp Leu Pro Leu Ile Asp Phe 657 662 667 672	2075
tgc gat acc cca gaa gca cac gtg gct gta gga tct gaa agc agg cct Cys Asp Thr Pro Glu Ala His Val Ala Val Gly Ser Glu Ser Arg Pro 673 678 683 688	2123
ctg atc gac ctc atg aca aac act cca gac atg aat aaa aat gtg gcc Leu Ile Asp Leu Met Thr Asn Thr Pro Asp Met Asn Lys Asn Val Ala 689 694 699 704	2171
aaa cct tca ccg gtg gtg gga cag ctc ata gac ctg agc tcc cct ctg Lys Pro Ser Pro Val Val Gly Gln Leu Ile Asp Leu Ser Ser Pro Leu 705 710 715 720	2219
atc cag ctg agc cct gag gct gac aag gag aac gtg gat tcc cca ctc Ile Gln Leu Ser Pro Glu Ala Asp Lys Glu Asn Val Asp Ser Pro Leu 721 726 731 736	2267

ctc aag ttc taa gcc gaaccaaatc ctttgccttg aaagaacago cctaaaagtgg	2322
Leu Lys Phe *	
737	
 tttcaaccc tcagaaaaca gctttaggct ggtcgcagtg gcttacactt gtaaccctag	2382
aacttgggag gctgagggtgg gcggattact tgagcccagg agttcgggac cagcctggga	2442
aatatagtga aactcctgtc cctacaaaaa atacaaaaat tagccgggtg tggtagtgca	2502
tgcctgttagt cccagctact tgggaggctg aagtgggagg atggcctgag ctcaaggaga	2562
tgcaggctgc agtgggctgt gattgtgcca ctgcactcca gcctggcac caatgtgaga	2622
acctgtcttg gaaaaaaaaaaaaaa acatggggatgtt agaagttta tttgaaaaag	2682
aaaaataaagc ataaatatat tcccagtgtc ggagagggtg ggctgaggga ctggggccag	2742
cacggaccac ccaaggcctc tgcttccgc cgccaccctc ctgcgtgcca ttctctggc	2802
tggaatgtga agcctcagtc actctaaatg aagaattttc ttttgaatgt tttgtatgt	2862
aaatagcaag tggctatttt taaagttaag tttgtataaa tagttagata ttctagattt	2922
acattaaatt gtaaaataaa tggacttatt gaagcatatc ttgattttt agcttatctt	2982
gattttcaaaa catgcatacg tatttttattc actctaatac gtaaggctac tatctagact	3042
cgaatgctt catacaagtg attttcaaaa attagtcaat aaaaattgtat gtcagtgcag	3102
gcccaggccc gccccagat acactagttt ctaggtctgg ggccagccctt gtaattgtt	3162
ctaggcacac aggtgatgct gactcgatgg cctgagacac acccccttgag aagaagctgc	3222
tctggggaga cgagggatgt agtggaaaga ggatggcga	3262

<210> 140
 <211> 3061
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(2078)

<400> 140

agcgggattc gatagcatac tcagtgtggt ggaattcgtg acttctgaca gctctctcc	59
atg gaa gga ggc ggc ggc cgc gat gag cct tca gcc tgc cgg gca ggg	107
Met Glu Gly Gly Gly Gly Arg Asp Glu Pro Ser Ala Cys Arg Ala Gly	
1 , 5 10 15	

gac gtg aac atg gat gac cct aag aag gaa gac att ctt ctt ttg gcc	155
Asp Val Asn Met Asp Asp Pro Lys Lys Glu Asp Ile Leu Leu Leu Ala	
17 22 27 32	

gat gaa aaa ttt gac ttc gat ctt tca ttg tct tct tcg agt gca aat			203
Asp Glu Lys Phe Asp Phe Asp Leu Ser Leu Ser Ser Ser Ala Asn			
33	38	43	48
gaa gat gat gaa gtc ttc ttc gga ccc ttt gga cat aaa gaa aga tgt			251
Glu Asp Asp Glu Val Phe Phe Gly Pro Phe Gly His Lys Glu Arg Cys			
49	54	59	64
att gct gcc agc ttg gaa tta aat aat ccg gtt ccc gaa cag cct ccg			299
Ile Ala Ala Ser Leu Glu Leu Asn Asn Pro Val Pro Glu Gln Pro Pro			
65	70	75	80
ttg ccc aca tct gag agt ccc ttt gcc tgg agc cct ctg gcc ggg gag			347
Leu Pro Thr Ser Glu Ser Pro Phe Ala Trp Ser Pro Leu Ala Gly Glu			
81	86	91	96
aag ttc gtg gag gtg tac aaa gaa gct cac tta ctg gct tta cac att			395
Lys Phe Val Glu Val Tyr Lys Glu Ala His Leu Leu Ala Leu His Ile			
97	102	107	112
gag agc agc agc cgg aac cag gca gcc caa gct gcc aag cct gaa gac			443
Glu Ser Ser Ser Arg Asn Gln Ala Ala Gln Ala Ala Lys Pro Glu Asp			
113	118	123	128
cct cggtt agc cag ggc gtg gaa aga ttc ata cag gag tca aaa tta aaa			491
Pro Arg Ser Gln Gly Val Glu Arg Phe Ile Gln Glu Ser Lys Leu Lys			
129	134	139	144
ata aac ctc ttt gag aaa gaa aag gaa atg aag aaa agc ccc acg tct			539
Ile Asn Leu Phe Glu Lys Glu Lys Glu Met Lys Lys Ser Pro Thr Ser			
145	150	155	160
ctt aaa agg gag aca tac tac ctg tca gac agc ccc ttg ctg ggg ccc			587
Leu Lys Arg Glu Thr Tyr Leu Ser Asp Ser Pro Leu Leu Gly Pro			
161	166	171	176
cct gtg ggt gag cct cgg ctc ttg gcc tcc tcc ccg gcc ctg ccc agc			635
Pro Val Gly Glu Pro Arg Leu Leu Ala Ser Ser Pro Ala Leu Pro Ser			
177	182	187	192
tct ggt gcc cag gcc cgc ctc acc cgg gcg ccg ggg cct ccg cac tct			683
Ser Gly Ala Gln Ala Arg Leu Thr Arg Ala Pro Gly Pro Pro His Ser			
193	198	203	208
gct cat gct ttg ccc agg gaa tca tgc act gct cat gct gca agt cag			731
Ala His Ala Leu Pro Arg Glu Ser Cys Thr Ala His Ala Ala Ser Gln			
209	214	219	224
gca gcg act cag agg aag ccc ggg acc aaa ttg ctg ctg cct cga gcg			779
Ala Ala Thr Gln Arg Lys Pro Gly Thr Lys Leu Leu Pro Arg Ala			
225	230	235	240
gcc tct gtt aga gga aga agc atc cct ggg gct gcg gag aag ccc aag			827
Ala Ser Val Arg Gly Arg Ser Ile Pro Gly Ala Ala Glu Lys Pro Lys			
241	246	251	256

aaa gag att cca gct agt cct tcc agg aca aaa atc cca gct gag aag		875
Lys Glu Ile Pro Ala Ser Pro Ser Arg Thr Lys Ile Pro Ala Glu Lys		
257	262	267
272		
gaa tcc cac cg ^g gat gtt ctc cct gac aaa cct gcc ccg ggt gct gtc		923
Glu Ser His Arg Asp Val Leu Pro Asp Lys Pro Ala Pro Gly Ala Val		
273	278	283
288		
aat gtg ccg gcc ggc gga agc cac ttg ggc cag ggc aag ccg ggc atc		971
Asn Val Pro Ala Ala Gly Ser His Leu Gly Gln Gly Lys Arg Ala Ile		
289	294	299
304		
cct gtt cca aac aag ttg ggg ctg aag aag acc ctg tta aaa gca ccc		1019
Pro Val Pro Asn Lys Leu Gly Leu Lys Lys Thr Leu Leu Lys Ala Pro		
305	310	315
320		
ggc tct acc agc aat ctc gca agg aag tcc tcc tcg ggg cct gtt tgg		1067
Gly Ser Thr Ser Asn Leu Ala Arg Lys Ser Ser Gly Pro Val Trp		
321	326	331
336		
-agc ggg gca tcc agt gcg tgc aca tcc cca gca gtg ggc aaa gct aaa		1115
Ser Gly Ala Ser Ser Ala Cys Thr Ser Pro Ala Val Gly Lys Ala Lys		
337	342	347
352		
tca agt gaa ttt gca agt att cct gca aat agc tcc ccg cct ctg tca		1163
Ser Ser Glu Phe Ala Ser Ile Pro Ala Asn Ser Ser Arg Pro Leu Ser		
353	358	363
368		
aac atc agc aag tca ggc aga atg gga ccc gcc atg ctg ccg cca gct		1211
Asn Ile Ser Lys Ser Gly Arg Met Gly Pro Ala Met Leu Arg Pro Ala		
369	374	379
384		
ctg cct gca ggc cct gtg ggg gca tcc tcc tgg cag gcc aag ccg gtc		1259
Leu Pro Ala Gly Pro Val Gly Ala Ser Ser Trp Gln Ala Lys Arg Val		
385	390	395
400		
gat gtt tct gag ctg gca gcg gag cag ctc acg gca ccc ccc tca gca		1307
Asp Val Ser Glu Leu Ala Ala Glu Gln Leu Thr Ala Pro Pro Ser Ala		
401	406	411
416		
tcc ccc acc caa ccc cag act ccg gaa ggt ggc ccg cag tgg ctg aac		1355
Ser Pro Thr Gln Pro Gln Thr Pro Glu Gly Gly Gln Trp Leu Asn		
417	422	427
432		
tcc agt tgc gct tgg tca gaa tct tct caa ttg aat aag act aga agt		1403
Ser Ser Cys Ala Trp Ser Glu Ser Ser Gln Leu Asn Lys Thr Arg Ser		
433	438	443
448		
atc aga ccg cga gat tcc tgt cta aat tcc aag aca aag gtt atg cct		1451
Ile Arg Arg Arg Asp Ser Cys Leu Asn Ser Lys Thr Lys Val Met Pro		
449	454	459
464		
act cct aca aat caa ttt aaa att cct aag ttt tct att ggt gac tcc		1499
Thr Pro Thr Asn Gln Phe Lys Ile Pro Lys Phe Ser Ile Gly Asp Ser		
465	470	475
480		
ccg gac agc tca aca cca aag ctt tcg cgg gca cag ccg cag tcg		1547

Pro	Asp	Ser	Ser	Thr	Pro	Lys	Leu	Ser	Arg	Ala	Gln	Arg	Pro	Gln	Ser		
481					486				491				496				
tgc	acg	tca	gtt	ggc	agg	gtc	act	gtc	cac	agc	acc	ccg	gtt	aga	cgc	1595	
Cys	Thr	Ser	Val	Gly	Arg	Val	Thr	Val	His	Ser	Thr	Pro	Val	Arg	Arg		
497					502				507				512				
tca	tct	ggg	cca	gca	cca	caa	agc	ctg	ctg	agc	gca	cgg	cgt	gtg	tca	1643	
Ser	Ser	Gly	Pro	Ala	Pro	Gln	Ser	Leu	Leu	Ser	Ala	Arg	Arg	Val	Ser		
513					518				523				528				
gcc	ttg	ccc	aca	ccc	gcc	agc	cgg	cgc	tgc	tct	ggc	ctt	cca	ccg	atg	1691	
Ala	Leu	Pro	Thr	Pro	Ala	Ser	Arg	Arg	Cys	Ser	Gly	Leu	Pro	Pro	Met		
529					534				539				544				
acc	ccc	aaa	acg	atg	ccc	agg	gcc	gtg	ggc	tct	ccc	ctg	tgt	gtg	cca	1739	
Thr	Pro	Lys	Thr	Met	Pro	Arg	Ala	Val	Gly	Ser	Pro	Leu	Cys	Val	Pro		
545					550				555				560				
gct	cgg	aga	cgt	tcc	tct	gag	ccc	cgc	aag	aac	tct	gca	atg	agg	gct	1787	
Ala	Arg	Arg	Arg	Ser	Ser	Glu	Pro	Arg	Lys	Asn	Ser	Ala	Met	Arg	Ala		
561					566				571				576				
ctt	ctt	gta	gat	atc	aaa	ctg	gaa	cca	ctc	gcg	gtc	act	cca	gat	gct	1835	
Leu	Leu	Val	Asp	Ile	Lys	Leu	Glu	Pro	Leu	Ala	Val	Thr	Pro	Asp	Ala		
577					582				587				592				
gca	agc	cag	ccc	ctc	att	gac	ctt	cct	ctc	atc	gac	ttc	tgc	gat	acc	1883	
Ala	Ser	Gln	Pro	Leu	Ile	Asp	Leu	Pro	Leu	Ile	Asp	Phe	Cys	Asp	Thr		
593					598				603				608				
cca	gaa	gca	cac	gtg	gct	gta	gga	tct	gaa	agc	agg	cct	ctg	atc	gac	1931	
Pro	Glu	Ala	His	Val	Ala	Val	Gly	Ser	Glu	Ser	Arg	Pro	Leu	Ile	Asp		
609					614				619				624				
ctc	atg	aca	aac	act	cca	gac	atg	aat	aaa	aat	gtg	gcc	aaa	cct	tca	1979	
Leu	Met	Thr	Asn	Thr	Pro	Asp	Met	Asn	Lys	Asn	Val	Ala	Lys	Pro	Ser		
625					630				635				640				
ccg	gtg	gtg	gga	cag	ctc	ata	gac	ctg	agc	tcc	cct	ctg	atc	cag	ctg	2027	
Pro	Val	Val	Gly	Gln	Leu	Ile	Asp	Leu	Ser	Ser	Pro	Leu	Ile	Gln	Leu		
641					646				651				656				
agc	cct	gag	gct	gac	aag	gag	aac	gtg	gat	tcc	cca	ctc	ctc	aag	ttc	2075	
Ser	Pro	Glu	Ala	Asp	Lys	Glu	Asn	Val	Asp	Ser	Pro	Leu	Leu	Lys	Phe		
657					662				667				672				
taa	gccg	aaccaa	atcc	tttg	cctt	ga	aaga	acag	cc	ctaa	agt	gg	ttt	caac	cc	2132	
*																	
673																	
cagaaaca	ag	ctt	tagg	ctg	gtc	gc	agt	gg	ctt	ac	act	cc	ct	gt	gg	agg	2192
ctg	aggt	gg	cg	gat	tt	cc	at	cc	at	cc	tc	tt	gg	gg	gg	gg	2252
act	cct	gt	tcc	at	aca	aaaa	at	aaaa	att	ag	cc	gg	gt	tg	tc	at	2312
act	cct	gt	tcc	at	aca	aaaa	at	aaaa	att	ag	cc	gg	gt	tg	tc	at	

ccagctactt gggaggctga agtgggagga tggcctgagc tcaaggagat gcaggctgca 2372
 gtgggctgtg atttgccac tgcactccag cctggcacc aatgtgagaa cctgtttgg 2432
 aaaaaaaaaaaa aaaaaaaaaaca tgtttagta gaagtttat ttgaaaaaga aaaataagca 2492
 taaatatatt cccagtgtg gagagggtgg gctgaggac tggggccagc acggaccacc 2552
 caaggcctct gcttcccgc gcccacccat tcgctgccat tctctggct ggaatgtgaa 2612
 gcctcagtca ctctaaatga agaattttct tttgaatgtt ttgtatgtaa aatagcaagt 2672
 ggctattttt aaagttaagt ttgtataaat agtagatat tctagattta cattaaattt 2732
 taaaataaat ggacttattt aagcatatct tgattttaa gcttatctt atttcaaacc 2792
 atgcatacgat attttatca ctctaaatcg taaggctact atctagactc gaatgcttc 2852
 atacaagtga ttttcaaaaa tttagtcaata aaaattgtg tcagtgcagg cccaggcccc 2912
 cccccagata cactagtttc taggtctggg gccagcctag taattgttac taggcacaca 2972
 ggtgatgctg actcgatggc ctgagacaca ccccttgaga agaagctgct ctggggagac 3032
 gagggtatga gtggaaagag gatgggcga 3061

<210> 141
 <211> 5102
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (284)..(4234)

<400> 141
 aggggggatt gacccttgcg gcaccggtcc ggaattccccg ggtcgaccac cgcgccggg 60
 ttccctgcaga tagagtctgc ctccccgtcc cccttctttt ctggattcct cgctgcccac 120
 cctcattctc ccgggggaag cctcgcaacg aagggccgga gccgccttcc tgctccgg 180
 atgcttcacc tgtccgcagc tccgccccgg ccaccccccgg aagtgacggc gaccgcgcgg 240
 ccctgccttt gttccgttgg gcgtccgcgg cgacggcggg aag atg gcg gcg gcg 295
 Met Ala Ala Ala
 1

gga gcc ctg gaa cgg agc ttc gtg gag cta agc gga gct gag cgc gaa 343
 Gly Ala Leu Glu Arg Ser Phe Val Glu Leu Ser Gly Ala Glu Arg Glu
 5 10 15 20

agg ccg agg cac ttt cgg gaa ttc aca gtc tgc agc att ggg act gca 391
 Arg Pro Arg His Phe Arg Glu Phe Thr Val Cys Ser Ile Gly Thr Ala

21	26	31	36	
aat gcc gtg gct ggc gcc gta aaa tac agt gaa agc gcg gga ggc ttt Asn Ala Val Ala Gly Ala Val Lys Tyr Ser Glu Ser Ala Gly Gly Phe 37 42 47 52				439
tac tac gtg gag agt ggc aag ttg ttc tcc gta acc aga aac agg ttc Tyr Tyr Val Glu Ser Gly Lys Leu Phe Ser Val Thr Arg Asn Arg Phe 53 58 63 68				487
att cat tgg aag acc tct gga gat aca ttg gag ctg atg gag gag tca Ile His Trp Lys Thr Ser Gly Asp Thr Leu Glu Leu Met Glu Glu Ser 69 74 79 84				535
ctg gac ata aat ctg ttg aat aat gcc att cgc cta aaa ttc caa aat Leu Asp Ile Asn Leu Leu Asn Asn Ala Ile Arg Leu Lys Phe Gln Asn 85 90 95 100				583
tgc agt gtt tta cct gga ggg gtt tat gtc tct gag act cag aat cgt Cys Ser Val Leu Pro Gly Gly Val Tyr Val Ser Glu Thr Gln Asn Arg 101 106 111 116				631
gtg ata atc ttg atg tta acc aat caa aca gtg cac agg tta ctt tta Val Ile Ile Leu Met Leu Thr Asn Gln Thr Val His Arg Leu Leu Leu 117 122 127 132				679
cca cac ccc tcc cgg atg'tat agg agt gag ttg gta gtt gac agt cag Pro His Pro Ser Arg Met Tyr Arg Ser Glu Leu Val Val Asp Ser Gln 133 138 143 148				727
atg cag tca ata ttc act gac att gga aaa gtt gat ttc aca gat cct Met Gln Ser Ile Phe Thr Asp Ile Gly Lys Val Asp Phe Thr Asp Pro 149 154 159 164				775
tgc aac tat cag tta att cca gca gta cct gga ata tct cct aat tcc Cys Asn Tyr Gln Leu Ile Pro Ala Val Pro Gly Ile Ser Pro Asn Ser 165 170 175 180				823
acc gcc tct aca gcc tgg ctc agc agt gat ggg gag gcc ctg ttt gcc Thr Ala Ser Thr Ala Trp Leu Ser Ser Asp Gly Glu Ala Leu Phe Ala 181 186 191 196				871
tta cca tgt gct tct ggg gga atc ttt gtt ctt aag cta cct cct tat Leu Pro Cys Ala Ser Gly Gly Ile Phe Val Leu Lys Leu Pro Pro Tyr 197 202 207 212				919
gac ata cct ggt atg gtg tca gtc gtg gaa ctg aaa cag agt tca gta Asp Ile Pro Gly Met Val Ser Val Val Glu Leu Lys Gln Ser Ser Val 213 218 223 228				967
atg caa cga ttg ctt aca ggc tgg atg cca aca gct atc agg ggt gac Met Gln Arg Leu Leu Thr Gly Trp Met Pro Thr Ala Ile Arg Gly Asp 229 234 239 244				1015
cag tcg cct tca gat cgt ccc ctc agt ctt gct gtt cat tgt gtg gag Gln Ser Pro Ser Asp Arg Pro Leu Ser Leu Ala Val His Cys Val Glu 245 250 255 260				1063 /

cat gat gcc ttc atc ttt gct ttg tgt cag gat cat aaa cta cga atg His Asp Ala Phe Ile Phe Ala Leu Cys Gln Asp His Lys Leu Arg Met 261 266 271 276	1111
tgg tct tac aag gag caa atg tgc cta atg gta gct gac atg ctg gag Trp Ser Tyr Lys Glu Gln Met Cys Leu Met Val Ala Asp Met Leu Glu 277 282 287 292	1159
aat gtc cct gtg aag aaa gac ctt cg ^g ctt act gct gga act gga cac Tyr Val Pro Val Lys Lys Asp Leu Arg Leu Thr Ala Gly Thr Gly His 293 298 303 308	1207
aaa tta cgg ctt gct tat tcc ccc acc atg gga ctc tac ctg ggg ata Lys Leu Arg Leu Ala Tyr Ser Pro Thr Met Gly Leu Tyr Leu Gly Ile 309 314 319 324	1255
atc atg cat gca cca aaa cga gga cag ttc tgc att ttc cag ttg gtg Tyr Met His Ala Pro Lys Arg Gly Gln Phe Cys Ile Phe Gln Leu Val 325 330 335 340	1303
agc act gag agt aat cgc tat agt ctc gat cat att tct tca ctg ttc Ser Thr Glu Ser Asn Arg Tyr Ser Leu Asp His Ile Ser Ser Leu Phe 341 346 351 356	1351
act tct cag gag aca ctg att gac ttt gcc tta act tcc acg gat atc Thr Ser Gln Glu Thr Leu Ile Asp Phe Ala Leu Thr Ser Thr Asp Ile 357 362 367 372	1399
tgg gcc ctg tgg cat gat gct gag aac caa aca gta gtg aaa tac atc Trp Ala Leu Trp His Asp Ala Glu Asn Gln Thr Val Val Lys Tyr Ile 373 378 383 388	1447
aac ttt gaa cat aat gtt gca ggt cag tgg aat cca gtt ttt atg cag Asn Phe Glu His Asn Val Ala Gly Gln Trp Asn Pro Val Phe Met Gln 389 394 399 404	1495
cct ctg cca gag gaa gag att gtc atc aga gat gat caa gac ccc aga Pro Leu Pro Glu Glu Ile Val Ile Arg Asp Asp Gln Asp Pro Arg 405 410 415 420	1543
gag atg tat ctg caa agt ctt ttt aca cca gga caa ttc aca aat gaa Glu Met Tyr Leu Gln Ser Leu Phe Thr Pro Gly Gln Phe Thr Asn Glu 421 426 431 436	1591
gct tta tgt aag gct tta cag att ttc tgc cga gga act gag agg aat Ala Leu Cys Lys Ala Leu Gln Ile Phe Cys Arg Gly Thr Glu Arg Asn 437 442 447 452	1639
ttg gat ctt tcc tgg agt gaa ctg aag aaa gaa gtt act tta gct gtt Leu Asp Leu Ser Trp Ser Glu Leu Lys Lys Glu Val Thr Leu Ala Val 453 458 463 468	1687
gaa aat gag ctt caa gga agt gta aca gag tat gaa ttc tcc cag gag Glu Asn Glu Leu Gln Gly Ser Val Thr Glu Tyr Glu Phe Ser Gln Glu 469 474 479 484	1735

gag ttt cga aat tta caa caa gaa ttc tgg tgc aag ttc tat gcc tgt Glu Phe Arg Asn Leu Gln Gln Glu Phe Trp Cys Lys Phe Tyr Ala Cys 485	490	495	500	1783
tgt ctt cag tat caa gaa gcc ctc tct cac cct ctt gcc cta cat ttg Cys Leu Gln Tyr Gln Glu Ala Leu Ser His Pro Leu Ala Leu His Leu 501	506	511	516	1831
aat cca cac aca aac atg gtg tgc ctg ctg aaa aaa ggg tac ctg tct Asn Pro His Thr Asn Met Val Cys Leu Leu Lys Lys Gly Tyr Leu Ser 517	522	527	532	1879
ttc ctt att ccc tca tcc tta gtg gat cat ttg tat ctc ctg cct tat Phe Leu Ile Pro Ser Ser Leu Val Asp His Leu Tyr ¹¹ Leu Leu Pro Tyr 533	538	543	548	1927
gag aac ctt ttg aca gaa gat gag aca acc ata tct gat gat gtg gat Glu Asn Leu Leu Thr Glu Asp Glu Thr Thr Ile Ser Asp Asp Val Asp 549	554	559	564	1975
atc gct cgg gat gtc ata tgt ctt ata aaa tgc ctc cgg ctg att gaa Ile Ala Arg Asp Val Ile Cys Leu Ile Lys Cys Leu Arg Leu Ile Glu 565	570	575	580	2023
gag tca gta act gtg gat atg tca gtt ata atg gaa atg agt tgt tat Glu Ser Val Thr Val Asp Met Ser Val Ile Met Glu Met Ser Cys Tyr 581	586	591	596	2071
aac cta cag tct ccg gaa aag gct gca gag cag att ctg gaa gat atg Asn Leu Gln Ser Pro Glu Lys Ala Ala Glu Gln Ile Leu Glu Asp Met 597	602	607	612	2119
atc act att gat gta gaa aat gtg atg gag gat att tgt agt aaa ctg Ile Thr Ile Asp Val Glu Asn Val Met Glu Asp Ile Cys Ser Lys Leu 613	618	623	628	2167
caa gag att agg aac cca atc cat gca att gga cta ctt ata cgg gaa Gln Glu Ile Arg Asn Pro Ile His Ala Ile Gly Leu Leu Ile Arg Glu 629	634	639	644	2215
atg gat tat gaa aca gaa gtg gaa atg gaa aag gga ttc aat cca gct Met Asp Tyr Glu Thr Glu Val Glu Met Glu Lys Gly Phe Asn Pro Ala 645	650	655	660	2263
cag cct ttg aat att cga atg aat ctt acc cag ctc tat ggt agt aac Gln Pro Leu Asn Ile Arg Met Asn Leu Thr Gln Leu Tyr Gly Ser Asn 661	666	671	676	2311
aca gca ggg tat att gtg tgc aga ggg gtg cat aaa atc gcc agt act Thr Ala Gly Tyr Ile Val Cys Arg Gly Val His Lys Ile Ala Ser Thr 677	682	687	692	2359
cgt ttc ctg atc tgc aga gat ctt ttg atc tta cag cag ctg tta atg Arg Phe Leu Ile Cys Arg Asp Leu Leu Ile Leu Gln Gln Leu Leu Met 693	698	703	708	2407
agg ctt gga gat gct gtg att tgg gga act ggt cag ctc ttt caa gct				2455

Arg Leu Gly Asp Ala Val Ile Trp Gly Thr Gly Gln Leu Phe Gln Ala			
709	714	719	724
cag caa gac cta cta cat cga aca gct ccc cta ctc tta tct tat tac			2503
Gln Gln Asp Leu Leu His Arg Thr Ala Pro Leu Leu Ser Tyr Tyr			
725	730	735	740
ctc att aaa tgg gga agt gag tgc ttg gca act gat gtt cca ctt gac			2551
Leu Ile Lys Trp Gly Ser Glu Cys Leu Ala Thr Asp Val Pro Leu Asp			
741	746	751	756
aca ctg gag tct aat ctc caa cac tta tca gta ctg gaa tta aca gac			2599
Thr Leu Glu Ser Asn Leu Gln His Leu Ser Val Leu Glu Leu Thr Asp			
757	762	767	772
tct ggt gct tta atg gca aat agg ttt gta tct agt cct cag act att			2647
Ser Gly Ala Leu Met Ala Asn Arg Phe Val Ser Ser Pro Gln Thr Ile			
773	778	783	788
gtg gag tta ttc ttc caa gaa gtt gca aga aaa cac att ata tct cac			2695
Val Glu Leu Phe Phe Gln Glu Val Ala Arg Lys His Ile Ile Ser His			
789	794	799	804
ctc ttc tct cag cca aag gca cct ctg agc caa act gga ttg aat tgg			2743
Leu Phe Ser Gln Pro Lys Ala Pro Leu Ser Gln Thr Gly Leu Asn Trp			
805	810	815	820
cct gaa atg att act gca att acc agt tat tta ttg cag ctt tta tgg			2791
Pro Glu Met Ile Thr Ala Ile Thr Ser Tyr Leu Leu Gln Leu Leu Trp			
821	826	831	836
cct agc aat cct ggt tgt ctc ttt cta gaa tgt ttg atg gga aat tgc			2839
Pro Ser Asn Pro Gly Cys Leu Phe Leu Glu Cys Leu Met Gly Asn Cys			
837	842	847	852
caa tat gta caa ttg cag gat tat att caa ctg cta cat ccc tgg tgt			2887
Gln Tyr Val Gln Leu Gln Asp Tyr Ile Gln Leu Leu His Pro Trp Cys			
853	858	863	868
caa gtc aat gtt ggt tcc tgt cga ttt atg ctg gga agg tgt tac cta			2935
Gln Val Asn Val Gly Ser Cys Arg Phe Met Leu Gly Arg Cys Tyr Leu			
869	874	879	884
gtt aca gga gaa gga cag aag gct ctg gaa tgt ttt tgt cag gca gca			2983
Val Thr Gly Glu Gly Gln Lys Ala Leu Glu Cys Phe Cys Gln Ala Ala			
885	890	895	900
tct gaa gta ggc aaa gag gaa ttc ttg gat cgc ttg att cgc tca gag			3031
Ser Glu Val Gly Lys Glu Glu Phe Leu Asp Arg Leu Ile Arg Ser Glu			
901	906	911	916
gat ggg gag atc gtg tct acc ccc agg ctg cag tat tat gac aag gtt			3079
Asp Gly Glu Ile Val Ser Thr Pro Arg Leu Gln Tyr Tyr Asp Lys Val			
917	922	927	932
tta cga cta cta gat gtc att ggt ttg cct gaa ctg gtt att cag ttg			3127
Leu Arg Leu Leu Asp Val Ile Gly Leu Pro Glu Leu Val Ile Gln Leu			

933	938	943	948	
gct aca tca gcc ata act gaa gca ggt gat gac tgg aaa agt cag gct Ala Thr Ser Ala Ile Thr Glu Ala Gly Asp Asp Trp Lys Ser Gln Ala 949	954	959	964	3175
act cta agg aca tgt att ttc aaa cat cat ttg gat ttg ggt cac aat Thr Leu Arg Thr Cys Ile Phe Lys His His Leu Asp Leu Gly His Asn 965	970	975	980	3223
agc caa gca tat gaa gcc tta acc caa att cct gat tcc agc agg caa Ser Gln Ala Tyr Glu Ala Leu Thr Gln Ile Pro Asp Ser Ser Arg Gln 981	986	991	996	3271
tta gat tgt tta cgg cag ttg gtg gta gtt ctt tgt gaa cgc tca cag Leu Asp Cys Leu Arg Gln Leu Val Val Val Leu Cys Glu Arg Ser Gln 997	1002	1007	1012	3319
cta cag gat ctt gta gag ttt ccc tat gtg aat ctg cat aat gag gtt Leu Gln Asp Leu Val Glu Phe Pro Tyr Val Asn Leu His Asn Glu Val 1013	1018	1023	1028	3367
gtg gga ata att gag tca cgt gct aga gct gtg gac ctt atg act cac Val Gly Ile Ile Glu Ser Arg Ala Arg Ala Val Asp Leu Met Thr His 1029	1034	1039	1044	3415
aat tac tat gaa ctt ctg tat gcc ttt cac atc tat cgc cac aat tac Asn Tyr Tyr Glu Leu Leu Tyr Ala Phe His Ile Tyr Arg His Asn Tyr 1045	1050	1055	1060	3463
cgc aag gct ggc aca gtg atg ttt gag tat gga atg cgg ctt ggc aga Arg Lys Ala Gly Thr Val Met Phe Glu Tyr Gly Met Arg Leu Gly Arg 1061	1066	1071	1076	3511
gaa gtt cga act ctc cgg gga ctt gag aaa caa ggc aac tgt tat ctg Glu Val Arg Thr Leu Arg Gly Leu Glu Lys Gln Gly Asn Cys Tyr Leu 1077	1082	1087	1092	3559
gct gct ctc aat tgt tta cga ctt att cgt cca gaa tat gcg tgg att Ala Ala Leu Asn Cys Leu Arg Leu Ile Arg Pro Glu Tyr Ala Trp Ile 1093	1098	1103	1108	3607
gtg cag cca gtg tct ggt gca gtg tat gat cgc cct gga gca tcc cct Val Gln Pro Val Ser Gly Ala Val Tyr Asp Arg Pro Gly Ala Ser Pro 1109	1114	1119	1124	3655
aag agg aat cat gat gga gaa tgc aca gct gcc ccc aca aat cga caa Lys Arg Asn His Asp Gly Glu Cys Thr Ala Ala Pro Thr Asn Arg Gln 1125	1130	1135	1140	3703
att gaa atc ctg gaa gat ctg gag aaa gag tgt tcc ttg gct Ile Glu Ile Leu Glu Leu Glu Asp Leu Glu Lys Glu Cys Ser Leu Ala 1141	1146	1151	1156	3751
cgc atc cgc ctc act ttg gct cag cat gat cca tca gcg gtt gca gtt Arg Ile Arg Leu Thr Leu Ala Gln His Asp Pro Ser Ala Val Ala Val 1157	1162	1167	1172	3799

gct gga agt tca tca gca gag gaa atg gtc act ctc ttg gtt cag gcg Ala Gly Ser Ser Ser Ala Glu Glu Met Val Thr Leu Leu Val Gln Ala	3847
1173 1178 1183 1188	
 ggc ctc ttt gac act gcc ata tca ctc tgt cag act ttt aag ctt ccc Gly Leu Phe Asp Thr Ala Ile Ser Leu Cys Gln Thr Phe Lys Leu Pro	3895
1189 1194 1199 1204	
 tta acg cca gtc ttt gaa ggg ctt gcc ttc aaa tgc atc aaa ttg caa Leu Thr Pro Val Phe Glu Gly Leu Ala Phe Lys Cys Ile Lys Leu Gln	3943
1205 1210 1215 1220	
 ttt gga gga gag gca gca caa gca gaa gcc tgg gcc tgg cta gca gcc Phe Gly Gly Glu Ala Ala Gln Ala Glu Ala Trp Ala Trp Leu Ala Ala	3991
1221 1226 1231 1236	
 aat cag ctc tca tct gtc atc act act aag gag tct agt gct aca gat Asn Gln Leu Ser Ser Val Ile Thr Thr Lys Glu Ser Ser Ala Thr Asp	4039
1237 1242 1247 1252	
 gaa gca tgg cga cta tta tcc act tac ctg gag agg tac aaa gtc cag Glu Ala Trp Arg Leu Leu Ser Thr Tyr Leu Glu Arg Tyr Lys Val Gln	4087
1253 1258 1263 1268	
 aat aac ttg tat cac cac tgt gta atc aac aag ctc ttg tct cat gga Asn Asn Leu Tyr His His Cys Val Ile Asn Lys Leu Leu Ser His Gly	4135
1269 1274 1279 1284	
 gtg cct ctg cct aat tgg ctt ata aac agt cac aac atc gca ctg tcc Val Pro Leu Pro Asn Trp Leu Ile Asn Ser His Asn Ile Ala Leu Ser	4183
1285 1290 1295 1300	
 caa aaa gtt gat aag gca aca cgg gat tta tta tat cgt cgg acc ttg Gln Lys Val Asp Lys Ala Thr Arg Asp Leu Leu Tyr Arg Arg Thr Leu	4231
1301 1306 1311 1316	
 tga tttg gattgtcacc tagcctttgt aaccgcttgg tgcccttttag gacttaagac *	4288
1317	
 taccctacag gaaccctgta ctcaaggccg atttttgtaa ctgtaaatga tgtgtacaac	4348
attcaagtct gcattctgca caagatagga gggcggaaaga gtcagaggac cctgtgcttg	4408
ctgggttgtc taacacaatt tctggtgttc aaccttggtc tcaaatact gttttgtat	4468
atgattcacg agcttttta gagtttatat tttttaaac taccgaagac attcattatc	4528
tgcaaattaa gactcacctt cactttccaa aatagctgag ggttgttgc ttgtttagc	4588
tgaccaccaa aagcagtcac tgcaaatctt ttaattcttc cctatcacct tttgtatTTT	4648
aatgcaatta ttttggtcca gaactgacct gtatTTCTG tattgtacac aaaagctaatt	4708
aatTTTGTGT acTTTTTATT TATTTGGAG GTTTATATG ATCTTCATT GAGTATTAaaa	4768

taatggcct agattaagcc taaaatgatg accagcta ataaagaagat atttgaatc	4828
tggttctgag ctaaagttga gtaaattctt agctaagaaa aaattggaaa tccatcatct	4888
atattagcaa cagattctca gagtaaattg ttaacttcta tgatttatga taatcaagct	4948
ggacttgatc atacaagtta gtctcataat gtattggacc aaaatgtaaa cttcattgg	5008
cagatttaga agcattcatg ctcacaagtt ttggaaagt gaaaaataat aaaatcatct	5068
tggattttat tctgtatatt aaaatttatac tttt	5102

<210> 142
 <211> 1510
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (60)..(884)

<400> 142

atggccct cgaggccaag aattcgac gaggaccact ctgcgtcccc gcctaagcc	59
atg cac ctc tgt ggg agc'aat ggg ctg ctg acc cag aca gac ccc aag	107
Met His Leu Cys Gly Ser Asn Gly Leu Leu Thr Gln Thr Asp Pro Lys	
1 5 10 15	

gag caa caa agg cag ctg aag aag cag aag aac cgg gca gcc gcc cag	155
Glu Gln Gln Arg Gln Leu Lys Lys Gln Lys Asn Arg Ala Ala Gln	
17 22 27 32	

cga agc cgg cag aag cac aca gac aag gca gac gcc ctg cac cag cag	203
Arg Ser Arg Gln Lys His Thr Asp Lys Ala Asp Ala Leu His Gln Gln	
33 38 43 48	

cac gag tct ctg gaa aaa gac aac ctc gcc ctg cgg aag gag atc cag	251
His Glu Ser Leu Glu Lys Asp Asn Leu Ala Leu Arg Lys Glu Ile Gln	
49 54 59 64	

tcc ctg cag gcc gag ctg gcg tgg tgg agc cgg acc ctg cac gtg cat	299
Ser Leu Gln Ala Glu Leu Ala Trp Trp Ser Arg Thr Leu His Val His	
65 70 75 80	

gag cgc ctg tgc ccc atg gat tgt gcc tcc tgc tca gct cca ggg ctc	347
Glu Arg Leu Cys Pro Met Asp Cys Ala Ser Cys Ser Ala Pro Gly Leu	
81 86 91 96	

ctg ggc tgc tgg gac cag gct gag ggg ctc ctg ggc cct ggc cca cag	395
Leu Gly Cys Trp Asp Gln Ala Glu Gly Leu Leu Gly Pro Gly Pro Gln	
97 102 107 112	

gga caa cat ggc tgc cgg gag cag ctg gag ttc cag acc ccg ggt	443
Gly Gln His Gly Cys Arg Glu Gln Leu Glu Leu Phe Gln Thr Pro Gly	
113 118 123 128	

tcc tgt tac cca gct cag ccg ctc tct cca ggt cca cag cct cat gat			491
Ser Cys Tyr Pro Ala Gln Pro Leu Ser Pro Gly Pro Gln Pro His Asp			
129	134	139	144
tct ccc agc ctc ctc cag tgc ccc ctg ccc tca ctg tcc ctt ggc ccc			539
Ser Pro Ser Leu Leu Gln Cys Pro Leu Pro Ser Leu Ser Leu Gly Pro			
145	150	155	160
gct gtg gtt gct gaa cct cct gtc cag ctg tcc ccc agc cct ctc ctg			587
Ala Val Val Ala Glu Pro Pro Val Gln Leu Ser Pro Ser Pro Leu Leu			
161	166	171	176
ttt gcc tcg cac act ggt tcc agc ctg cag ggg tct tcc tct aag ctc			635
Phe Ala Ser His Thr Gly Ser Ser Leu Gln Gly Ser Ser Ser Lys Leu			
177	182	187	192
agt gcc ctc cag ccc agc ctc acg gcc caa act gcc cct cca cag ccc			683
Ser Ala Leu Gln Pro Ser Leu Thr Ala Gln Thr Ala Pro Pro Gln Pro			
193	198	203	208
ctc gag ctg gag cat ccc acc aga ggg aag ctg ggg tcc tct ccc gac			731
Leu Glu Leu Glu His Pro Thr Arg Gly Lys Leu Gly Ser Ser Pro Asp			
209	214	219	224
aac cct tcc tct gcc ctg ggg ctt gca cgt ctg cag agc agg gag cac			779
Asn Pro Ser Ser Ala Leu Gly Leu Ala Arg Leu Gln Ser Arg Glu His			
225	230	235	240
aaa cct gct ctc tca gca gcc act tgg caa ggg ctg gtt gtg gat ccc			827
Lys Pro Ala Leu Ser Ala Ala Thr Trp Gln Gly Leu Val Val Asp Pro			
241	246	251	256
agc cct cac cct ctc ctg gcc ttt cct ctg ctc tcc tct gct caa gtc			875
Ser Pro His Pro Leu Leu Ala Phe Pro Leu Leu Ser Ser Ala Gln Val			
257	262	267	272
cac ttc taa cctggtc ttccggagctg gggtggcccc ttctttggc tcaggaagca			931
His Phe *			
273			
gccttagcac acggggctct cctccctcac tactgggtgc tgccctgcgt ggctgaccag			991
ctggcccccagg atttcacagt cgaaaaggaa gccaccactg atgcctccca ctgtgacagg			1051
ccctgtcacc accaatatct tatttcaacc tcacagttga cctgagaaaaat cgagattatc			1111
actccacttt ttcagacaag gaaactgagg ctcagggaaag ccaagtgaca agtccaaggt			1171
cacgaagact ttcttgagc ccgaaacacc accctctgtc cctccttctc ctgtcctggg			1231
cccaggcatc ctagggctg aaatcctgga aaaccctgg ggccttgggt gggtgaaaaaa			1291
aagggttttt gccaatggcc tccaagaagg ccaagaaaaaa aaagggggct ttctttcccc			1351
ccactggttt tgtgattcca agggcccaga gccatgccag tccccagaaa accccaaccc			1411

taaacttggg gcaagtccca gagtccaagc ccctgggtggg gtaagaggcc aaagcaagaa 1471
gccctgaagt gggactctt gttcccccta agaagggg 1510

<210> 143
<211> 2995
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (285)..(2351)

<400> 143

gcgtgttcta tataactatc tattcgatga tgaagataacc ccaccaaacc caaaaaaaaaga 60

gatctctcgaa ggatccgaat tcgcggccgc gtcgaccgcg gccgcgtcga cagaagattg 120

tgggtgttagt ggccacagcc ttacaggcag gcaggggtgg ttgggtgtcaa caggggggccc 180

aacagggtac cagagccaag accctcgccc tcctcccccgc ccgccttcct gcagatctgc 240

ttggctttga ggaagagtg 296
cagta 296
ctg 296
tcactgcata 296
aggg 296
atg 296
gga 296
tca 296
gag 296
Met 296
Gly 296
Ser 296
Glu 296
1 296

aac agt gct tta aag agc tat aca ctg aga gaa cca cca ttt acc tta 344
Asn Ser Ala Leu Lys Ser Tyr Thr Leu Arg Glu Pro Pro Phe Thr Leu
5 10 15 20

ccc tct gga ctt gct tat ccc gct gta ctg caa gat ggc aaa ttt 392
Pro Ser Gly Leu Ala Val Tyr Pro Ala Val Leu Gln Asp Gly Lys Phe
21 26 31 36

gct tca gtt ttt gtg tat aag aga gaa aat gaa gac aag gtt aat aaa 440
Ala Ser Val Phe Val Tyr Lys Arg Glu Asn Glu Asp Lys Val Asn Lys
37 42 47 52

gct gcc aag cat ttg aag aca ctt cgt cac cct tgc ttg cta aga ttt 488
Ala Ala Lys His Leu Lys Thr Leu Arg His Pro Cys Leu Leu Arg Phe
53 58 63 68

tta tct tgt act gtg gaa gcg gat ggc att cat ctt gtc act gag cga 536
Leu Ser Cys Thr Val Glu Ala Asp Gly Ile His Leu Val Thr Glu Arg
69 74 79 84

gta cag ccc ctg gaa gtg gct ttg gaa aca ttg tct tct gca gag gtc 584
Val Gln Pro Leu Glu Val Ala Leu Glu Thr Leu Ser Ser Ala Glu Val
85 90 95 100

tgt gct ggg atc tat gac ata ttg ctg gct ctt atc ttc ctt cat gac 632
Cys Ala Gly Ile Tyr Asp Ile Leu Leu Ala Leu Ile Phe Leu His Asp
101 106 111 116

aga gga cac cta aca cac aat aat gtc tgt tta tca tct gtg ttt gtg		680	
Arg Gly His Leu Thr His Asn Asn Val Cys Leu Ser Ser Val Phe Val			
117	122	127	132
agt gaa gat gga cac tgg aag cta gga gga atg gaa act gtt tgt aaa		728	
Ser Glu Asp Gly His Trp Lys Leu Gly Gly Met Glu Thr Val Cys Lys			
133	138	143	148
gtt tct cag gcc aca cca gag ttt ctg agg agt att cag tca ata aga		776	
Val Ser Gln Ala Thr Pro Glu Phe Leu Arg Ser Ile Gln Ser Ile Arg			
149	154	159	164
gac cca gca tct atc cct cct gaa gag atg tct cca gaa ttc aca act		824	
Asp Pro Ala Ser Ile Pro Pro Glu Glu Met Ser Pro Glu Phe Thr Thr			
165	170	175	180
ctc cca gag tgt cat gga cat gcc cgg gat gcc ttt tca ttt gga aca		872	
Leu Pro Glu Cys His Gly His Ala Arg Asp Ala Phe Ser Phe Gly Thr			
181	186	191	196
ttg gtg gaa agt ttg ctc aca atc tta aat gaa cag gtt tca gcg gat		920	
Leu Val Glu Ser Leu Leu Thr Ile Leu Asn Glu Gln Val Ser Ala Asp			
197	202	207	212
gtt ctc tcc agc ttt caa cag acc ttg cac tca act ttg ctg aat ccc		968	
Val Leu Ser Ser Phe Gln Gln Thr Leu His Ser Thr Leu Leu Asn Pro			
213	218	223	228
att cca aaa tgt cgg cca gcg ctc tgc acc tta cta tct cat gac ttc		1016	
Ile Pro Lys Cys Arg Pro Ala Leu Cys Thr Leu Leu Ser His Asp Phe			
229	234	239	244
ttc aga aat gat ttt ctg gaa gtt gtg aat ttc ttg aaa agt tta aca		1064	
Phe Arg Asn Asp Phe Leu Glu Val Val Asn Phe Leu Lys Ser Leu Thr			
245	250	255	260
ttg aag agt gaa gag gag aaa acg gaa ttc ttt aaa ttt ctg ctg gac		1112	
Leu Lys Ser Glu Glu Lys Thr Glu Phe Phe Lys Phe Leu Leu Asp			
261	266	271	276
aga gtc agc tgc ttg tca gag gaa ttg ata gct tca agg ttg gtg cct		1160	
Arg Val Ser Cys Leu Ser Glu Glu Leu Ile Ala Ser Arg Leu Val Pro			
277	282	287	292
ctt ctg ctt aat cag ttg gtg ttt gca gag cca gtg gct gtt aag agt		1208	
Leu Leu Leu Asn Gln Leu Val Phe Ala Glu Pro Val Ala Val Lys Ser			
293	298	303	308
ttt ctt cct tat ctg ctt ggc ccc aaa aaa gat cat gcg cag gga gaa		1256	
Phe Leu Pro Tyr Leu Leu Gly Pro Lys Lys Asp His Ala Gln Gly Glu			
309	314	319	324
act cct tgc ttg ctc tca cca gcc ctg ttc cag tca cgg gtg atc ccc		1304	
Thr Pro Cys Leu Leu Ser Pro Ala Leu Phe Gln Ser Arg Val Ile Pro			
325	330	335	340
gtg ctt ctc cag ttg ttt gaa gtt cat gaa gag cat gtg cgg atg gtg		1352	

Val	Leu	Leu	Gln	Leu	Phe	Glu	Val	His	Glu	Glu	His	Val	Arg	Met	Val	
341				346			351				356					
ctg	ctg	tct	cac	atc	gag	gcc	tac	gtg	gag	cac	ttc	act	cag	gag	cag	1400
Leu	Leu	Ser	His	Ile	Glu	Ala	Tyr	Val	Glu	His	Phe	Thr	Gln	Glu	Gln	
357				362				367				372				
ctg	aag	aaa	gtc	atc	ttg	cca	cag	gtt	ttg	ctg	ggc	ctg	cgt	gat	act	1448
Leu	Lys	Lys	Val	Ile	Leu	Pro	Gln	Val	Leu	Leu	Gly	Leu	Arg	Asp	Thr	
373				378				383				388				
agc	gat	tcc	att	gtg	gca	att	act	ctg	cat	agc	cta	gca	gtg	ctg	gtc	1496
Ser	Asp	Ser	Ile	Val	Ala	Ile	Thr	Leu	His	Ser	Leu	Ala	Val	Leu	Val	
389				394				399				404				
tct	ctg	ctt	gga	cca	gag	gtg	gtt	gtg	gga	gaa	cga	acc	aag	atc		1544
Ser	Leu	Leu	Gly	Pro	Glu	Val	Val	Val	Gly	Gly	Glu	Arg	Thr	Lys	Ile	
405				410				415				420				
ttc	aaa	cgc	act	gcc	cca	agt	ttt	act	aaa	aat	act	gac	ctt	tct	cta	1592
Phe	Lys	Arg	Thr	Ala	Pro	Ser	Phe	Thr	Lys	Asn	Thr	Asp	Leu	Ser	Leu	
421				426				431				436				
gaa	ggc	gat	cca	ttt	tct	cag	cct	att	aaa	ttt	ccc	ata	aat	gga	ctc	1640
Glu	Gly	Asp	Pro	Phe	Ser	Gln	Pro	Ile	Lys	Phe	Pro	Ile	Asn	Gly	Leu	
437				442				447				452				
tca	gat	gta	aaa	aat	act	tcg	gag	gac	agt	gaa	aac	ttc	cca	tca	agt	1688
Ser	Asp	Val	Lys	Asn	Thr	Ser	Glu	Asp	Ser	Glu	Asn	Phe	Pro	Ser	Ser	
453				458				463				468				
tct	aaa	aag	tct	gag	gag	tgg	cct	gac	tgg	agt	gaa	cct	gag	gag	cct	1736
Ser	Lys	Ser	Glu	Glu	Trp	Pro	Asp	Trp	Ser	Glu	Pro	Glu	Glu	Pro		
469				474				479				484				
gaa	aat	caa	act	gtc	aac	ata	cag	att	tgg	cct	aga	gaa	cct	tgt	gat	1784
Glu	Asn	Gln	Thr	Val	Asn	Ile	Gln	Ile	Trp	Pro	Arg	Glu	Pro	Cys	Asp	
485				490				495				500				
gat	gtc	aag	tcc	cag	tgc	act	acc	ttg	gat	gtg	gaa	gag	tca	tct	tgg	1832
Asp	Val	Lys	Ser	Gln	Cys	Thr	Thr	Leu	Asp	Val	Glu	Glu	Ser	Ser	Trp	
501				506				511				516				
gat	gac	tgc	gag	ccc	agc	agc	tta	gat	act	aaa	gta	aac	cca	gga	ggt	1880
Asp	Asp	Cys	Glu	Pro	Ser	Ser	Leu	Asp	Thr	Lys	Val	Asn	Pro	Gly	Gly	
517				522				527				532				
gga	atc	act	gct	aca	aaa	cct	gtt	acc	tca	ggg	gag	cag	aag	cct	att	1928
Gly	Ile	Thr	Ala	Thr	Lys	Pro	Val	Thr	Ser	Gly	Glu	Gln	Lys	Pro	Ile	
533				538				543				548				
cct	gct	ttg	ctt	tca	ctc	act	gaa	gag	tct	atg	cct	tgg	aaa	tca	agc	1976
Pro	Ala	Leu	Leu	Ser	Leu	Thr	Glu	Glu	Ser	Met	Pro	Trp	Lys	Ser	Ser	
549				554				559				564				
tta	ccc	cga	aag	att	agc	ctt	gta	caa	agg	ggg	gat	gac	gca	gac	caa	2024
Leu	Pro	Arg	Lys	Ile	Ser	Leu	Val	Gln	Arg	Gly	Asp	Asp	Ala	Asp	Gln	

565	570	575	580	
atc gag ccg cca aaa gta tca tca caa gaa agg ccc ctt aag gtt cca Ile Glu Pro Pro Lys Val Ser Ser Gln Glu Arg Pro Leu Lys Val Pro				2072
581	586	591	596	
tca gaa ctt ggt tta gga gag gaa ttc acc att caa gta aaa aag aag Ser Glu Leu Gly Leu Gly Glu Phe Thr Ile Gln Val Lys Lys Lys				2120
597	602	607	612	
cca gta aaa gat cct gag atg gat tgg ttt gct gat atg atc cca gaa Pro Val Lys Asp Pro Glu Met Asp Trp Phe Ala Asp Met Ile Pro Glu				2168
613	618	623	; 628	
att aag cct tct gct gct ttt ctt ata tta cct gaa ctg agg aca gaa Ile Lys Pro Ser Ala Ala Phe Leu Ile Leu Pro Glu Leu Arg Thr Glu				2216
629	634	639	644	
atg gtc cca aaa aag gat gat gtc tcc cca gtg atg cag ttt tcc tca Met Val Pro Lys Lys Asp Asp Val Ser Pro Val Met Gln Phe Ser Ser				2264
645	650	655	660	
aaa ttt gct gca gca gaa att act gag gga gag gct gaa ggc tgg gaa Lys Phe Ala Ala Ala Glu Ile Thr Glu Gly Glu Ala Glu Gly Trp Glu				2312
661	666	671	676	
gaa gaa ggg gag ctg aac tgg gaa gat aat aac tgg tga caatagatgt Glu Glu Gly Glu Leu Asn Trp Glu Asp Asn Asn Trp *				2361
677	682	687		
gagttaaact ttagaaaaaa ggattccctt tttttaaaaaa aaatcaatac ctcaaaagca ggctttggga caagaaaacc ccaaagtggc ctgctttcc catcccagga gtcattatc				2421
cagtctgtgc caactgaagt aggagactga ctgtgagtgc tggctaaaag ccctgggtgg				2481
tgaggctcac agtactggtt tccaggagga agagcctttg tgcatttgac tgaggccagt				2541
ttcttatgaag agcaagtagc tgaggagagg tcgaatttac tgcttttcc aggacaattc				2601
tggaagtaaa gaaaatgtaa ttcaagctgg ttagcttaat tttgtgccat tctttcttt				2661
aacataagag taagctctat tatgaaatac aactttaaaa aatttttagct ataaattata				2721
taaatgattt taaattgctg aggtttcctt aggcagctta tttatgttt tacagttaga				2781
ctatctgagt aaatggttct ttgtggacct aggcagttcc tgactgttcc acatgttagta				2841
cattgtacca aagttcttaa taagaatatt ccccacaatac ctgttctcta aatgtcaaat				2901
aaagattatt ttcactagat tcaaaaaaaaaaaa aaaa				2961
				2995

/

/

<210> 144
<211> 1031

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (138)..(950)

<220>
<221> misc_feature
<222> (1)..(1031)
<223> n = a,t,c or g

<400> 144

atttggccct	cgaggccaag	aattcggcac	gagagggggg	atcgctggga	gcgggttcgg	60										
cgtgcggggg	gctgagttat	agctgtgact	tctgccctgc	caggccgcac	acaagctggc	120										
tgaccgggtt	tgtaaaa	atg	gaa	ttt	caa	gca	gta	gtg	atg	gca	gta	ggt	170			
		Met	Glu	Phe	Gln	Ala	Val	Val	Met	Ala	Val	Gly				
		1				5										
gga	gga	tct	cgg	atg	aca	gac	cta	act	tcc	agc	att	ccc	aaa	cct	ctg	218
Gly	Gly	Ser	Arg	Met	Thr	Asp	Leu	Thr	Ser	Ser	Ile	Pro	Lys	Pro	Leu	
12		17				22					27					
ctt	cca	gtt	ggg	aac	aaa	cct	tta	att	tgg	tac	cca	ttg	aac	ctg	ctt	266
Leu	Pro	Val	Gly	Asn	Lys	Pro	Leu	Ile	Trp	Tyr	Pro	Leu	Asn	Leu	Leu	
28		33				38			43							
gag	cgt	gtt	gga	ttt	gaa	gaa	gtc	att	gtg	gtt	aca	acc	agg	gat	gtt	314
Glu	Arg	Val	Gly	Phe	Glu	Glu	Val	Ile	Val	Val	Thr	Thr	Arg	Asp	Val	
44		49				54					59					
caa	aag	gct	cta	tgt	gca	gaa	ttc	aag	atg	aaa	atg	aag	cca	gat	att	362
Gln	Lys	Ala	Leu	Cys	Ala	Glu	Phe	Lys	Met	Lys	Met	Lys	Pro	Asp	Ile	
60		65				70			75							
gtg	tgt	att	cct	gat	gac	gct	gac	atg	gga	act	gca	gat	tct	ttg	cgc	410
Val	Cys	Ile	Pro	Asp	Asp	Ala	Asp	Met	Gly	Thr	Ala	Asp	Ser	Leu	Arg	
76		81				86			91							
tac	ata	tat	cca	aaa	ctt	aag	aca	gat	gtg	ctg	gtg	ctg	agc	tgt	gat	458
Tyr	Ile	Tyr	Pro	Lys	Leu	Lys	Thr	Asp	Val	Leu	Val	Leu	Ser	Cys	Asp	
92		97				102			107							
ctg	ata	aca	gac	gtt	gcc	tta	cat	gag	gtt	gtg	gac	ctg	ttt	aga	gct	506
Leu	Ile	Thr	Asp	Val	Ala	Leu	His	Glu	Val	Val	Asp	Leu	Phe	Arg	Ala	
108		113				118			123							
tat	gat	gca	tca	ctt	gtc	atg	ttg	atg	aga	aaa	ggc	caa	gat	agc	ata	554
Tyr	Asp	Ala	Ser	Leu	Ala	Met	Leu	Met	Arg	Lys	Gly	Gln	Asp	Ser	Ile	
124		129				134			139							
gaa	cct	gtt	ccc	ggt	caa	aag	ggg	aaa	aaa	aaa	gca	gtg	gag	cag	cgt	602
Glu	Pro	Val	Pro	Gly	Gln	Lys	Gly	Lys	Lys	Lys	Ala	Val	Glu	Gln	Arg	
140		145				150			155							

gac ttc att gga gtg gac agc aca gga aag agg ctg ctc ttc atg got		650
Asp Phe Ile Gly Val Asp Ser Thr Gly Lys Arg Leu Leu Phe Met Ala		
156	161	166
		171
aat gaa gca gac ttg gat gaa gag ctg gtc att aag gga tcc atc cta		698
Asn Glu Ala Asp Leu Asp Glu Leu Val Ile Lys Gly Ser Ile Leu		
172	177	182
		187
cag aag cat cct aga ata cgt ttc cac acg ggt ctt gtg gat gcc cac		746
Gln Lys His Pro Arg Ile Arg Phe His Thr Gly Leu Val Asp Ala His		
188	193	198
		203
ctc tac tgt ttg aaa aaa tac atc gtg gat ttc cta atg gaa aat ggg		794
Leu Tyr Cys Leu Lys Tyr Ile Val Asp Phe Leu Met Glu Asn Gly		
204	209	214
		219
tca ata act tct atc cgg agt gaa ctg att cca tat tta gtg aga aaa		842
Ser Ile Thr Ser Ile Arg Ser Glu Leu Ile Pro Tyr Leu Val Arg Lys		
220	225	230
		235
cag ttt tcc tca gct tcc tca caa cag ggg aca agg aag gaa aaa gag		890
Gln Phe Ser Ser Ala Ser Ser Gln Gln Gly Thr Arg Lys Glu Lys Glu		
236	241	246
		251
gga ggg tct aaa gga aaa agg ggc ttg aag tcc ttt agg ata tct tac		938
Gly Gly Ser Lys Gly Lys Arg Gly Leu Lys Ser Phe Arg Ile Ser Tyr		
252	257	262
		267
agt ttt tat taa aag gaagccaatt acactggaac cggggctccc tatggatggc		993
Ser Phe Tyr *		
268		
ctgctgggaa ttgcctgttc gagggnggac ggttgggg		1031

<210> 145
 <211> 2130
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (184)..(1236)

<400> 145

gttttctcca catggaaact tattggcggt tgccctcgca gacagaaccg tgagactctg		60
---	--	----

gattcctgat aagagaggaa aattctcata atttaaagct catacagctc cagttcgaag		120
---	--	-----

tggagacttt tcacctgatg gccagttct agctacagct tctgaagaca aatccataat		180
--	--	-----

agt atg gag cat gta tcg cca gcg ctt cct gta ttc ctt gga tcg aca		228
Met Glu His Val Ser Pro Ala Leu Pro Val Phe Leu Gly Ser Thr		
1	5	10

tac aca ctg tgt acg ctg tgc cca att gta ccc gat gga aga cta att		276
Tyr Thr Leu Cys Thr Leu Cys Pro Ile Val Pro Asp Gly Arg Leu Ile		
16 21 26 31		
gtg tca tgt agt gag gat aaa act att aaa att tgg gat acc aca aat		324
Val Ser Cys Ser Glu Asp Lys Thr Ile Lys Ile Trp Asp Thr Thr Asn		
32 37 42 47		
aag caa tgt gtt aat aac ttc tca gat tcc gtt gga ttt gca aat ttt		372
Lys Gln Cys Val Asn Asn Phe Ser Asp Ser Val Gly Phe Ala Asn Phe		
48 53 58 63		
gtg gac ttt aac cct agt ggt aca tgc ata gct tca gca ggt tct gat		420
Val Asp Phe Asn Pro Ser Gly Thr Cys Ile Ala Ser Ala Gly Ser Asp		
64 69 74 79		
caa act gtg aaa gtc tgg gat gta aga gtg aac aaa tta cta cag cat		468
Gln Thr Val Lys Val Trp Asp Val Arg Val Asn Lys Leu Leu Gln His		
80 85 90 95		
tac caa gtt cac agc ggt gga gtt aat tgc ata tca ttc cat cct tcg		516
Tyr Gln Val His Ser Gly Gly Val Asn Cys Ile Ser Phe His Pro Ser		
96 101 106 111		
ggt aac tat ctc atc aca gct tct tca gat ggt acc ctt aag att ctg		564
Gly Asn Tyr Leu Ile Thr Ala Ser Ser Asp Gly Thr Leu Lys Ile Leu		
112 117 122 127		
gac ctc tta gaa gga agg ctc atc tat aca ctt caa gga cat acg gga		612
Asp Leu Leu Glu Gly Arg Leu Ile Tyr Thr Leu Gln Gly His Thr Gly		
128 133 138 143		
cct gtc ttt act gtt tca ttt tca aaa ggt gga gag cta ttt gca tca		660
Pro Val Phe Thr Val Ser Phe Ser Lys Gly Gly Glu Leu Phe Ala Ser		
144 149 154 159		
gga ggt gca gac aca cag gtc tta tta tgg agg act aac ttt gat gaa		708
Gly Gly Ala Asp Thr Gln Val Leu Leu Trp Arg Thr Asn Phe Asp Glu		
160 165 170 175		
ttg cat tgt aaa ggt ctt acc aaa aga aat ctc aaa aga tta cat ttt		756
Leu His Cys Lys Gly Leu Thr Lys Arg Asn Leu Lys Arg Leu His Phe		
176 181 186 191		
gat tca cca cca cat ctt ctt gat atc tac cca aga aca cca cat ccc		804
Asp Ser Pro Pro His Leu Leu Asp Ile Tyr Pro Arg Thr Pro His Pro		
192 197 202 207		
cat gag gaa aaa gtt gag act gta gaa att aat cca aag ctt gag gta		852
His Glu Glu Lys Val Glu Thr Val Glu Ile Asn Pro Lys Leu Glu Val		
208 213 218 223		
atc gat ttg cag atc tct act ccc cct gtt atg gat atc ctt tct ttt		900
Ile Asp Leu Gln Ile Ser Thr Pro Pro Val Met Asp Ile Leu Ser Phe		
224 229 234 239		
gat tct acc aca aca gaa acc agt ggt agg act ctg cca gac aag		948

Asp Ser Thr Thr Thr Glu Thr Ser Gly Arg Thr Leu Pro Asp Lys			
240	245	250	255
ggt gaa gag gcc tgt gga tat ttc ttg aac cct tcc tta atg tca cca			996
Gly Glu Ala Cys Gly Tyr Phe Leu Asn Pro Ser Leu Met Ser Pro			
256	261	266	271
gaa tgt ttg cca aca acc acg aaa aag aaa aca gaa gac atg agt gac			1044
Glu Cys Leu Pro Thr Thr Lys Lys Thr Glu Asp Met Ser Asp			
272	277	282	287
ctc ccc tgt gaa agtcaa agg agc ata cct ctc gct gtg act gat gct			1092
Leu Pro Cys Glu Ser Gln Arg Ser Ile Pro Leu Ala Val Thr Asp Ala			
288	293	298	303
tta gag cat att atg gaa caa ctc aat gtt ttg aca cag act gtt tca			1140
Leu Glu His Ile Met Glu Gln Leu Asn Val Leu Thr Gln Thr Val Ser			
304	309	314	319
atc ttg gag cag cga ctg act ttg aca gag gat aag ctg aaa gac tgc			1188
Ile Leu Glu Gln Arg Leu Thr Leu Thr Glu Asp Lys Leu Lys Asp Cys			
320	325	330	335
ctt gaa aat cag caa aag ctt ttc agt gct gtc caa cag aaa agc tga			1236
Leu Glu Asn Gln Gln Lys Leu Phe Ser Ala Val Gln Gln Lys Ser *			
336	341	346	351
ataaaaaatt cattttcatt tggtggcag aggcccaata aatgaacaaa tgtacataca			1296
ctcaggaagg tagtacaaga tactccatac aacacaacca tgtgctattt atcatggcat			1356
ttcttaaaag ggtgagcaac agaacaaaag gcagaaaagg catacctaag gactaattta			1416
aacacatatac aatgtgaagg actaatttaa attactatca tttatgattt cagtaataaa			1476
gtgataagca ttcaagcaac tctgtatttt cccatatta tttaaatgt ccattttcat			1536
ttataggcca aatcctgccca ggaaagtaac ccagatctct ggatttcact gttaagtcat			1596
ttcagattga ccatattcag acagtcatgg ggtgaaataa ttcacttacc tccaaaatag			1656
cattctatat ggccaataat gagttattga tctgactagt tgtatgtctt tctgttcaaa			1716
atagaaattt tccttctta ctaatgcctt gaaagaatga acaaataaaa attcccagac			1776
cacagaattt ccacagcaag aatacactt ttttaattaa caatagcaca gatatagcat			1836
agggcagtgg gtttttagt taatttatgg ccgactttgt ttatccattt gccaacctga			1896
agggaaatgaa actcacctat ctttctatca cagatgaatg cgctagatga atgatttggg			1956
ctggatctga ccatggttca cacaaattat gtcagggtgg tgttagtgacg gtaaatgtct			2016
gagtgattcg agagtgattt ttatcatcct attccactgt agggcactt gctcgagaaa			2076
tattgctgtt atgctgactt cggctgcttt tcgtatctcc tttataatc ttgc			2130

<210> 146
<211> 4515
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (44)..(1381)

<400> 146

cggaattgcc	ggaccgacga	tttcgtgttag	aggccgcggc	aaa	atg	gct	gct	cct	55
					Met	Ala	Ala	Pro	
					1				
gag gag cgg gat cta acc cag gag cag aca gag aag ctg ctg cag ttt									103
Glu	Glu	Arg	Asp	Leu	Thr	Gln	Glu	Gln	
5					10				
Glu Lys Leu Leu Gln Phe									20
cag gat ctc act ggc atc gaa tct atg gat cag tgt cgc cat acc ttg									151
Gln	Asp	Leu	Thr	Gly	Ile	Glu	Ser	Met	
21					26				
Asp Gln Cys Arg His Thr Leu									36
gaa cag cat aac tgg aac ata gag gct gct gta cag gac aga ttg aat									199
Glu	Gln	His	Asn	Trp	Asn	Ile	Glu	Ala	
37					42				
Val Gln Asp Arg Leu Asn									52
gag caa gag ggc gta cct agt gtt ttc aac cca cct cca tca cga ccc									247
Glu	Gln	Glu	Gly	Val	Pro	Ser	Val	Phe	
53					58				
Asn Pro Pro Pro Ser Arg Pro									68
ctg cag gtt aat aca gct gac cac agg atc tac agc tat gtt gtc tca									295
Leu	Gln	Val	Asn	Thr	Ala	Asp	His	Arg	
69					74				
Ile Tyr Ser Tyr Val Val Ser									84
aga cct caa cca agg ggg ctg ctt gga tgg ggt tat tac ttg ata atg									343
Arg	Pro	Gln	Pro	Arg	Gly	Leu	Leu	Gly	
85					90				
Trp Gly Tyr Tyr Leu Ile Met									100
ctt cca ttc cgg ttt acc tat tac acg ata ctt gat ata ttt agg ttt									391
Leu	Pro	Phe	Arg	Phe	Thr	Tyr	Thr	Ile	
101					106				
Leu Asp Ile Phe Arg Phe									116
gct ctt cgt ttt ata cgg cct gac cct cgc agc cgg gtc act gac ccc									439
Ala	Leu	Arg	Phe	Ile	Arg	Pro	Asp	Pro	
117					122				
Ser Arg Val Thr Asp Pro									132
gtt ggg gac att gtt tca ttt atg cac tct ttt gaa gag aaa tat ggg									487
Val	Gly	Asp	Ile	Val	Ser	Phe	Met	His	
133					138				
Ser Phe Glu Glu Lys Tyr Gly									148
agg gca cac cct gtc ttc tac cag gga acg tac agc cag gca ctt aac									535
Arg	Ala	His	Pro	Val	Phe	Tyr	Gln	Gly	
149					154				
Thr Tyr Ser Gln Ala Leu Asn									164

gat gcc aaa agg gag ctt cgc ttt ctt ttg gtt tat ctt cat gga gat		583	
Asp Ala Lys Arg Glu Leu Arg Phe Leu Leu Val Tyr Leu His Gly Asp			
165	170	175	180
 gat cac cag gac tct gat gag ttt tgt cgc aac aca ctc tgt gca cct		631	
Asp His Gln Asp Ser Asp Glu Phe Cys Arg Asn Thr Leu Cys Ala Pro			
181	186	191	196
 gaa gtt att tca cta ata aac act agg atg ctc ttc tgg gca tgc tct		679	
Glu Val Ile Ser Leu Ile Asn Thr Arg Met Leu Phe Trp Ala Cys Ser			
197	202	207	212
 aca aac aaa cct gag gga tac agg gtc tca cag gct tta cga gag aac		727	
Thr Asn Lys Pro Glu Gly Tyr Arg Val Ser Gln Ala Leu Arg Glu Asn			
213	218	223	228
 acc tat cca ttc ctg gcc atg att atg ctg aag gat cga agg atg act		775	
Thr Tyr Pro Phe Leu Ala Met Ile Met Leu Lys Asp Arg Arg Met Thr			
229	234	239	244
 gtg gtg gga cgg cta gaa ggc ctc att caa cct gat gac ctc att aac		823	
Val Val Gly Arg Leu Glu Gly Leu Ile Gln Pro Asp Asp Leu Ile Asn			
245	250	255	260
 caa ctg aca ttt atc atg gat gct aac cag act tac ctg gtg tca gaa		871	
Gln Leu Thr Phe Ile Met Asp Ala Asn Gln Thr Tyr Leu Val Ser Glu			
261	266	271	276
 cgc cta gaa agg gaa gaa aga aac cag acc caa gtg ctg aga caa cag		919	
Arg Leu Glu Arg Glu Arg Asn Gln Thr Gln Val Leu Arg Gln Gln			
277	282	287	292
 cag gat gag gcc tac ctg gcc tct ctc aga gct gac cag gag aaa gaa		967	
Gln Asp Glu Ala Tyr Leu Ala Ser Leu Arg Ala Asp Gln Glu Lys Glu			
293	298	303	308
 aga aag aaa cgg gag gag cgg gag cgt aag cgg cgg aag gag gag gag		1015	
Arg Lys Lys Arg Glu Glu Arg Glu Arg Lys Arg Arg Lys Glu Glu Glu			
309	314	319	324
 gtg caa cag caa aag ttg gca gag gag aga cgg cgg cag aat tta cag		1063	
Val Gln Gln Gln Lys Leu Ala Glu Glu Arg Arg Arg Gln Asn Leu Gln			
325	330	335	340
 gag gaa aag gaa agg aag ttg gaa tgc ctg ccc cct gaa cct tcc cct		1111	
Glu Glu Lys Glu Arg Lys Leu Glu Cys Leu Pro Pro Glu Pro Ser Pro			
341	346	351	356
 gat gac cct gaa agt gtc aag atc atc ttc aaa tta cct aat gat tct		1159	
Asp Asp Pro Glu Ser Val Lys Ile Ile Phe Lys Leu Pro Asn Asp Ser			
357	362	367	372
 cga gta gag aga cga ttc cac ttt tca cag tct cta aca gta atc cac		1207	
Arg Val Glu Arg Arg Phe His Phe Ser Gln Ser Leu Thr Val Ile His			
373	378	383	388
 gac ttc tta ttc tcc ttg aag gaa agc cca gaa aag ttt cag att gaa		1255	

Asp Phe Leu Phe Ser Leu Lys Glu Ser Pro Glu Lys Phe Gln Ile Glu				
389	394	399	404	
gcc aat ttt ccc agg cga gtg ccc tgc atc cct tca gag gag tgg				1303
Ala Asn Phe Pro Arg Arg Val Leu Pro Cys Ile Pro Ser Glu Glu Trp				
405	410	415	420	
ccc aat ccc cct acg cta cag gag gcc gga ctc agc cac aca gaa gtt				1351
Pro Asn Pro Pro Thr Leu Gln Glu Ala Gly Leu Ser His Thr Glu Val				
421	426	431	436	
ctt ttt gtt cag gac cta act gac gaa tga c attttttct tcctgtcccc				1402
Leu Phe Val Gln Asp Leu Thr Asp Glu *				
437	442			
tcctacccca gtccctaaaa gaaatgggaa aaaaagaaaa caacagcaag tcagaaaaaa				1462
aaaacaagag agagaaattc atattattat tattattata atacaatatt tttttaaaa				1522
gactgctgca tccttaggaa ggatcagaaa ccatgctgcc cgtaagagtc acaacctgtg				1582
tgtgcgcgca aggttagcaa caaacgtacc cgcttggcaa gcccacccctt cctgtggcct				1642
ctgtgcacgc accttccagt gaacagagac tcttcacctt cgaccatcc attgtcccag				1702
ctgggaaggg gacattccca cttagttctca ttcatcttg cttttatgaa aaataaaaagt				1762
aaaaaacctc catcaaccag ctacttgca catctcctga ggacttgctt ctccctgcctc				1822
tggggaaagag agggaaagaga aagcacagag cagagaagca gagatgttcc ttgaactgcc				1882
cacaagttt caataacttt tatttctgtt ttgtaatgac caaaggaatg aggctgacat				1942
aggtatatat atatattttt ttcccttatt tgataaaagag ccaattcttt aaacccatga				2002
gtttatgccc tgggctcctt agcccacaat agtgtaataa aagtgcggcg ggctggtttg				2062
tgcttatttc tgccattgtc cctctcacgt tcccagagag gtcattctt ttggtccaac				2122
tcttgctgtc ctttcttacc acctgtgcac cccacttggaa gcagtggag gaaatctggg				2182
tttgtggccc cacaaaggct gtatatgtaa agatacacct atgtatgtgg tggaactcac				2242
ctttacacac aactgcagct tttccttggaa gtctgtacca ggtgggtggtt atggggtctg				2302
aaccaaagga tagcagctct tcattcctct tctgacatgt gcatgctgct ccccccagcc				2362
ctgggctttc ctgaattgcc aagcctggtg ctttccaaa ggactagcag ggcctgtgg				2422
ggagccagca gaaccacagg agagtgcctt gcctgtctca gtggaaagtgtt attattgttt				2482
taaggataga accagaggcc ttgaagggag ccaagacaga actcccagcc tgtgtaatct				2542
atggaaaggc acatttcat ttctgtatgca gccacccctt ggaggcagct ttatccctt				2602
ctctctattt ctatgtgaa gtaatagggt ttttttaac ctctggatgt ctcgtctgtg				2662

gttgagttta tggtaatggg tacatgggc aggccatgta ttaacagatg ccagtgcgc 2722
ctgacaagta ttccaaagtg ttccgtagct agactggtgc aggctcggtt taccactgca 2782
accgactgac gttactgttag ttcctagaat gctgtgaggg cgggggggtc agatcaacat 2842
aaagcctaac ttgctggagt tgttagtctca aggcttctc tcttgcttaa ctAAAaccta 2902
aggaccactg ttttggtag caattatacg gttactatcc actgcagtc tcagttgtt 2962
gggtaaatcc cacatggcag agtaaggcac cccacagaaa ttaacttggg gagcctgaga 3022
aattcccagt ggccttggca tagctgtcta gaacaccatc tcttaggaaaa tttaattctg 3082
tccctggcca gctattgttcc ttccacttgc tttctgctg tcccaaggcc agatgagtgg 3142
aatcaccatc tgactgttgt cagtaaaatg tatctggcgt gaacagcagg ataaccatg 3202
ttctccacat aaggataacc ttacgtgaaa ctttcctgct gacaaccatg cagaggaatt 3262
tttccactt aagtcagagc cttccccc atctggatt cacagctgtt ccctggcag 3322
cacacaggag ggtattaagg acctttgtga ggcttaggtac actgtccaca cctctttggg 3382
gaagttacga tttttttt ccatcataat tcagtctttt cttattctac agtgtgcact 3442
ttatgcctct cgcctttga taatagttgt tcagtgaagg aagtcagctg ccagaatatt 3502
aagaagggtc tcccttatg tcagtacaac tgtagggcg gcctcccat ttactttagg 3562
tttcaagagg attcaccgga agcacatgcc cccgtctagt cccatttggaa acagttctgc 3622
tttactgaga ccctaggccg gtctccttgc tgaccctagc gctgctgcct aggtgccatt 3682
tccttcctc ctcagtcataa tacaggctgc acatgggtc acttaatgcc agtacaatct 3742
gtgttactcc taaggacttt tgggattttt atgagacctg cgagggagaa gacactgaga 3802
agccagtgtat ctgcaagcat ttgctttgt ttccacatca cctctggat atttcagctg 3862
ttgtttccaa atggcaaatc atcaactaaa agcacttggtt tcaagttttt ttctgcactc 3922
ccacgactga agtttagat tgagctgaat aaccatgggaa agtgcaccaag caaagacact 3982
cgattggagt cagttgaata tttgtaccct cagtgagcc cttctggtct tttcttccac 4042
ttctgcagaa ttccctctag caaatacttc ttctccttg cttgcctcca ccatgatatt 4102
tgaataagag atggccagag gataacactt gtctttaaa aactaagctt aaaagaacct 4162
agaaccttca attgagcagt tgtgaaaatt gctaattggc ccaaggccaa gcaaaagagtt 4222
tcagaaaatg actgagaagg agcgataacc cccagaatgc aaaatcaggg gcatcattat 4282
ccggtgcttg aacaaggagc tccgctctac aactggttt tttaggactt gtgaggaaca 4342
cagcaacgga aatccatcca caaaggatgc agtgccccaa cttgtactgc gcctgaatag 4402

tcatgtgata atttactgaa gaaatctagt gtactttaaa ttttttcat aaaagttac 4462
attgtattgt aggttaacat taaatgttt atagcaaaaa cttcaaaaaa aaa 4515

<210> 147
<211> 5761
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (168) .. (2885)

<400> 147
tttcgtcagg aatttccctt caaggttagca ggagatgaac gcgtgctgct ccaggatttt 60
acagaactga ttctgcagca aagacaaatg ttgcctgtat ttgccagata gtataaacag 120
gagcaaaagt tgcacagcta aaccaggggc tcattcccag gacagac atg cag tta 176
Met Gln Leu
1
tgg att ccg aaa gac aag tca agg aca ctg atg aca ttg aaa gtc cta 224
Trp Ile Pro Lys Asp Lys Ser Arg Thr Leu Met Thr Leu Lys Val Leu
4 9 14 19
aac gca gta tcc gag aca gtg gct aca tcg act gct ggg att ccg agc 272
Asn Ala Val Ser Glu Thr Val Ala Thr Ser Thr Ala Gly Ile Pro Ser
20 25 30 35
gca gcg act ccc tct ctc ctc gcc acg gca gag atg att cct tcg 320
Ala Ala Thr Pro Ser Leu Leu Ala Thr Ala Glu Met Ile Pro Ser
36 41 46 51
aca gcc tgg att cct ttg gct ctc gct cgt cgg cag acg cct tca cca 368
Thr Ala Trp Ile Pro Leu Ala Leu Ala Arg Arg Gln Thr Pro Ser Pro
52 57 62 67
gat gta gtc ctc agg gga agc agc gat ggg aga gga agc gac tct gaa 416
Asp Val Val Leu Arg Gly Ser Ser Asp Gly Arg Gly Ser Asp Ser Glu
68 73 78 83
tcc gac ttg cct cat cgg aag ctg cca gat gtg aag aag gat gac atg 464
Ser Asp Leu Pro His Arg Lys Leu Pro Asp Val Lys Lys Asp Asp Met
84 89 94 99
tct gca cgg cgg act tcc cat ggt gag ccg aaa tca gca gtg cct ttt 512
Ser Ala Arg Arg Thr Ser His Gly Glu Pro Lys Ser Ala Val Pro Phe
100 105 110 115
aac cag tac ctc ccg aac aaa agc aat cag acg gcc tac gtc ccc gcg 560
Asn Gln Tyr Leu Pro Asn Lys Ser Asn Gln Thr Ala Tyr Val Pro Ala
116 121 126 131

cct ctg aga aag aag aaa gca gag aga gag gaa tac cgc aag agc tgg		608
Pro Leu Arg Lys Lys Ala Glu Arg Glu Tyr Arg Lys Ser Trp		
132	137	142
		147
agt acc gcc acc tcc ccg ctg ggt ggg gag agg ccc ttc aga tac ggt		656
Ser Thr Ala Thr Ser Pro Leu Gly Gly Glu Arg Pro Phe Arg Tyr Gly		
148	153	158
		163
ccg aga act cct gtg tct gat gac gca gag agc acc agc atg ttt gac		704
Pro Arg Thr Pro Val Ser Asp Asp Ala Glu Ser Thr Ser Met Phe Asp		
164	169	174
		179
atg cgg tgt gag gag gag gcc gcg gtg cag ccg cac agc agg gcc cgc		752
Met Arg Cys Glu Glu Ala Ala Val Gln Pro His Ser Arg Ala Arg		
180	185	190
		195
cag gag cag ctg cag ctg ata aat aac cag ctg agg gaa gag gac gac		800
Gln Glu Gln Leu Gln Ile Asn Asn Gln Leu Arg Glu Glu Asp Asp		
196	201	206
		211
aaa tgg caa gat gac ctg gct cgt tgg aag agt cgt aga aga agt gtt		848
Lys Trp Gln Asp Asp Leu Ala Arg Trp Lys Ser Arg Arg Arg Ser Val		
212	217	222
		227
tct cag gac tta atc aag aaa gag gaa gaa agg aaa aaa atg gag aag		896
Ser Gln Asp Leu Ile Lys Lys Glu Glu Arg Lys Lys Met Glu Lys		
228	233	238
		243
tta ctg gct gga gaa gat ggg aca agt gaa cga agg aaa agc atc aaa		944
Leu Leu Ala Gly Glu Asp Gly Thr Ser Glu Arg Arg Lys Ser Ile Lys		
244	249	254
		259
acc tac aga gaa att gtt caa gaa aaa gag cgg aga gag aga gag ctg		992
Thr Tyr Arg Glu Ile Val Gln Glu Lys Glu Arg Arg Glu Arg Glu Leu		
260	265	270
		275
cat gaa gca tat aag aac gct cgg tcc cag gag gag gca gag ggg atc		1040
His Glu Ala Tyr Lys Asn Ala Arg Ser Gln Glu Glu Ala Glu Gly Ile		
276	281	286
		291
ctt caa cag tac att gag agg ttc acc atc agt gag gct gtt ctc gaa		1088
Leu Gln Gln Tyr Ile Glu Arg Phe Thr Ile Ser Glu Ala Val Leu Glu		
292	297	302
		307
cgc ttg gag atg cca aaa att ctg gaa aga agc cat tca aca gag cca		1136
Arg Leu Glu Met Pro Lys Ile Leu Glu Arg Ser His Ser Thr Glu Pro		
308	313	318
		323
aat tta tcc tcc ttc ctg aat gac ccc aat ccc atg aaa tac ctg cgg		1184
Asn Leu Ser Ser Phe Leu Asn Asp Pro Asn Pro Met Lys Tyr Leu Arg		
324	329	334
		339
caa cag tca ctg cct cca ccc aaa ttc act gcc act gtt gaa acc acc		1232
Gln Gln Ser Leu Pro Pro Pro Lys Phe Thr Ala Thr Val Glu Thr Thr		
340	345	350
		355

att gct cgt gcc agt gtt ctg gat acc agc atg tca gca ggc agt ggg Ile Ala Arg Ala Ser Val Leu Asp Thr Ser Met Ser Ala Gly Ser Gly 356	361	366	371	1280
tct cca agc aaa act gtc act ccc aaa gca gtg cct atg ctg aca ccc Ser Pro Ser Lys Thr Val Thr Pro Lys Ala Val Pro Met Leu Thr Pro 372	377	382	387	1328
aag cct tac tcc cag ccc aaa aat tct caa gat gtt ctg aag acc ttt Lys Pro Tyr Ser Gln Pro Lys Asn Ser Gln Asp Val Leu Lys Thr Phe 388	393	398	403	1376
aag gta gac ggg aaa gtc agt gtg aat gga gag acg gtt cat aga gag Lys Val Asp Gly Lys Val Ser Val Asn Gly Glu Thr Val His Arg Glu 404	409	414	419	1424
gag gag aag gaa aga gag tgt ccc acg gtg gca cct gcc cac tcc tta Glu Glu Lys Glu Arg Glu Cys Pro Thr Val Ala Pro Ala His Ser Leu 420	425	430	435	1472
acc aaa tcc cag atg ttt gaa ggt gtg gcc aga gtg cac ggg tct cca Thr Lys Ser Gln Met Phe Glu Gly Val Ala Arg Val His Gly Ser Pro 436	441	446	451	1520
ctg gag ctg aaa caa gac aac ggt agc atc gag atc aac ata aag aag Leu Glu Leu Lys Gln Asp Asn Gly Ser Ile Glu Ile Asn Ile Lys Lys 452	457	462	467	1568
cca aac tct gtt ccc caa gag ctc gca gca acc act gag aaa acg gaa Pro Asn Ser Val Pro Gln Glu Leu Ala Ala Thr Thr Glu Lys Thr Glu 468	473	478	483	1616
ccg aat agt caa gag gac aag aat gat ggt gga aaa tca aga aaa ggg Pro Asn Ser Gln Glu Asp Lys Asn Asp Gly Gly Lys Ser Arg Lys Gly 484	489	494	499	1664
aat ata gaa ctt gcc tca tca gaa cca cag cat ttt aca aca act gtg Asn Ile Glu Leu Ala Ser Ser Glu Pro Gln His Phe Thr Thr Thr Val 500	505	510	515	1712
act cga tgc agc ccg acc gtg gcc ttt gtg gaa ttt ccc tcc agc ccc Thr Arg Cys Ser Pro Thr Val Ala Phe Val Glu Phe Pro Ser Ser Pro 516	521	526	531	1760
cag ctg aag aat gat gtg tcg gaa gaa aaa gac cag aag aaa cca gaa Gln Leu Lys Asn Asp Val Ser Glu Glu Lys Asp Gln Lys Lys Pro Glu 532	537	542	547	1808
aat gaa atg agt gga aag gtg gag ttg gtg ctg tca caa aag gtg gta Asn Glu Met Ser Gly Lys Val Glu Leu Val Leu Ser Gln Lys Val Val 548	553	558	563	1856
aag cca aaa tct cca gaa ccc gaa gca acg ctg aca ttt cca ttt ctg Lys Pro Lys Ser Pro Glu Pro Glu Ala Thr Leu Thr Phe Pro Phe Leu 564	569	574	579	1904
gac aaa atg cct gaa gcc aac caa cta cat ttg cca aat ctc aat tct				1952

Asp Lys Met Pro Glu Ala Asn Gln Leu His Leu Pro Asn Leu Asn Ser			
580	585	590	595
caa gtg gat tct cca agc agt gag aag tca cct gtt acg aca cct ttt			2000
Gln Val Asp Ser Pro Ser Ser Glu Lys Ser Pro Val Thr Thr Pro Phe			
596	601	606	611
aag ttc tgg gca tgg gac cca gaa gag gag cgc agg cga cag gaa aaa			2048
Lys Phe Trp Ala Trp Asp Pro Glu Glu Arg Arg Arg Gln Glu Lys			.
612	617	622	627
tgg caa cag gaa cag gaa cgt ttg ctc cag gag aga tac cag aag gag			2096
Trp Gln Gln Glu Gln Glu Arg Leu Leu Gln Glu Arg Tyr Gln Lys Glu			
628	633	638	643
cag gac aag ctg aaa gaa qag tgg gaa aag gcc caa aag gag gtg gaa			2144
Gln Asp Lys Leu Lys Glu Glu Trp Glu Lys Ala Gln Lys Glu Val Glu			
644	649	654	659
gag gaa gaa cgc aga tac tat gag gag gag cgt aag ata att gaa gac			2192
Glu Glu Glu Arg Arg Tyr Tyr Glu Glu Glu Arg Lys Ile Ile Glu Asp			
660	665	670	675
act gtg gtt cca ttt act gtt tct tca agt tcc gct gac cag ctg tct			2240
Thr Val Val Pro Phe Thr Val Ser Ser Ser Ala Asp Gln Leu Ser			
676	681	686	691
acc tct tcc tcc atg act gaa ggc agt ggg aca atg aat aag ata gac			2288
Thr Ser Ser Ser Met Thr Glu Gly Ser Gly Thr Met Asn Lys Ile Asp			
692	697	702	707
ctg gga aac tgt caa gat gaa aaa caa gac aga aga tgg aag aaa tca			2336
Leu Gly Asn Cys Gln Asp Glu Lys Gln Asp Arg Arg Trp Lys Lys Ser			
708	713	718	723
tcc cag gga gat gac agt gac tta ttg ctg aag act agg gaa agt gat			2384
Phe Gln Gly Asp Asp Ser Asp Leu Leu Leu Lys Thr Arg Glu Ser Asp			
724	729	734	739
cga ctg gag gag aag ggc agc cta act gaa ggg gcc ttg gct cat tct			2432
Arg Leu Glu Glu Lys Gly Ser Leu Thr Glu Gly Ala Leu Ala His Ser			
740	745	750	755
ggg aac cct gta tca aaa gga gtc cat gaa gac cat cag ctg gat acc			2480
Gly Asn Pro Val Ser Lys Gly Val His Glu Asp His Gln Leu Asp Thr			
756	761	766	771
gag gct ggg gcc cca cac tgt gga aca aac cca cag ctt gct cag gat			2528
Glu Ala Gly Ala Pro His Cys Gly Thr Asn Pro Gln Leu Ala Gln Asp			
772	777	782	787
cca tcc cag aat cag cag aca tca aat cca acg cac agt tca gaa gat			2576
Pro Ser Gln Asn Gln Gln Thr Ser Asn Pro Thr His Ser Ser Glu Asp			
788	793	798	803
gtg aag cca aaa acc ctc ccg ctg gat aaa agc att aac cat cag atc			2624
Val Lys Pro Lys Thr Leu Pro Leu Asp Lys Ser Ile Asn His Gln Ile			

804	809	814	819	
gag tct ccc agt gaa agg cg ^g aag tct ata agt gga aag aag ctg tgc Glu Ser Pro Ser Glu Arg Arg Lys Ser Ile Ser Gly Lys Lys Leu Cys				2672
820	825	830	835	
tct tcc tgt ggg ctt cct ttg ggt aaa gga gct gca atg atc atc gag Ser Ser Cys Gly Leu Pro Leu Gly Lys Gly Ala Ala Met Ile Ile Glu				2720
836	841	846	851	
acc ctc aat ctc tat ttt cac atc cag tgt ttc agg tgt gga att tgt Thr Leu Asn Leu Tyr Phe His Ile Gln Cys Phe Arg Cys Gly Ile Cys				2768
852	857	862	867	
aaa ggc cag ctt gga gat gca gtg agt ggg acg gat gtt agg att cga Lys Gly Gln Leu Gly Asp Ala Val Ser Gly Thr Asp Val Arg Ile Arg				2816
868	873	878	883	
aat ggt ctc ctg aac tgt aat gat tgc tac atg cga tcc aga agt gcc Asn Gly Leu Leu Asn Cys Asn Asp Cys Tyr Met Arg Ser Arg Ser Ala				2864
884	889	894	899	
ggg cag cct aca aca ttg tga ca cggcttcaa gcttccggat cactcaccat Gly Gln Pro Thr Thr Leu *				2917
900	905			
ttctttactg agagtgtccc ctggcaactg cttaacaaaa tcccaagctc aggggcttct				2977
caccatttac ctaatttctg aaaggctctt ctgaaaggtg gtatctgttc tttcgtagca				3037
cagtgtttat gttttccctg tttattgttt tggtttttt ttttttttg cattgcaca				3097
gtatacacaa aagaatatgg ggttgtaatg atcctgaata gctaaaaaaaaa ggtttagca				3157
tggtaaaca ggcttatggt taaaaatgtt ttattctttt ctttggaaat tagtaaatg				3217
atgcaataaa cctgttttgt tttagaatgtt ctaggaatta aacactttt gtttacagaa				3277
ttgagctgca gaaagtgcaa gacatgccaa tttgagacac acggcttct aagactgaag				3337
gataaattta atgcatttca gaaactaaac atcacagcaa gctctatctc tgagctataa				3397
tttggtttta atgcaaagac actagttga taatataac tgtaatcctg aaacatttgt				3457
gttacttacc tttggaggtt gaaattatac caataaatta ttgcaccgtt agtatttagat				3517
tctgtgtacc ttggaaagtta tgtcattaat ataggctggt tcataaataa aagcaaaacc				3577
ttgcaatatac agctagattt acactccggg acgttgccta aaggttaggaa gaaagcagag				3637
ggaaatattt cagtcatcat ttccaaagtc attatcaaaa tctgtgagga agttaatct				3697
tccaaagagt caatgtcaga catcaggcct ctgttgcttg cttctctcga ggcactagat				3757
taggagtctt caataagaga cttaacatga ggttatatgga agatgaggca ccgagataag				3817
ttcatcatta ggtgtgagca ctgctcaccc ttgctggcaa gttctcctta agggccctga				3877

agcacaggtg tccaaagaaa agcgttaagt ccatcttaat agaatctatg tggtatatga 3937
tgtgggtcag cccctgggtc tgtgatcagc aagaacctac agcacagatt atgccctgcc 3997
cacttcaatg aatacctact ctcctccatt ctccatcaact tttttgctg tcaagaactc 4057
cgAACCTTGC ccatggagaa gtttagagag gaactcttgt ggagagctgg tttatTTCT 4117
GCCCTGTGC gacgagttc agctggccaa gaaaggagtc aagttattaa aaagcatcac 4177
aatgttagatc tccaggctgg tttttgttt tttgttgtta agactgggaa aagggggact 4237
atTTATTCTG ccttaaatca atggcaaata agtcaagatg acATTTGTG aatgttagact 4297
atggatacac tcctaataaga ttgatgttgtt cataaaaggg ggtcaagtag atgttttct 4357
gttatgttaag caataatttt tccgtgtctt attgagtatg gctagcgatt atttattaca 4417
tgcttagatgg gttcttgca tgtgggttcc atataagggtgc agaaatttcc tcagccactg 4477
gagggatttc gaccatattt gtcatttggta tgagctgttta ttagattgaa atctacacat 4537
catTTcatta aaaattgtgc ctttagaaaac gcaaagctgt tgacatggc gataaattat 4597
ggatgcagta cattgaagag agatgaagtc acttccaagt ttccaagact tctcatggag 4657
gtgtttgctg ttttacagga aaaaataaaaa ataaaaaaaaag aaaaaaaagaa aaaattaaaa 4717
agaaaaaatttgg ttttggaaat gtacagatca agtccaatat tttgattatc cacctgcatg 4777
ttttattaaa tattttgata atgtggatgt ttacactttg catgatatta gcagagtacc 4837
actagtaatg cacaacatg tacaatatgg tcattcataa ccgattttta tagaataactt 4897
tttacatgtg caactccatc cgttatgtaa ggattacatg aatattgcac attcccttct 4957
ggTTTcacaa acccatttat acatatttct tagtgaggct cattgtacat gtattgaagc 5017
tagaatcgag tcaagaaaaa taaagccccca ttctccaact gcaaaatgtg ctTTCCATA 5077
atgaacacta gtcaccagca cagaataatc tccaacattt tctaaattct aattgccaac 5137
tggTTTCTat ttatatttga tttatatttc atttggagtc tgTTACATGG cagcttaagc 5197
agactagatc ttgtttttc caatgcagca taatgagtat gatctatttc ttTTCAAATA 5257
atctttgaga tcccaggaaa aaaaaatgc tctgctccat tgagctataa tgtaatgtg 5317
tttggTTAA aaacaggtga ggcaagttag tgattattg ttccTGAGGA agtataatctg 5377
atTTTTTTC tcataactcca aaagcttagtc cctactctt aataaaaata atggtaact 5437
tttggTTTTT cactagcgaa cttccatgac atttccTTTC tatgttagtgtt gattaatgca 5497
atacatatta tagttatcta tacacagtgt aagatttaac aaactgaaat gatccacctc 5557

atatgtgagt ccgtccaaaa gatgttactg ctctgggtgg gccagtgttc tatatcggtt	5617
atactaactt tcatttaaag tatttattct aaaatgcctc tgagaaaacag taaaaaaataa	5677
aaacaacaag ttgtctaaaa tgcaacagct tttatagtaa atgtacattt ataaaataaaa	5737
tactcaaatc aaaaaaaaaa aaaa	5761

<210> 148
 <211> 2622
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (336)..(1799)

<400> 148	
gcaagttcct gagagccggg aagaactgta ggaatagtca cagcttgaca accgaacaca	60
acctgagtgt gctgagaact catggcgttg accacctgag ctataatgag ctatgccaac	120
tcttgtttca gaacgacccc tggctttgc cagaaatttg ccaacattac aacaaaggag	180
atggaccccc ca cggtctttgt gcctttcaaa agcagtgcataa caagctccat atctgccagt	240
attttttaca gggggaatgc aagtttggca ctagctgtaa gagatcccat gatttctcta	300
attctgagaa tctggaaaaa ttggagaagt tgggt atg agc tca gac ctg gtg	353
Met Ser Ser Asp Leu Val	
1	
agc agg ctg cct acc att tat aga aat gca cat gac atc aag aat aag	401
Ser Arg Leu Pro Thr Ile Tyr Arg Asn Ala His Asp Ile Lys Asn Lys	
7 12 17 22	
agc tct gcc ccc agc aga gtg cct ctt ttt gtc cca cag ggg act	449
Ser Ser Ala Pro Ser Arg Val Pro Pro Leu Phe Val Pro Gln Gly Thr	
23 28 33 38	
tct gaa aga aaa gac agt tca ggt tct gtg tcc cca aac act ctt agc	497
Ser Glu Arg Lys Asp Ser Ser Gly Ser Val Ser Pro Asn Thr Leu Ser	
39 44 49 54	
cag gag gag ggt gat cag atc tgt ttg tac cat atc cgg aaa agt tgt	545
Gln Glu Gly Asp Gln Ile Cys Leu Tyr His Ile Arg Lys Ser Cys	
55 60 65 70	
agc ttt caa gat aag tgc cat aga gtt cat ttc cat ttg ccg tat cga	593
Ser Phe Gln Asp Lys Cys His Arg Val His Phe His Leu Pro Tyr Arg	
71 76 81 86	
/	
tgg caa ttc ttg gat aga ggc aaa tgg gag gat ttg gac aac atg gaa	641
Trp Gln Phe Leu Asp Arg Gly Lys Trp Glu Asp Leu Asp Asn Met Glu	

87	92	97	102	
ctt att gaa gag gca tat tgc aat ccc aaa ata gaa agg atc ctg tgc Leu Ile Glu Glu Ala Tyr Cys Asn Pro Lys Ile Glu Arg Ile Leu Cys 103 108 113 118				689
tct gag tca gcc agt acc ttt cac tct cat tgt ctg aac ttt aac gcc Ser Glu Ser Ala Ser Thr Phe His Ser His Cys Leu Asn Phe Asn Ala 119 124 129 134				737
atg act tac ggt gct acc cag gct cgc cgc ctc tcc acg gcc tcc tct Met Thr Tyr Gly Ala Thr Gln Ala Arg Arg Leu Ser Thr Ala Ser Ser 135 140 145 150				785
gtc acc aaa cct cca cac ttc atc ctc acc act gac tgg att tgg tac Val Thr Lys Pro Pro His Phe Ile Leu Thr Thr Asp Trp Ile Trp Tyr 151 156 161 166				833
tgg agt gat gag ttt ggt tct tgg cag gaa tat gga aga cag ggc acg Trp Ser Asp Glu Phe Gly Ser Trp Gln Glu Tyr Gly Arg Gln Gly Thr 167 172 177 182				881
gtg cac cct gtg acc act gtc agc agt agc gac gtg gag aag gcc tac Val His Pro Val Thr Thr Val Ser Ser Ser Asp Val Glu Lys Ala Tyr 183 188 193 198				929
ctg gcc tac tgt aca ccg ggg tct gac ggc cag gca gcc acc ttg aag Leu Ala Tyr Cys Thr Pro Gly Ser Asp Gly Gln Ala Ala Thr Leu Lys 199 204 209 214				977
ttc cag gcc gga aag cac aac tac gag tta gat ttc aaa gcc ttc gtt Phe Gln Ala Gly Lys His Asn Tyr Glu Leu Asp Phe Lys Ala Phe Val 215 220 225 230				1025
cag aaa aac ctg gtc tat ggc aca act aaa aag gtt tgc cgc aga ccc Gln Lys Asn Leu Val Tyr Gly Thr Thr Lys Lys Val Cys Arg Arg Pro 231 236 241 246				1073
aaa tac gtg tct ccc cag gat gtg acg acc atg caa acc tgc aat acc Lys Tyr Val Ser Pro Gln Asp Val Thr Thr Met Gln Thr Cys Asn Thr 247 252 257 262				1121
aag ttt cca ggc ccg aag agc atc cca gac tat tgg gac tcc tct gcc Lys Phe Pro Gly Pro Lys Ser Ile Pro Asp Tyr Trp Asp Ser Ser Ala 263 268 273 278				1169
ctg cca gac cca ggc ttt cag aag atc acc ctt agt tct tcc tcg gaa Leu Pro Asp Pro Gly Phe Gln Lys Ile Thr Leu Ser Ser Ser Glu 279 284 289 294				1217
gag tat cag aag gtc tgg aac ctc ttt aac cgc acg ctg cct ttc tac Glu Tyr Gln Lys Val Trp Asn Leu Phe Asn Arg Thr Leu Pro Phe Tyr 295 300 305 310				1265
ttt gtt cag aag att gag cga gta cag aac ctg gcc ctc tgg gaa gtc Phe Val Gln Lys Ile Glu Arg Val Gln Asn Leu Ala Leu Trp Glu Val 311 316 321 326				1313

tac cag tgg caa aaa gga cag atg cag aag cag aac gga ggg aag gcc Tyr Gln Trp Gln Lys Gly Gln Met Gln Lys Gln Asn Gly Gly Lys Ala 327 . 332 . 337 . 342	1361
gtg gac gag cgg cag ctg ttc cac ggc acc agc gcc att ttt gtg gac Val Asp Glu Arg Gln Leu Phe His Gly Thr Ser Ala Ile Phe Val Asp 343 . 348 . 353 . 358	1409
gcc atc tgc cag cag aac ttt gac tgg cgg gtc tgt ggt gtt cat ggc Ala Ile Cys Gln Gln Asn Phe Asp Trp Arg Val Cys Gly Val His Gly 359 . 364 . 369 . 374	1457
act tcc tac ggc aag ggg agc tac ttt gcc cga gat gct gca tat tcc Thr Ser Tyr Gly Lys Gly Ser Tyr Phe Ala Arg Asp Ala Ala Tyr Ser 375 . 380 . 385 . 390	1505
cac cac tac agc aaa tcc gac acg cag acc cac acg atg ttc ctg gcc His His Tyr Ser Lys Ser Asp Thr Gln Thr His Thr Met Phe Leu Ala 391 . 396 . 401 . 406	1553
cgg gtg ctg gtg ggc gag ttc gtc agg ggc aat gcc tcc ttt gtc cgt Arg Val Leu Val Gly Glu Phe Val Arg Gly Asn Ala Ser Phe Val Arg 407 . 412 . 417 . 422	1601
ccg ccg gcc aag gag ggc tgg agc aac gcc ttc tat gat agc tgc gtg Pro Pro Ala Lys Glu Gly Trp Ser Asn Ala Phe Tyr Asp Ser Cys Val 423 . 428 . 433 . 438	1649
aac agt gtg tcc gac ccc tcc atc ttt gtg atc ttt gag aaa cac cag Asn Ser Val Ser Asp Pro Ser Ile Phe Val Ile Phe Glu Lys His Gln 439 . 444 . 449 . 454	1697
gtc tac cca gag tat gtc atc cag tac acc acc tcc tcc aag ccc tcg Val Tyr Pro Glu Tyr Val Ile Gln Tyr Thr Ser Ser Lys Pro Ser 455 . 460 . 465 . 470	1745
gtc aca ccc tcc atc ctg ctg gcc ttg ggc tcc ctg ttc agc agc cga Val Thr Pro Ser Ile Leu Leu Ala Leu Gly Ser Leu Phe Ser Ser Arg 471 . 476 . 481 . 486	1793
cag tga gcgcacagga gtgtccagg ccttcacct gctctgcctt gaaatggcta Gln * 487	1849
tttggcctt tcctttctt tttaaacaga aactttaat gaactgttct cttaacattg acctctcaat gaagttatgt tcttaatctc ttgctaataa tgattttac tttaagtca ctttgggtt cactagtgga ttaaccagaa gtgattgttag ttgagtccag tttgcttt taataatgtg ttgaagttt agttttact ctttgtgac tttgctgctt attggcacca gggacagagt ttctagatac aatttatgg attggttta attttatga gtttgtctct / gcaagtgattc ggtttctcag agtctcatgg catcatagtt tttccagaat gacacagtag 2209	1909 1969 2029 2089 2149 2209

ccaccgggtgg atgacagccc acggggcggca cagtcacttc tgcctgtgc tctgacacca	2269
acccaggcag ctctgctgtg gcttctcctg ggctctggca tttagttggtc tgtgtcacat	2329
tgtcagaaca ggtggctgct gtgtggtgcc atcgagtccc tgctggttcc ccttgcctg	2389
ggagggtcac ccattgccc aggaagtgc tccacactggc aggtgacctg gaggagtagc	2449
ttccccgagg acccccaggc ttggcctgtg attgcgcaaa cccacatttc ctaagcacac	2509
tggacaccct tcgagtgtgg gtttaacat ccctgtgaga ttgaatactt gtgccacaca	2569
tgtcacaaaa gagtatggaa ataaaaaggaa atttatccga aaaaaaaaaaaa aaa	2622

<210> 149
 <211> 4285
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (346)..(3285)

<400> 149	.
taagcttgcg gccgctctgc ctgcgcgcctg ctccctgctct gctacacctgaa tgggttacca	60
tctttgggta ggcagacttc cctgacgaca tcagtgatac ccaaagctga gcagagcgtg	120
gcttacaaag actttatcta ttttactgtc tttgaaggaa acgttcgcaa cgtttctgaa	180
gtctcggttg agtattttatg ctctcagcct tgggttgtca atttggaaagc agttgtttca	240
tctgagttca gaagtagcat tcccgtgtac aaaaaaaggt ggaagaatga gaaacatctt	300
cacaccagca ggacacaaat agtacatgtg aaatttccaa gcatt atg gtt tac	354
	Met Val Tyr
	1

aga gat gat tat ttc atc aga cat tcc atc tct gta tct gca gtg ata	402
Arg Asp Asp Tyr Phe Ile Arg His Ser Ile Ser Val Ser Ala Val Ile	
4 9 14 19	

gtt cgc gcc tgg att act cac aaa tac agt ggc aga gac tgg aat gtt	450
Val Arg Ala Trp Ile Thr His Lys Tyr Ser Gly Arg Asp Trp Asn Val	
20 25 30 35	

aaa tgg gag gaa aac ttg ctc cat gct gta gca aag aat tat acc ctc	498
Lys Trp Glu Glu Asn Leu Leu His Ala Val Ala Lys Asn Tyr Thr Leu	
36 41 46 51	

ctg cag acc atc ccg cct ttt gaa cgc cct ttc aaa gat cat caa gtg	546
Leu Gln/Thr Ile Pro Pro Phe Glu Arg Pro Phe Lys Asp His Gln Val	
52 57 62 67	

tgc ctt gag tgg aac atg ggt tat att tgg aac ctt cg ^g gca aac agg Cys Leu Glu Trp Asn Met Gly Tyr Ile Trp Asn Leu Arg Ala Asn Arg 68 73 78 83	594
att cca cag tgt cct ctg gaa aat gat gtg gtt gcc ctg ctt ggc ttt Ile Pro Gln Cys Pro Leu Glu Asn Asp Val Val Ala Leu Leu Gly Phe 84 89 94 99	642
cct tat gcc tcc agt gga gaa aac aca ggc att gtc aag aag ttc ccg Pro Tyr Ala Ser Ser Gly Glu Asn Thr Gly Ile Val Lys Lys Phe Pro 100 105 110 115	690
agg ttt cgg aac cga gag ctg gag gcc act cga cgc cag agg atg gat Arg Phe Arg Asn Arg Glu Leu Glu Ala Thr Arg Arg Gln Arg Met Asp 116 121 126 131	738
tac cca gtg ttt act gtt tca ttg tgg ctt tat tta ctc cat tat tgc Tyr Pro Val Phe Thr Val Ser Leu Trp Leu Tyr Leu Leu His Tyr Cys 132 137 142 147	786
aag gcc aac ctc tgt ggg att ctg tac ttt gtt gac tct aat gag atg Lys Ala Asn Leu Cys Gly Ile Leu Tyr Phe Val Asp Ser Asn Glu Met 148 153 158 163	834
tac ggc aca cct tct gta ttt ctt acg gaa gag ggc tat ttg cat att Tyr Gly Thr Pro Ser Val Phe Leu Thr Glu Glu Gly Tyr Leu His Ile 164 169 174 179	882
cag atg cat ctt gtc aaa ggg gaa gac ctt gct gta aaa act aaa ttc Gln Met His Leu Val Lys Gly Glu Asp Leu Ala Val Lys Thr Lys Phe 180 185 190 195	930
atc ata cct ttg aag gag tgg ttt cga ctg gat atc tct ttt aac gga Ile Ile Pro Leu Lys Glu Trp Phe Arg Leu Asp Ile Ser Phe Asn Gly 196 201 206 211	978
ggc cag ata gta gta acc act agc att gga cag gat ttg aaa agc tac Gly Gln Ile Val Val Thr Ser Ile Gly Gln Asp Leu Lys Ser Tyr 212 217 222 227	1026
cac aat cag acc att agc ttc cgg gag gat ttc cat tat aat gac aca His Asn Gln Thr Ile Ser Phe Arg Glu Asp Phe His Tyr Asn Asp Thr 228 233 238 243	1074
gct ggg tac ttc att att gga ggg agc agg tat gtg gct ggc att gaa Ala Gly Tyr Phe Ile Ile Gly Gly Ser Arg Tyr Val Ala Gly Ile Glu 244 249 254 259	1122
ggg ttt ttt gga ccc ctg aag tac tat cgc ctt cgc agt ctg cac tca Gly Phe Phe Gly Pro Leu Lys Tyr Tyr Arg Leu Arg Ser Leu His Ser 260 265 270 275	1170
gcc ctg att ttt aat ccc ctc ctt gag aag caa ctt gct gaa caa atc Ala Leu Ile Phe Asn Pro Leu Leu Glu Lys Gln Leu Ala Glu Gln Ile 276 281 286 291	1218
aag tta tat tat gaa agg tgt gct gag gtt caa gaa ata gta tct gtg	1266

Lys	Leu	Tyr	Tyr	Glu	Arg	Cys	Ala	Glu	Val	Gln	Glu	Ile	Val	Ser	Val		
292		297						302				307					
tat gca tct gca gca aag cac ggg ggc gag aga caa gaa gca tgc cac															1314		
Tyr	Ala	Ser	Ala	Ala	Lys	His	Gly	Gly	Glu	Arg	Gln	Glu	Ala	Cys	His		
308		313						318				323					
ctc cac aac tcc tac ctg gac ctc cag cgc agg tat ggg aga ccc tcg															1362		
Leu	His	Asn	Ser	Tyr	Leu	Asp	Leu	Gln	Arg	Arg	Tyr	Gly	Arg	Pro	Ser		
324		329						334				339					
atg tgc aga gcc ttc ccc tgg gag aag gag ctg aaa gac aaa cac ccc															1410		
Met	Cys	Arg	Ala	Phe	Pro	Trp	Glu	Lys	Glu	Leu	Lys	Asp	Lys	His	Pro		
340		345						350				355					
agc ttg ttc cag gca ttg ctg gag atg gat ctg ctg acc gtg cca agg															1458		
Ser	Leu	Phe	Gln	Ala	Leu	Leu	Glu	Met	Asp	Leu	Leu	Thr	Val	Pro	Arg		
356		361						366				371					
aaccaaataatgaaatctgtatcaaaaaatcggtggaaatataatgtttgaggaaat															1506		
Asn	Gln	Asn	Glu	Ser	Val	Ser	Glu	Ile	Gly	Gly	Lys	Ile	Phe	Glu	Lys		
372		377						382				387					
gct gta aag aga ctc tct agc att gat ggt ctt cac caa att agc tct															1554		
Ala	Val	Lys	Arg	Leu	Ser	Ser	Ile	Asp	Gly	Leu	His	Gln	Ile	Ser	Ser		
388		393						398				403					
atc gtc ccc ttt ctg acg gat tcc agc tgc tgt gga tac cat aaa gca															1602		
Ile	Val	Pro	Phe	Leu	Thr	Asp	Ser	Ser	Cys	Cys	Gly	Tyr	His	Lys	Ala		
404		409						414				419					
tcc tac tac ctt gca gtc ttt tat gag act gga tta aat gtt cct cg															1650		
Ser	Tyr	Tyr	Leu	Ala	Val	Phe	Tyr	Glu	Thr	Gly	Leu	Asn	Val	Pro	Arg		
420		425						430				435					
gat cag ctg cag ggc atg ttg tat agt ttg gtt gga ggc cag ggg agt															1698		
Asp	Gln	Leu	Gln	Gly	Met	Leu	Tyr	Ser	Leu	Val	Gly	Gly	Gln	Gly	Ser		
436		441						446				451					
gag agg ctg tct tca atg aat ctt ggg tat aaa cac tac cag ggt att															1746		
Glu	Arg	Leu	Ser	Ser	Met	Asn	Leu	Gly	Tyr	Lys	His	Tyr	Gln	Gly	Ile		
452		457						462				467					
gac aac tac ccc ctg gac tgg gaa ctg tcg tat gcc tac tac agc aac															1794		
Asp	Asn	Tyr	Pro	Leu	Asp	Trp	Glu	Leu	Ser	Tyr	Ala	Tyr	Tyr	Ser	Asn		
468		473						478				483					
att gcc acc aag aca ccc ctt gac cag cac aca ctg caa gga gat cag															1842		
Ile	Ala	Thr	Lys	Thr	Pro	Leu	Asp	Gln	His	Thr	Leu	Gln	Gly	Asp	Gln		
484		489						494				499					
gca tat gtt gaa aca att aga cta aaa gat gat gaa ata ctc aag gta															1890		
Ala	Tyr	Val	Glu	Thr	Ile	Arg	Leu	Lys	Asp	Asp	Glu	Ile	Leu	Lys	Val		
500		505						510				515					
caa acc aaa gaa gat gga gat gtc ttt atg tgg ttg aag cat gaa gct															1938		
Gln	Thr	Lys	Glu	Asp	Gly	Asp	Val	Phe	Met	Trp	Leu	Lys	His	Glu	Ala		

516	521	526	531		
acc cga ggc aat gca gca gct cag caa cga ttg gcc cag atg ctg ttc Thr Arg Gly Asn Ala Ala Gln Gln Arg Leu Ala Gln Met Leu Phe	532	537	542	547	1986
tgg ggg cag caa ggt gtg gcc aag aat ccc gaa gca gca att gag tgg Trp Gly Gln Gln Gly Val Ala Lys Asn Pro Glu Ala Ala Ile Glu Trp	548	553	558	563	2034
tac gcc aag ggc gcc ctg gag acg gag gat cct gcg tta atc tat gac Tyr Ala Lys Gly Ala Leu Glu Thr Glu Asp Pro Ala Leu Ile Tyr Asp	564	569	574	579	2082
tat gcc att gtg cta ttc aag ggt caa gga gta aaa aag aac aga cgg Tyr Ala Ile Val Leu Phe Lys Gly Gln Gly Val Lys Lys Asn Arg Arg	580	585	590	595	2130
ctt gcc tta gag ctg atg aag aaa gca gct tcc aag gga ttg cat cag Leu Ala Leu Glu Leu Met Lys Lys Ala Ala Ser Lys Gly Leu His Gln	596	601	606	611	2178
gca gtc aat ggc ctg gga tgg tat tac cac aaa ttc aag aaa aat tac Ala Val Asn Gly Leu Gly Trp Tyr Tyr His Lys Phe Lys Lys Asn Tyr	612	617	622	627	2226
gcc aaa gca gca aag tac tgg tta aaa gca gaa gaa atg ggg aac cca Ala Lys Ala Ala Lys Tyr Trp Leu Lys Ala Glu Glu Met Gly Asn Pro	628	633	638	643	2274
gat gcg tca tac aat ctt gga gtc ctg cat ttg gat ggc atc ttc cct Asp Ala Ser Tyr Asn Leu Gly Val Leu His Leu Asp Gly Ile Phe Pro	644	649	654	659	2322
gga gtt cct gga agg aat caa act tta gct ggt gaa tat ttc cat aag Gly Val Pro Gly Arg Asn Gln Thr Leu Ala Gly Glu Tyr Phe His Lys	660	665	670	675	2370
gct gcg caa ggt gga cac atg gaa ggg acc ttg tgg tgt tct ctc tac Ala Ala Gln Gly Gly His Met Glu Gly Thr Leu Trp Cys Ser Leu Tyr	676	681	686	691	2418
tat atc aca ggc aac ctg gag aca ttc cct aga gat cct gag aaa gct Tyr Ile Thr Gly Asn Leu Glu Thr Phe Pro Arg Asp Pro Glu Lys Ala	692	697	702	707	2466
gtt gta tgg gca aaa cat gta gct gag aaa aat ggc tac ttg ggc cat Val Val Trp Ala Lys His Val Ala Glu Lys Asn Gly Tyr Leu Gly His	708	713	718	723	2514
gtc atc cgc aaa ggc ctc aat gcc tac ctg gaa ggt tca tgg cat gaa Val Ile Arg Lys Gly Leu Asn Ala Tyr Leu Glu Gly Ser Trp His Glu	724	729	734	739	2562
gct ttg ctg tat tat gtt tta gca gca gaa act gga att gaa gtg tca Ala Leu Leu Tyr Tyr Val Leu Ala Ala Glu Thr Gly Ile Glu Val Ser	740	745	750	755	2610

cag aca aat tta gca cac atc tgt gag gag agg cca gac ctg gcc agg Gln Thr Asn Leu Ala His Ile Cys Glu Glu Arg Pro Asp Leu Ala Arg	756	761	766	771	2658
aga tac ttg ggt gtt aac tgt gtt tgg aga tac tat aat ttc tct gtt Arg Tyr Leu Gly Val Asn Cys Val Trp Arg Tyr Tyr Asn Phe Ser Val	772	777	782	787	2706
ttt caa atc gat gct cct tcc ttt gca tat ttg aag atg gga gac ctt Phe Gln Ile Asp Ala Pro Ser Phe Ala Tyr Leu Lys Met Gly Asp Leu	788	793	798	803	2754
tac tac tat ggc cac caa aac cag tca caa gac ctg gag ttg tct gtg Tyr Tyr Tyr Gly His Gln Asn Gln Ser Gln Asp Leu Glu Leu Ser Val	804	809	814	819	2802
cag atg tac gcc caa gcc gcc ctg gat gga gac tcc cag gga ttt ttt Gln Met Tyr Ala Gln Ala Ala Leu Asp Gly Asp Ser Gln Gly Phe Phe	820	825	830	835	2850
aac ctg gcc ctg cta atc gag gaa ggt acg ata atc cca cac cat atc Asn Leu Ala Leu Leu Ile Glu Glu Gly Thr Ile Ile Pro His His Ile	836	841	846	851	2898
ttg gat ttc ttg gaa att gac tca act ctc cat tct aat aac atc tcc Leu Asp Phe Leu Glu Ile Asp Ser Thr Leu His Ser Asn Asn Ile Ser	852	857	862	867	2946
att ctc cag gaa ctg tac gaa agg tgc tgg agc cac agt aac gag gag Ile Leu Gln Glu Leu Tyr Glu Arg Cys Trp Ser His Ser Asn Glu Glu	868	873	878	883	2994
tcc ttc agc ccc tgc tcc ttg gcc tgg ctt tac ctg cac ttg cgg ctt Ser Phe Ser Pro Cys Ser Leu Ala Trp Leu Tyr Leu His Leu Arg Leu	884	889	894	899	3042
ctc tgg ggt gct atc ctg cac tca gcc ctg atc tac ttt ctg gga acc Leu Trp Gly Ala Ile Leu His Ser Ala Leu Ile Tyr Phe Leu Gly Thr	900	905	910	915	3090
ttt ctg cta tcc ata ttg atc gcc tgg act gtg cag tat ttc cag tct Phe Leu Leu Ser Ile Leu Ile Ala Trp Thr Val Gln Tyr Phe Gln Ser	916	921	926	931	3138
gtc tca gca agc gat ccc cct cca aga cca tcc cag gcc tcc cca gac Val Ser Ala Ser Asp Pro Pro Pro Arg Pro Ser Gln Ala Ser Pro Asp	932	937	942	947	3186
act gcc acg tcc act gca agt cca gct gtg act cca gct gca gat gcc Thr Ala Thr Ser Thr Ala Ser Pro Ala Val Thr Pro Ala Ala Asp Ala	948	953	958	963	3234
tct gac caa gac cag ccc aca gta act aat aac ccg gag cca cgt ggg Ser Asp Gln Asp Gln Pro Thr Val Thr Asn Asn Pro Glu Pro Arg Gly	964	969	974	979	3282

tga actg tgcactccag ttctctccag atgagagaga atctttcaa cagctggat	3339
*	
980	
tggttgcggc atgatcctga taaacacctt aaatgtcttgc tcaactggat	3399
gcaaaattttt caattggtgt cattttttt aaagtcaaata tacaagggaa tacccagatc	3459
aggcagtggt aataccaaag gtcatcaaacc acatacaagg aacatcttgc tcatagggca	3519
tgtggggaaat tttactgggc catcacagac ttttgcgttgc gtgattgtat gtattaggag	3579
tcatagcatg ccctacggca gatctggatt cttataactt aagatgtgtc ttaagaatca	3639
cagtgcgtgc ttcatccctt tattgaagaa cagaaaatta tgactactt acaagggtgga	3699
taatattttt gtacctgtgc ttgccacagc cctgttcctc aaagctgaat tgatagattt	3759
ctctttgact tccaagacctt agcagttata aggacacccat aaataaatttgc tttgtgcctg	3819
gaaatgcagg gagggcaata gctttgtaaa ttgggttaca tttttctcct tgaatttttc	3879
tagggtccta gtgcttccga atcatttaat ggcattgtcg gatatctttt acatttcaat	3939
tgcaatccat gaaattacat tttagaagatt cttagtactt aactgtgtc ttctccatga	3999
attacacgtt agaatacgact ggcagcaact gaatatgcag caagtaagcc tctagcttat	4059
agtttcatcc ctaccctca tgcctgcgtg agtctgtaca gggatatgtg tgtgtgtgt	4119
tgtgtgtgtg tgtagagag gaagagggaa agcagaatgt ctgtataacta catgctgcta	4179
aggttagtgaa taaatcagta atgcaatattt gtgggtccaa actactctt gcactacttt	4239
atttacagta gtaaaaaaaa ttatttttt aaaaaaaaaaaaaaaa	4285

<210> 150
 <211> 4618
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (282)..(4043)

<400> 150	
cggaattccc gggtcgacga ttctgttttc gcttgcgtat ttcgttagggg aggaggccga	60
gtgtttcctg ggcattcccc ggccagcccg agtgcgttac tcggccaagg aaactcccaag	120
ggccccccca ggaccggccaa gccggccgg acgcagaatg tggctcgttgc gcccctggc	180
ccatcccagg gcagagctcc tcctgagttac cttgcgttac ggagcagatt cagcagaagg	240

cagattgccc cctctccctg gagctggctc tgaagccca g	atg gcg gcc cag	293
	Met Ala Ala Gln	
	1	
gtg act ctg gag gac gcg ctg tcc aac gtg gac ctc ctg gag gag ctg		341
Val Thr Leu Glu Asp Ala Leu Ser Asn Val Asp Leu Leu Glu Glu Leu		
5 10 15 20		
ccc ctg ccc gac cag cag ccc tgc atc gag ccc ccg cca tcc tcg ctg		389
Pro Leu Pro Asp Gln Gln Pro Cys Ile Glu Pro Pro Pro Ser Ser Leu		
21 26 31 36		
ctc tac cag cca aat ttc aac act aac ttt gaa gac aga aat gca ttt		437
-Leu Tyr Gln Pro Asn Phe Asn Thr Asn Phe Glu Asp Arg Asn Ala Phe		
37 42 47 52		
gtt act ggc atc gca aga tac att gaa caa gcc acc gtc cac tct agc		485
Val Thr Gly Ile Ala Arg Tyr Ile Glu Gln Ala Thr Val His Ser Ser		
53 58 63 68		
atg aac gag atg ctg gag gag ggc caa gaa tat gct gtc atg ctg tac		533
Met Asn Glu Met Leu Glu Glu Gly Gln Glu Tyr Ala Val Met Leu Tyr		
69 74 79 84		
acc tgg agg agc tgc tcc cgg gcc atc cca cag gtg aaa tgt aac gag		581
Thr Trp Arg Ser Cys Ser Arg Ala Ile Pro Gln Val Lys Cys Asn Glu		
85 90 95 100		
cag cct aac aga gtg gaa atc tac gag aaa acc gtg gag gtt ctg gag		629
Gln Pro Asn Arg Val Glu Ile Tyr Glu Lys Thr Val Glu Val Leu Glu		
101 106 111 116		
cct gag gtc aca aaa ctg atg aat ttc atg tac ttc cag aga aat gcc		677
Pro Glu Val Thr Lys Leu Met Asn Phe Met Tyr Phe Gln Arg Asn Ala		
117 122 127 132		
att gag cgt ttc tgc ggg gaa gtg agg cgc ctg tgc cat gcc gag agg		725
Ile Glu Arg Phe Cys Gly Glu Val Arg Arg Leu Cys His Ala Glu Arg		
133 138 143 148		
agg aag gac ttc gtg tca gaa gcc tac ctg atc aca ctg ggc aaa ttc		773
Arg Lys Asp Phe Val Ser Glu Ala Tyr Leu Ile Thr Leu Gly Lys Phe		
149 154 159 164		
atc aac atg ttc gct gtg ctg gac gag ctg aag aac atg aag tgc agt		821
Ile Asn Met Phe Ala Val Leu Asp Glu Leu Lys Asn Met Lys Cys Ser		
165 170 175 180		
gtg aag aac gac cac tca gcg tac aag agg gcc gct cag ttt tta cgt		869
Val Lys Asn Asp His Ser Ala Tyr Lys Arg Ala Ala Gln Phe Leu Arg		
181 186 191 196		
aaa atg gca gat cca cag tcc atc cag gaa tcg cag aat ctg tcc atg		917
Lys Met Ala Asp Pro Gln Ser Ile Gln Glu Ser Gln Asn Leu Ser Met		
197 202 207 212		
ttc ctg gcc aat cat aac aag atc aca cag tct ctg cag cag ctc		965

Phe	Leu	Ala	Asn	His	Asn	Lys	Ile	Thr	Gln	Ser	Leu	Gln	Gln	Leu	
213									223					228	
gaa gtg att tct ggc tac gaa gag ctc ctg gca gat att gtg aat ctg														1013	
Glu	Val	Ile	Ser	Gly	Tyr	Glu	Glü	Leu	Leu	Ala	Asp	Ile	Val	Asn	Leu
229									239					244	
tgt gtg gat tac tac gag aac agg atg tat ttg acg ccc agt gag aaa														1061	
Cys	Val	Asp	Tyr	Tyr	Glu	Asn	Arg	Met	Tyr	Leu	Thr	Pro	Ser	Glu	Lys
245									255					260	
cac atg ctt ctc aaa gtc atg gga ttt ggt ctg tac ctg atg gat ggg														1109	
His	Met	Leu	Leu	Lys	Val	Met	Gly	Phe	Gly	Leu	Tyr	Leu	Met	Asp	Gly
261									271					276	
agt gtc agt aac atc tat aag ttg gat gcc aag aaa aga ata aac tta														1157	
Ser	Val	Ser	Asn	Ile	Tyr	Lys	Leu	Asp	Ala	Lys	Lys	Arg	Ile	Asn	Leu
277									287					292	
tcc aaa atc gac aag tac ttc aag caa ctc cag gtg gtt cca cta ttt														1205	
Ser	-Lys	Ile	Asp	-Lys	Tyr	Phe	Lys	Gln	-Leu	Gln	-Val	-Val	Pro	Leu	Phe
293									303					308	
ggg gac atg caa ata gaa ctg gca aga tat atc aag acc agc gcc cac														1253	
Gly	Asp	Met	Gln	Ile	Glu	Leu	Ala	Arg	Tyr	Ile	Lys	Thr	Ser	Ala	His
309									319					324	
tac gag gaa aat aaa tct cga tgg acg tgc aca tcc tcc ggc agc agc														1301	
Tyr	Glu	Glu	Asn	Lys	Ser	Arg	Trp	Thr	Cys	Thr	Ser	Ser	Gly	Ser	Ser
325									335					340	
cct cag tac aac atc tgc gag cag atg atc cag atc cgc gag gac cac														1349	
Pro	Gln	Tyr	Asn	Ile	Cys	Glu	Gln	Met	Ile	Gln	Ile	Arg	Glu	Asp	His
341									351					356	
atg cgc ttc att tcg gag ctg gcg cgc tac agc aac agc gag gtg gtc														1397	
Met	Arg	Phe	Ile	Ser	Glu	Leu	Ala	Arg	Tyr	Ser	Asn	Ser	Glu	Val	Val
357									367					372	
acg ggc tcg ggc cgc cag gag gcc cag aag acg gac gcg gag tac cgc														1445	
Thr	Gly	Ser	Gly	Arg	Gln	Glu	Ala	Gln	Lys	Thr	Asp	Ala	Glu	Tyr	Arg
373									383					388	
aag ctc ttc gac ctg gcg ctg cag ggc ctg cag ctg ttg tcg cag tgg														1493	
Lys	Leu	Phe	Asp	Leu	Ala	Leu	Gln	Gly	Leu	Gln	Leu	Leu	Ser	Gln	Trp
389									399					404	
agc gcg cac gtg atg gaa gtg tat tcc tgg aag ctt gtg cac ccc acc														1541	
Ser	Ala	His	Val	Met	Glu	Val	Tyr	Ser	Trp	Lys	Leu	Val	His	Pro	Thr
405									415					420	
gac aag tac tcc aac aag gac tgc ccc gac agc gct gaa gag tac gag														1589	
Asp	Lys	Tyr	Ser	Asn	Lys	Asp	Cys	Pro	Asp	Ser	Ala	Glu	Glu	Tyr	Glu
421									431					436	
cgt gcc acg cgc tac aac tac acc agc gag gag aag ttt gcc cta gtg														1637	
Arg	Ala	Thr	Arg	Tyr	Asn	Tyr	Thr	Ser	Glu	Glu	Lys	Phe	Ala	Leu	Val

437	442	447	452													
gag	gtg	atc	gcc	atg	atc	aaa	ggc	ctg	cag	gtg	ctg	atg	ggc	agg	atg	1685
Glu	Val	Ile	Ala	Met	Ile	Lys	Gly	Leu	Gln	Val	Leu	Met	Gly	Arg	Met	
453					458					463					468	
gag	agc	gtg	tcc	aac	cac	gcc	atc	cg	cac	acc	gtc	tat	gcc	gca	ctg	1733
Glu	Ser	Val	Phe	Asn	His	Ala	Ile	Arg	His	Thr	Val	Tyr	Ala	Ala	Leu	
469						474				479					484	
cag	gac	ttc	tcc	cag	gtg	acc	ctt	agg	gag	ccg	ctg	cg	cag	gcc	atc	1781
Gln	Asp	Phe	Ser	Gln	Val	Thr	Leu	Arg	Glu	Pro	Leu	Arg	Gln	Ala	Ile	
485						490				495					500	
aag	aag	aag	aag	aac	gtc	atc	cag	agt	gtc	ctg	cag	gcc	atc	agg	aag	1829
Lys	Lys	Lys	Lys	Asn	Val	Ile	Gln	Ser	Val	Leu	Gln	Ala	Ile	Arg	Lys	
501						506				511					516	
acc	gtg	tgt	gac	tgg	gag	acg	ggg	cat	gag	ccc	ttc	aat	gac	cca	gcc	1877
Thr	Val	Cys	Asp	Trp	Glu	Thr	Gly	His	Glu	Pro	Phe	Asn	Asp	Pro	Ala	
517						522				527					532	
ttg	cgg	ggc	gag	aag	gac	ccc	tcc	agc	gac	ata	aaa	gta	cca		1925	
Leu	Arg	Gly	Glu	Lys	Asp	Pro	Lys	Ser	Gly	Phe	Asp	Ile	Lys	Val	Pro	
533						538				543					548	
cgc	cgc	gcc	gtg	gga	ccc	tcc	agc	act	cag	ctt	tac	atg	gtg	aga	acc	1973
Arg	Arg	Ala	Val	Gly	Pro	Ser	Ser	Thr	Gln	Leu	Tyr	Met	Val	Arg	Thr	
549						554				559					564	
atg	cta	gag	tcc	ctc	att	gca	gac	aaa	agt	ggt	tcc	aag	aaa	acc	ttg	2021
Met	Leu	Glu	Ser	Leu	Ile	Ala	Asp	Lys	Ser	Gly	Ser	Lys	Lys	Thr	Leu	
565						570				575					580	
aga	agt	agc	ctt	gag	ggg	ccc	acc	ata	ttg	gac	ata	gaa	aaa	ttt	cat	2069
Arg	Ser	Ser	Leu	Glu	Gly	Pro	Thr	Ile	Leu	Asp	Ile	Glu	Lys	Phe	His	
581						586				591					596	
cga	gag	tca	ttc	ttc	tac	act	cac	ttg	ata	aat	ttc	agt	gaa	acg	ctg	2117
Arg	Glu	Ser	Phe	Phe	Tyr	Thr	His	Leu	Ile	Asn	Phe	Ser	Glu	Thr	Leu	
597						602				607					612	
cag	cag	tgc	tgt	gac	ctt	tcg	cag	ctg	tgg	ttc	cga	gag	ttc	ttc	ctg	2165
Gln	Gln	Cys	Cys	Asp	Leu	Ser	Gln	Leu	Trp	Phe	Arg	Glu	Phe	Phe	Leu	
613						618				623					628	
gag	ctg	acc	atg	ggc	agg	agg	atc	cag	ttc	ccc	att	gag	atg	tcg	atg	2213
Glu	Leu	Thr	Met	Gly	Arg	Arg	Ile	Gln	Phe	Pro	Ile	Glu	Met	Ser	Met	
629						634				639					644	
ccc	tgg	atc	ctg	acg	gac	cac	atc	ctg	gag	acc	aag	gag	gca	tcg	atg	2261
Pro	Trp	Ile	Leu	Thr	Asp	His	Ile	Leu	Glu	Thr	Lys	Glu	Ala	Ser	Met	
645						650				655					660	
atg	gag	tac	gtg	ctc	tac	tcc	ctg	tac	ctg	tac	aat	gac	agc	gcc	cac	2309
Met	Glu	Tyr	Val	Leu	Tyr	Ser	Leu	Tyr	Leu	Tyr	Asn	Asp	Ser	Ala	His	
661						666				671					676	

tac	gcf	ctc	acc	agg	ttc	aac	aag	cag	ttc	ctg	tac	gac	gaa	att	gag		2357
Tyr	Ala	Leu	Thr	Arg	Phe	Asn	Lys	Gln	Phe	Leu	Tyr	Asp	Glu	Ile	Glu		
677						682				687				692			
gcc	gag	gtg	aat	cta	tgt	ttt	gac	caa	ttt	gtt	tac	aag	cta	gca	gac		2405
Ala	Glu	Val	Asn	Leu	Cys	Phe	Asp	Gln	Phe	Val	Tyr	Lys	Leu	Ala	Asp		
693						698				703				708			
cag	ata	ttt	gcc	tat	tat	aag	gtt	atg	gca	gga	agt	ttg	ctt	ctt	gat		2453
Gln	Ile	Phe	Ala	Tyr	Tyr	Lys	Val	Met	Ala	Gly	Ser	Leu	Leu	Leu	Asp		
709						714				719				724			
aaa	cgf	tta	cga	tca	gaa	tgc	aag	aat	cag	gga	gcc	acg	atc	cac	ctc		2501
Lys	Arg	Leu	Arg	Ser	Glu	Cys	Lys	Asn	Gln	Gly	Ala	Thr	Ile	His	Leu		
725						730				735				740			
ccg	ccg	tct	aac	cgc	tac	gag	acg	ctg	ctg	aag	cag	agg	cat	gtg	cag		2549
Pro	Pro	Ser	Asn	Arg	Tyr	Glu	Thr	Leu	Leu	Lys	Gln	Arg	His	Val	Gln		
741						746				751				756			
ctc	ctc	ggc	aga	tca	ata	gac	ctc	aat	cgt	ctg	atc	acc	cag	cgc	gtc		2597
Leu	Leu	Gly	Arg	Ser	Ile	Asp	Leu	Asn	Arg	Leu	Ile	Thr	Gln	Arg	Val		
757						762				767				772			
tca	gca	gcc	atg	tat	aag	tcc	cta	gaa	ctg	gcg	att	gga	cga	ttt	gaa		2645
Ser	Ala	Ala	Met	Tyr	Lys	Ser	Leu	Glu	Leu	Ala	Ile	Gly	Arg	Phe	Glu		
773						778				783				788			
agt	gaa	gat	ttg	acc	tcc	ata	gtt	gag	ctg	gat	ggc	ctg	ttg	gaa	atc		2693
Ser	Glu	Asp	Leu	Thr	Ser	Ile	Val	Glu	Leu	Asp	Gly	Leu	Leu	Glu	Ile		
789						794				799				804			
aac	cgc	atg	acc	cac	aag	ctg	ctg	agc	cgg	tac	ctg	acg	ctg	gac	ggc		2741
Asn	Arg	Met	Thr	His	Lys	Leu	Leu	Ser	Arg	Tyr	Leu	Thr	Leu	Asp	Gly		
805						810				815				820			
ttc	gac	gcc	atg	ttc	cgf	gag	gcc	aac	cac	aat	gtg	tca	gcf	ccc	tac		2789
Phe	Asp	Ala	Met	Phe	Arg	Glu	Ala	Asn	His	Asn	Val	Ser	Ala	Pro	Tyr		
821						826				831				836			
ggg	agg	atc	acc	ctg	cac	gtc	ttc	tgg	gag	ctc	aac	tat	gac	ttc	ctg		2837
Gly	Arg	Ile	Thr	Leu	His	Val	Phe	Trp	Glu	Leu	Asn	Tyr	Asp	Phe	Leu		
837						842				847				852			
ccc	aac	tac	tgc	tac	aac	ggc	tct	acc	aac	cgg	ttt	gtt	cgf	aca	gtg		2885
Pro	Asn	Tyr	Cys	Tyr	Asn	Gly	Ser	Thr	Asn	Arg	Phe	Val	Arg	Thr	Val		
853						858				863				868			
tta	cca	ttt	tct	cag	gaa	ttt	caa	aga	gat	aag	cag	cct	aat	gca	cag		2933
Leu	Pro	Phe	Ser	Gln	Glu	Phe	Gln	Arg	Asp	Lys	Gln	Pro	Asn	Ala	Gln		
869						874				879				884			
cct	cag	tat	ctg	cat	gga	tcc	aag	gct	ttg	aac	ttg	gcc	tac	tcc	agc		2981
Pro	Gln	Tyr	Leu	His	Gly	Ser	Lys	Ala	Leu	Asn	Leu	Ala	Tyr	Ser	Ser		
885						890				895				900			

att tac ggc agc tac cgg aac ttc gtg gga cct cca cac ttt caa gtc Ile Tyr Gly Ser Tyr Arg Asn Phe Val Gly Pro Pro His Phe Gln Val 901 906 911 916	3029
atc tgc cgg ctt ctc ggc tac cag ggt atc gcc gtg gtc atg gag gag Ile Cys Arg Leu Leu Gly Tyr Gln Gly Ile Ala Val Val Met Glu Glu 917 922 927 932	3077
ctg ctg aag gtc aag agc ctg ctg caa ggc aca atc ctg cag tac Leu Leu Lys Val Val Lys Ser Leu Leu Gln Gly Thr Ile Leu Gln Tyr 933 938 943 948	3125
gtg aag acg ctg atg gag gtg atg ccc aag atc tgc cgc ctg ccc cgg Val Lys Thr Leu Met Glu Val Met Pro Lys Ile Cys Arg Leu Pro Arg 949 954 959 964	3173
cac gag tac ggc tct cct ggt atc ctg gag ttc ttc cac cac cag ctg His Glu Tyr Ser Pro Gly Ile Leu Glu Phe Phe His His Gln Leu 965 970 975 980	3221
aag_gac_atc_gtg_gag_tac_gca_gag_ctg_aag_acg_gtg_tgc_ttc_cag_aac Lys Asp Ile Val Glu Tyr Ala Glu Leu Lys Thr Val Cys Phe Gln Asn 981 986 991 996	3269
ctg cgg gag gtg ggg aac gcc atc ctc ttc tgc ctg ctc atc gag cag Leu Arg Glu Val Gly Asn Ala Ile Leu Phe Cys Leu Leu Ile Glu Gln 997 1002 1007 1012	3317
agc ctg tct tta gaa gaa gtg tgt gac ctg ctg cac gcg gct cct ttc Ser Leu Ser Leu Glu Glu Val Cys Asp Leu Leu His Ala Ala Pro Phe 1013 1018 1023 1028	3365
cag aac atc ttg ccg cga gtc cat gtg aaa gag ggg gag aga ctt gat Gln Asn Ile Leu Pro Arg Val His Val Lys Glu Gly Glu Arg Leu Asp 1029 1034 1039 1044	3413
gcc aaa atg aaa aga cta gaa tca aag tac gcc ccg ctg cat ctt gtc Ala Lys Met Lys Arg Leu Glu Ser Lys Tyr Ala Pro Leu His Leu Val 1045 1050 1055 1060	3461
cca ctg att gaa aga ctg ggg acc cct cag caa att gcc atc gca aga Pro Leu Ile Glu Arg Leu Gly Thr Pro Gln Gln Ile Ala Ile Ala Arg 1061 1066 1071 1076	3509
gag ggg gac ctg ctg aca aag gag cgc ctc tgc tgc ggc ctg tcc atg Glu Gly Asp Leu Leu Thr Lys Glu Arg Leu Cys Cys Gly Leu Ser Met 1077 1082 1087 1092	3557
ttt gag gtc atc ctg aca cgg atc cgg agc ttt ctg gat gac ccc atc Phe Glu Val Ile Leu Thr Arg Ile Arg Ser Phe Leu Asp Asp Pro Ile 1093 1098 1103 1108	3605
tgg cgc ggg cct ctg ccc agc aat ggg gtc atg cat gtg gac gag tgt Trp Arg Gly Pro Leu Pro Ser Asn Gly Val Met His Val Asp Glu Cys 1109 1114 1119 1124	3653
gtg gag ttt cac aga ctg tgg agt gcc atg cag ttt gtc tac tgc att	3701

Val Glu Phe His Arg Leu Trp Ser Ala Met Gln Phe Val Tyr Cys Ile				
1125	1130	1135	1140	
ccc gtg ggg aca cac gag ttc aca gtc gag cag tgc ttt ggt gat ggg				3749
Pro Val Gly Thr His Glu Phe Thr Val Glu Gln Cys Phe Gly Asp Gly				
1141	1146	1151	1156	
cta cac tgg gct ggc tgt atg atc atc gta ctt ctt ggg cag cag cgg				3797
Leu His Trp Ala Gly Cys Met Ile Ile Val Leu Leu Gly Gln Gln Arg				
1157	1162	1167	1172	
cgt ttt gct gtg ctg gat ttc tgc tac cat cta ctt aaa gtc cag aaa				3845
Arg Phe Ala Val Leu Asp Phe Cys Tyr His Leu Leu Lys Val Gln Lys				
1173	1178	1183	1188	
cat gat ggc aaa gat gag att att aaa aat gtg cct ttg aag aag atg				3893
His Asp Gly Lys Asp Glu Ile Ile Lys Asn Val Pro Leu Lys Lys Met				
1189	1194	1199	1204	
gtg gag aga att cgc aag ttc cag att ctc aat gat gag atc atc acc				3941
Val Glu Arg Ile Arg Lys Phe Gln Ile Leu Asn Asp Glu Ile Ile Thr				
1205	1210	1215	1220	
atc ctg gat aag tac ctg aag tca ggc gac ggg gag ggc acg cca gtg				3989
Ile Leu Asp Lys Tyr Leu Lys Ser Gly Asp Gly Glu Gly Thr Pro Val				
1221	1226	1231	1236	
gag cat gtg cgc tgc ttc cag ccg ccc atc cac cag tcc ctc gcc agc				4037
Glu His Val Arg Cys Phe Gln Pro Pro Ile His Gln Ser Leu Ala Ser				
1237	1242	1247	1252	
agc tga gggcacgcgc tgcaactccgt aactcaacat ggcacatgcctt tctctccgt				4093
Ser *				
1253				
aactatTTAG TgAGATTTT AGGGACTATT TTTCAGTATC TCTGTACCTG TTAAAGGGGG				4153
TGCTTTTCGA TCTAAAAACT TAATTTATA AAATTGACTT ATTTTCTAG ACTAAAATTG				4213
TATATGCTTT TGGAATTAG GAACTCTTGA GAATATTGGC TGCTGATTGT TGCCATCACG				4273
TTCCCTACAAA ATTGTTTTC TATGGGATGT TCTGGCAGCT GTGTCAAAA ATGCTGCTGG				4333
GTCATTATCAT TCATTCATA AGAAAACCTAA TACCAAGCAAA TGCATTAAT CCCTTGCCAG				4393
TTACCACTAA CTGTAACTAT TTGCTTTG TTAGGGATC TTCTGTATGG TCTTTATGA				4453
GCAATCTTAG TTCTAAGTCA TTGTTCCAT CCCTTTTG TGTGTTCAAG AAAATAGTGA				4513
ACTTGATTCC CCTGCTTCCA CTAATCCAG TTGTGACAAA ATCTAACGTG ACATCAGATC				4573
GAAAGGTTAT AGAAATAAAA CTAATGAGAT CTAATGAGAT AAAAAA				4618

<211> 4244

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (230)..(2311)

<400> 151

gcacgagccc tgccgggtgg aaccgaggcg gcggcggccg tggcgcggcg tggcgcggga 60

gggacgggtgg agacggctgc octagtggga gaggcggcgc ggccgcgatg aggaggaggg 120

tgaagcggcg gcgtcgaagg agaatgcttg gacagaagag atgactata tttccactaa 180

ggcctataat tgcctactgt acaaatagtc ctgatcaggc aatatacga atg gcc 235
Met Ala
1

caa gga agc cac caa att gat ttt cag gtt tta cat gac ctg cga caa 283
Gln Gly Ser His Gln Ile Asp Phe Gln Val Leu His Asp Leu Arg Gln

3 8 13 18

aaa ttc cct gaa gta cct gaa gtt gtt gta tcc agg tgc atg tta cag 331
Lys Phe Pro Glu Val Pro Glu Val Val Val Ser Arg Cys Met Leu Gln
19 24 29 34

aat aat aat aac ctg gat gcc tgc tgt gct gtt ctc tct cag gag agt 379
Asn Asn Asn Leu Asp Ala Cys Cys Ala Val Leu Ser Gln Glu Ser
35 40 45 50

aca aga tat ctt tat ggt gaa gga gac ttg aat ttt tca gat gat tct 427
Thr Arg Tyr Leu Tyr Gly Glu Asp Leu Asn Phe Ser Asp Asp Ser
51 56 61 66

gga att tct ggt cta cgc aat cac atg act tct ctc aac ttg gac ttg 475
Gly Ile Ser Gly Leu Arg Asn His Met Thr Ser Leu Asn Leu Asp Leu
67 72 77 82

caa tca cag aac att tac cac cat gga aga gaa ggg agt agg atg aat 523
Gln Ser Gln Asn Ile Tyr His His Gly Arg Glu Gly Ser Arg Met Asn
83 88 93 98

gga agt agg act cta acg cac agc att agt gat gga caa ctt caa ggt 571
Gly Ser Arg Thr Leu Thr His Ser Ile Ser Asp Gly Gln Leu Gln Gly
99 104 109 114

ggc cag tcc aat agt gaa cta ttt cag cag gag cca cag aca gca cca 619
Gly Gln Ser Asn Ser Glu Leu Phe Gln Gln Glu Pro Gln Thr Ala Pro
115 120 125 130

gct caa gtt cct caa ggc ttt aat gtt ttt gga atg tcc agt tcc tct 667
Ala Gln Val Pro Gln Gly Phe Asn Val Phe Gly Met Ser Ser Ser Ser
131 136 141 146

ggt gct tca aat tca gca cca cat ctt gga ttt cac tta ggc agc aaa 715
Gly Ala Ser Asn Ser Ala Pro His Leu Gly Phe His Leu Gly Ser Lys

147	152	157	162	
gga aca tct agc ctt tct caa caa act ccc aga ttt aat ccc att atg Gly Thr Ser Ser Leu Ser Gln Gln Thr Pro Arg Phe Asn Pro Ile Met				763
163	168	173	178	
gta act tta gcc cca aat atc cag act ggt cgt aat act cct aca tct Val Thr Leu Ala Pro Asn Ile Gln Thr Gly Arg Asn Thr Pro Thr Ser				811
179	184	189	194	
ttg cac ata cat ggt gta cct cca cct gta ctt aac agt cca cag gga Leu His Ile His Gly Val Pro Pro Pro Val Leu Asn Ser Pro Gln Gly				859
195	200	205	210	
aat tct atc tat att agg cct tac att aca act cct ggt ggt aca act Asn Ser Ile Tyr Ile Arg Pro Tyr Ile Thr Thr Pro Gly Gly Thr Thr				907
211	216	221	226	
cga cag aca caa cag cat tct ggc tgg gta tct cag ttt aat ccc atg Arg Gln Thr Gln Gln His Ser Gly Trp Val Ser Gln Phe Asn Pro Met				955
227	232	237	242	
aac cct cag caa gtt tat cag cct tca cag cct ggt ccc tgg act act Asn Pro Gln Gln Val Tyr Gln Pro Ser Gln Pro Gly Pro Trp Thr Thr				1003
243	248	253	258	
tgt cct gca tct aat cct ctg tca cat acc tca tct caa cag cca aat Cys Pro Ala Ser Asn Pro Leu Ser His Thr Ser Ser Gln Gln Pro Asn				1051
259	264	269	274	
cag caa ggc cac cag acc tct cat gtc tac atg cca atc agt tca cct Gln Gln Gly His Gln Thr Ser His Val Tyr Met Pro Ile Ser Ser Pro				1099
275	280	285	290	
act act tca caa cca cca acc att cat tca tct ggt agc tca cag tct Thr Thr Ser Gln Pro Pro Thr Ile His Ser Ser Gly Ser Ser Gln Ser				1147
291	296	301	306	
tct gcc cat agc caa tat aac att cag aat att tca aca gga cct cga Ser Ala His Ser Gln Tyr Asn Ile Gln Asn Ile Ser Thr Gly Pro Arg				1195
307	312	317	322	
aaa aac cag att gaa atc aaa ctt gaa ccc cca caa aga aat aat tct Lys Asn Gln Ile Glu Ile Lys Leu Glu Pro Pro Gln Arg Asn Asn Ser				1243
323	328	333	338	
tca aaa ctg cgt tct tct gga cct cga acc tcc agc act tcc tct tca Ser Lys Leu Arg Ser Ser Gly Pro Arg Thr Ser Ser Thr Ser Ser Ser				1291
339	344	349	354	
gtc aat agc cag acc tta aac aga aat cag ccc act gtt tac ata gct Val Asn Ser Gln Thr Leu Asn Arg Asn Gln Pro Thr Val Tyr Ile Ala				1339
355	360	365	370	
gcc agc ccc cca aat acg gat gag ctg atg tcc cgt agt caa cct aag Ala Ser Pro Pro Asn Thr Asp Glu Leu Met Ser Arg Ser Gln Pro Lys				1387 /
371	376	381	386	

gtc tat att tca gcg aat gct gcc aca gga gat gaa cag gtc atg cgg Val Tyr Ile Ser Ala Asn Ala Ala Thr Gly Asp Glu Gln Val Met Arg 387 392 397 402	1435
aat cag ccc aca ctc ttc ata tcc aca aac tct gga gca tct gct gcc Asn Gln Pro Thr Leu Phe Ile Ser Thr Asn Ser Gly Ala Ser Ala Ala 403 408 413 418	1483
tcc agg aac atg tct ggg caa gtg agc atg ggt cct gcc ttt att cat Ser Arg Asn Met Ser Gly Gln Val Ser Met Gly Pro Ala Phe Ile His 419 424 429 434	1531
cac cat cct ccc aaa agt cga gca ata ggc aat aac tct gca acc tct His His Pro Pro Lys Ser Arg Ala Ile Gly Asn Asn Ser Ala Thr Ser 435 440 445 450	1579
cct cga gtg gta gtc act cag ccc aat acg aaa tac act ttc aaa att Pro Arg Val Val Val Thr Gln Pro Asn Thr Lys Tyr Thr Phe Lys Ile 451 456 461 466	1627
aca gtc tct ccc aat aag ccc cct gca gtt tca cca ggg gtg gtg tcc Thr Val Ser Pro Asn Lys Pro Pro Ala Val Ser Pro Gly Val Val Ser 467 472 477 482	1675
cct acc ttt gaa ctt aca aat ctt ctt aat cat cct gat cat tat gta Pro Thr Phe Glu Leu Thr Asn Leu Leu Asn His Pro Asp His Tyr Val 483 488 493 498	1723
gaa acc gag aat att cag cac ctc acg gac cct aca tta gca cat gtg Glu Thr Glu Asn Ile Gln His Leu Thr Asp Pro Thr Leu Ala His Val 499 504 509 514	1771
gat aga ata agt gaa aca cgg aaa ctg agt atg gga tct gat gat gct Asp Arg Ile Ser Glu Thr Arg Lys Leu Ser Met Gly Ser Asp Asp Ala 515 520 525 530	1819
gcc tac aca caa gct ctt ttg gta cac cag aag gcc aga atg gaa cga Ala Tyr Thr Gln Ala Leu Leu Val His Gln Lys Ala Arg Met Glu Arg 531 536 541 546	1867
ctt caa aga gaa ctt gag att caa aag aaa aag ctg gat aaa tta aaa Leu Gln Arg Glu Leu Glu Ile Gln Lys Lys Lys Leu Asp Lys Leu Lys 547 552 557 562	1915
tct gag gtt aat gaa atg gaa aat aat cta act cga agg cgc ctg aaa Ser Glu Val Asn Glu Met Glu Asn Asn Leu Thr Arg Arg Arg Leu Lys 563 568 573 578	1963
aga tca aat tct ata tcc cag ata cct tcc ctt gaa gaa atg cag cag Arg Ser Asn Ser Ile Ser Gln Ile Pro Ser Leu Glu Glu Met Gln Gln 579 584 589 594	2011
ctg aga agt tgt aat aga caa ctc cag att gac att gac tgc tta acc Leu Arg Ser Cys Asn Arg Gln Leu Gln Ile Asp Ile Asp Cys Leu Thr 595 600 605 610	2059

aaa gaa att gat ctt ttt caa gcc cga gga cca cat ttt aac ccc agc Lys Glu Ile Asp Leu Phe Gln Ala Arg Gly Pro His Phe Asn Pro Ser 611 616 621 626	2107
gct att cat aac ttt tat gac aat att gga ttt gta ggt cct gtg cca Ala Ile His Asn Phe Tyr Asp Asn Ile Gly Phe Val Gly Pro Val Pro 627 632 637 642	2155
cca aaa ccc aaa gat caa agg tcc atc atc aaa aca cca aag act caa Pro Lys Pro Lys Asp Gln Arg Ser Ile Ile Lys Thr Pro Lys Thr Gln 643 648 653 658	2203
gac aca gaa gat gat gag gga gct cag tgg aat tgt acc gcc tgt act Asp Thr Glu Asp Asp Glu Gly Ala Gln Trp Asn Cys Thr Ala Cys Thr 659 664 669 674	2251
ttt ttg aac cat cca gcc tta att cgc tgt gaa cag tgt gag atg cca Phe Leu Asn His Pro Ala Leu Ile Arg Cys Glu Gln Cys Glu Met Pro 675 680 685 690	2299
agg cat ttc tga gcc aaatggccct gtatcttctc taaaaccaca tctaaagttc Arg His Phe *	2354
691	
aagaaaactag tctgtcatcg ggaaaaagtt tcactgctac ataggatttt gtcaaattga	2414
aggtgtgaca agatgggttt ctgctaattgt taaatgtcag cccacagagc taataatacc	2474
tcaagtataat gtcatgagca gttgaaattc atcacatgaa aagtaatctg ctgaaagact	2534
tggttgccca ctgcctaact gtgtacagt ttaccagtgt cccattatgg ataattctca	2594
atatgttaac accttaggtgt tcccaatacc tttttccct catgtacta ctgaattttg	2654
acaggagggaa ggaatagaat gatacgttgt tttatttgta aagctttcag tgaaacacta	2714
catacacgaa gaaaaggaac aaggtttaac tatttaagaa ccatttgctg ccgcatactg	2774
ccattggata gggaaact tcagaaatct gtggtaactct tggccttgc tttgtcttcc	2834
ctgaacgtgt ctccactctg tgaagccagc atctaggggc taaagatgca aaggaaagca	2894
gcattgcattg tctgtacaaa tggcagcga aataccccaa agctttcct actgtacaga	2954
tctctcgagt ctgcttaag tgatttctt tcttcttgat tattttctta tatttctata	3014
tgtatagtgt aatagccttt tgtaactaa ttttctttt tccttttagt aattaagcac	3074
gatcatgtcc ctttttaagc cttacctgag aggaacaatg cctaaaaata aaaaagcatt	3134
aatgagatga aagtatgcac agaataactt tcctctactt attctgtact ttgcctcat	3194
gagttccaat gttgtgtgaa gacaggcaga tgctgcacag tgaattgcag atgatattac	3254
agaagtgtatg tctgttaggtc acattaaata ctgacttgag cagtgggtga cacaacacag	3314
tgtttgtctt ccacagggaa gcttaaaaaca aaagatattt ttaacccact gacagaacaa	3374

caaggtaag cttcatctgc ttgggtccc acagaacttg cacaaggcgt tgttattggg	3434
aaagtacagt ctcaaaacca gcaacagcag cagtacctac agccctttt ttggagagaa	3494
gtttaaatgc tttactgttg gggcagtc当地 tttctaattcc tgacttggtg acagtatcat	3554
gtgtatttat aaaacaaggc tagccatatt taggacaact gaagaaaagc tggaaaaaaaa	3614
aacaagcaaa cttgaacact gaagcaacct caagcatctc tttatggta tgatataattt	3674
ttgtaaggaa aatattcaga tgatcaggaa tgtatataac tgaaatcaag aaaaagaaca	3734
gtatgcattt aaaaagacag aattatgaaa ttatatgagt gcttagaatg gggctaaggg	3794
aagtgctgaa atagagcaaa ggatgaaaga taatatagac taccacccac tgtaaatgtt	3854
tgcaagtggc tggatggtaa atgggattat tacagttgat ctctatgaat gtcagagccc	3914
taactttcag gctttgcatt ttgtatatgg gaagaaaatat gacaatccta ggtaattaaa	3974
ccatagaccc aaagccctta cgtttgatgc aatttatttt taaaataggc cttgttttc	4034
agcttcatct gcagttctat gtgaagattg ataaatcagt tttacttgt tttattaata	4094
aaacgtaatt tggatatctt gagttgatgg ttttgatgatt tagctggta aactatctt	4154
gtaacagata agttatttat aaaaataaaa aaacttataat tctaaaaaaaaaaaaaaaaaa	4214
aaaaaaaaaaaaaaa aaaagggcgcccccagctta	4244

<210> 152
<211> 2703
<212> DNA
<213> *Homo sapiens*

<220>
<221> CDS
<222> (398) .. (2329)

<400> 152

atttggccct cgaggccaag aattcggcac gagccgtagg ctccttcagg gctgagccat	60
cctgcgtgtc ttgcgctcggtggaaatgcc cagccgaggg acgcgaccag aggacagctc	120
tgtgctgatcccacccgaca attcgaccccc acacaaggag gatctaagca gcaagattaa	180
agaacaaaaattgtggtgg atgaactttc taaccttaag aagaatagga aagtatata	240
gcaacaacag aacagcaata tattcttct tgccagaccga acagaaaatgc tgtctgagag	300
caagaatata ttggatgaac tgaaaaaaga ataccaagaa atagaaaact tagacaagac	360
caaaatcaag aaatagtcaa cctgatttca cataaca atgttgtggcatttgttgt	415

		Met Cys Gly Ile Cys Cys	
		1	
tct gta aac ttt tct gct gag cat ttc agt caa gat tta aaa gag gac Ser Val Asn Phe Ser Ala Glu His Phe Ser Gln Asp Leu Lys Glu Asp	7	12	463
		17	22
tta cta tat aat ctt aaa cag cgg gga ccc aat agt agt aaa caa ttg Leu Leu Tyr Asn Leu Lys Gln Arg Gly Pro Asn Ser Ser Lys Gln Leu	23	28	511
		33	38
tta aag tct gat gtt aac tac cag tgt tta ttt tct gct cac gtc cta Leu Lys Ser Asp Val Asn Tyr Gln Cys Leu Phe Ser Ala His Val Leu	39	44	559
		49	54
cac ttg agg ggt gtt ttg act acc cag cct gtg gaa gat gaa aga ggc His Leu Arg Gly Val Leu Thr Thr Gln Pro Val Glu Asp Glu Arg Gly	55	60	607
		65	70
aat gtg ttt cta tgg aat gga gaa att ttt agt gga ata aag gtt gaa Asn Val Phe Leu Trp Asn Gly Glu Ile Phe Ser Gly Ile Lys Val Glu	71	76	655
		81	86
gct gaa gag aat gac act caa att ttg ttt aat tat ctt tcc tcc tgt Ala Glu Glu Asn Asp Thr Gln Ile Leu Phe Asn Tyr Leu Ser Ser Cys	87	92	703
		97	102
aag aat gaa tct gag att ttg tca ctc ttc tca gaa gta caa ggt ccc Lys Asn Glu Ser Glu Ile Leu Ser Leu Phe Ser Glu Val Gln Gly Pro	103	108	751
		113	118
tgg tca ttt ata tat tat caa gca tct agt cat tat tta tgg ttt ggt Trp Ser Phe Ile Tyr Tyr Gln Ala Ser Ser His Tyr Leu Trp Phe Gly	119	124	799
		129	134
agg gat ttt ttt ggt cgc cgt agc ttg ctt tgg cat ttt agt aat ttg Arg Asp Phe Phe Gly Arg Arg Ser Leu Leu Trp His Phe Ser Asn Leu	135	140	847
		145	150
ggc aag agt ttc tgc ctc tct tca gtt ggc acc caa aca tct gga ttg Gly Lys Ser Phe Cys Leu Ser Ser Val Gly Thr Gln Thr Ser Gly Leu	151	156	895
		161	166
gca aat cag tgg caa gaa gtt cca gca tct gga ctt ttc aga att gat Ala Asn Gln Trp Gln Glu Val Pro Ala Ser Gly Leu Phe Arg Ile Asp	167	172	943
		177	182
ctt aag tct act gtc att tcc aga tgc att att tta caa ctg tat cct Leu Lys Ser Thr Val Ile Ser Arg Cys Ile Ile Leu Gln Leu Tyr Pro	183	188	991
		193	198
tgg aaa tat att tct agg gag aat att att gaa gaa aat gtt aat agc Trp Lys Tyr Ile Ser Arg Glu Asn Ile Ile Glu Glu Asn Val Asn Ser	199	204	1039
		209	214
ctg agt caa att tca gca gac tta cca gca ttt gta tca gtg gta gca Leu Ser Gln Ile Ser Ala Asp Leu Pro Ala Phe Val Ser Val Val Ala			1087

215	220	225	230	
aat gaa gcc aaa ctg tat ctt gaa aaa cct gtt gtc cct tta aat atg Asn Glu Ala Lys Leu Tyr Leu Glu Lys Pro Val Val Pro Leu Asn Met 231	236	241	246	1135
atg ttg cca caa gct gca ttg gag act cat tgc agt aat att tcc aat Met Leu Pro Gln Ala Ala Leu Glu Thr His Cys Ser Asn Ile Ser Asn 247	252	257	262	1183
gtg cca cct aca aga gag ata ctt caa gtc ttt ctt act gat gta cac Val Pro Pro Thr Arg Glu Ile Leu Gln Val Phe Leu Thr Asp Val His 263	268	273	278	1231
atg aag gaa gta att cag cag ttc att gat gtc ctg agt gta gca gtc Met Lys Glu Val Ile Gln Gln Phe Ile Asp Val Leu Ser Val Ala Val 279	284	289	294	1279
aag aaa cgt gtc ttg tgt tta cct agg gat gaa aac ctg aca gca aat Lys Lys Arg Val Leu Cys Leu Pro Arg Asp Glu Asn Leu Thr Ala Asn 295	300	305	310	1327
gaa gtt ttg aaa acg tgt gat agg aaa gca aat gtt gca atc ctg ttt Glu Val Leu Lys Thr Cys Asp Arg Lys Ala Asn Val Ala Ile Leu Phe 311	316	321	326	1375
tct ggg ggc att gat tcc atg gtt att gca acc ctt gct gac cgt cat Ser Gly Gly Ile Asp Ser Met Val Ile Ala Thr Leu Ala Asp Arg His 327	332	337	342	1423
att cct tta gat gaa cca att gat ctt ctt aat gta gct ttc ata gct Ile Pro Leu Asp Glu Pro Ile Asp Leu Leu Asn Val Ala Phe Ile Ala 343	348	353	358	1471
gaa gaa aag acc atg cca act acc ttt aac aga gaa ggg aat aaa cag Glu Glu Lys Thr Met Pro Thr Phe Asn Arg Glu Gly Asn Lys Gln 359	364	369	374	1519
aaa aat aaa tgt gaa ata cct tca gaa gaa ttc tct aaa gat gtt gct Lys Asn Lys Cys Glu Ile Pro Ser Glu Glu Phe Ser Lys Asp Val Ala 375	380	385	390	1567
gct gct gct gac agt cct aat aaa cat gtc agt gta cca gat cga Ala Ala Ala Ala Asp Ser Pro Asn Lys His Val Ser Val Pro Asp Arg 391	396	401	406	1615
atc aca gga agg gcg gga cta aag gaa cta caa gct gtt agc cct tcc Ile Thr Gly Arg Ala Gly Leu Lys Glu Leu Gln Ala Val Ser Pro Ser 407	412	417	422	1663
cga att tgg aat ttt gtt gaa att aat gtt tct atg gaa gaa ctg cag Arg Ile Trp Asn Phe Val Glu Ile Asn Val Ser Met Glu Glu Leu Gln 423	428	433	438	1711
aaa tta aga aga act cga ata tgt cac tta att cgg cca ttg gat aca Lys Leu Arg Arg Thr Arg Ile Cys His His Leu Ile Arg Pro Leu Asp Thr 439	444	449	454	1759

gtt ttg gat gat agc att ggc tgt gca gtc tgg ttt gct tct aga gga Val Leu Asp Asp Ser Ile Gly Cys Ala Val Trp Phe Ala Ser Arg Gly	455	460	465	470	1807
att ggt tgg tta gtg gcc cag gaa gga gtg aaa tcc tat cag agc aat Ile Gly Trp Leu Val Ala Gln Glu Gly Val Lys Ser Tyr Gln Ser Asn	471	476	481	486	1855
gca aag gta gtt ctc act gga att ggt gca gat gag caa ctt gca ggt Ala Lys Val Val Leu Thr Gly Ile Gly Ala Asp Glu Gln Leu Ala Gly	487	492	497	502	1903
tat tct cgt cat cgt gtc cgc ttt cag tcg cat ggg ctg gaa gga ttg Tyr Ser Arg His Arg Val Arg Phe Gln Ser His Gly Leu Glu Gly Leu	503	508	513	518	1951
aat aag gaa ata atg atg gaa ctg ggt cga att tct tct aga aat ctt Asn Lys Glu Ile Met Met Glu Leu Gly Arg Ile Ser Ser Arg Asn Leu	519	524	529	534	1999
ggt cgt gat gac aga gtt att ggt gat cat gga aaa gaa gca aga ttt Gly Arg Asp Asp Arg Val Ile Gly Asp His Gly Lys Glu Ala Arg Phe	535	540	545	550	2047
cct ttc ctg gat gaa aat gtt gtc tcc ttt cta aat tct ctg ccg att Pro Phe Leu Asp Glu Asn Val Val Ser Phe Leu Asn Ser Leu Pro Ile	551	556	561	566	2095
tgg gaa aaa gca aac ttg act tta ccc cga gga att ggt gaa aaa tta Trp Glu Lys Ala Asn Leu Thr Leu Pro Arg Gly Ile Gly Glu Lys Leu	567	572	577	582	2143
ctt tta cgc ctt gca gct gtg gaa ctt ggt ctt aca gcc tct gct ctt Leu Leu Arg Leu Ala Ala Val Glu Leu Gly Leu Thr Ala Ser Ala Leu	583	588	593	598	2191
ctg ccc aaa cgg gcc atg cag ttt gga tca aga att gca aaa atg gaa Leu Pro Lys Arg Ala Met Gln Phe Gly Ser Arg Ile Ala Lys Met Glu	599	604	609	614	2239
aaa att aat gaa aag gca tct gat aaa tgt gga cgg ctc caa atc atg Lys Ile Asn Glu Lys Ala Ser Asp Lys Cys Gly Arg Leu Gln Ile Met	615	620	625	630	2287
tcc tta gaa aat ctt tct att gaa aag gag act aaa ttg taa tggtgatt Ser Leu Glu Asn Leu Ser Ile Glu Lys Glu Thr Lys Leu *	631	636	641		2336
cacaatgtaa caataaaaaa ataagttttt atataattat ataaaaagtaa gatactctgc					2396
tgctttacta ttgtataata tagtagttt aaagttcatt tggttgaatt ttcatttttt					2456
cctgtcacag agcttctaaa accatggaat ttccttagtg atagggata tctttgttg					2516
ttcataataa gccccttttg atcacacctg agtttatgct aatgcggtaa cttagggta					2576

ggtctctaaa tagccttaa cacctgcagc ttggaggcc aaggcagagg gatctttga	2636
gtccaggagt ttgagaacag cctggcaac atgatgaaac ctcatctcta caaaaaaaaa	2696
aaaaaaaaa	2703

<210> 153
 <211> 5092
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (455)..(4195)

<400> 153

ctcagaacaa cgacagcggc cgcctttgt gtttgactca atagcatccg gggatgaaac	60
aggagaacctt ttctgttact gtttcaacac aaaagacagc gcccgcctct ttatataacc	120
caggacgatt ttctgtctta cttgctcacc tcatcatgaa gattttagtag ccattggcta	180
caaggatggc atagtggtga taattgacat cagtaagaaa ggagaaggta ttcataggct	240
tcgaggccat gatgatgaaa tccactccat agcctggtgt cccctgcctg gtgaagattg	300
tttatctata aaccaagagg aaacttcaga agaagctgaa attaccaacg ggaatgctgt	360
agcacaagct ccagtaacaa aaggttgcta cttagccact ggaagcaaag atcaaaccat	420
tcgaatctgg agctgttcta gaggccgagg ggtg atg att ttg aaa ttg ccc	472
Met Ile Leu Lys Leu Pro	
1	

ttt ctg aag aga aga gga ggg ggt ata gac cca act gtt aaa gag cgc	520
Phe Leu Lys Arg Arg Gly Gly Ile Asp Pro Thr Val Lys Glu Arg	
7 12 17 22	

ctt tgg ttg aca ctc cat tgg ccc agc aat caa cca aca cag ctg gta	568
Leu Trp Leu Thr Leu His Trp Pro Ser Asn Gln Pro Thr Gln Leu Val	
23 28 33 38	

tct agc tgt ttt gga ggt gaa ctg ttg caa tgg gat ctc act caa tct	616
Ser Ser Cys Phe Gly Gly Glu Leu Leu Gln Trp Asp Leu Thr Gln Ser	
39 44 49 54	

tgg aga cgg aaa tac acc ctc ttc agt gcc tca tca gaa ggg caa aat	664
Trp Arg Arg Lys Tyr Thr Leu Phe Ser Ala Ser Ser Glu Gly Gln Asn	
55 60 65 70	

cat tca aga att gtg ttt aat tta tgt cct tta caa aca gag gat gac	712
His Ser Arg Ile Val Phe Asn Leu Cys Pro Leu Gln Thr Glu Asp Asp	
71 76 81 86	

aaa cag ctg tta ctt tct aca tca atg gat aga gat gta aaa tgt tgg		760
Lys Gln Leu Leu Leu Ser Thr Ser Met Asp Arg Asp Val Lys Cys Trp		
87	92	97
		102
gac ata gcc acc ttg gag tgc agc tgg acc ctt cct tcc ctt ggt ggg		808
Asp Ile Ala Thr Leu Glu Cys Ser Trp Thr Leu Pro Ser Leu Gly Gly		
103	108	113
		118
ttt gca tac agc ctg gct ttc tct tct gtg gac ata ggc tct ttg gcc		856
Phe Ala Tyr Ser Leu Ala Phe Ser Ser Val Asp Ile Gly Ser Leu Ala		
119	124	129
		134
ata ggt gtt ggg gat ggc atg atc cgt gta tgg aat aca ctc tcc ata		904
Ile Gly Val Gly Asp Gly Met Ile Arg Val Trp Asn Thr Leu Ser Ile		
135	140	145
		150
aag aac aac tat gat gtg aaa aat ttt tgg caa ggc gtg aag tcc aag		952
Lys Asn Asn Tyr Asp Val Lys Asn Phe Trp Gln Gly Val Lys Ser Lys		
151	156	161
		166
gtt aca gcg ctg tgc tgg cac cca acc aag gaa ggt tgc tta gct ttt		1000
Val Thr Ala Leu Cys Trp His Pro Thr Lys Glu Gly Cys Leu Ala Phe		
167	172	177
		182
gga act gat gat gga aaa gtg gga ttg tat gac acc tac tcc aac aag		1048
Gly Thr Asp Asp Gly Lys Val Gly Leu Tyr Asp Thr Tyr Ser Asn Lys		
183	188	193
		198
cct cca cag att tct agc aca tat cat aag aag act gta tat acg tta		1096
Pro Pro Gln Ile Ser Ser Thr Tyr His Lys Lys Thr Val Tyr Thr Leu		
199	204	209
		214
gcc tgg ggg cca cca gta ccc ccc atg tca ctt gga gga gaa gga gac		1144
Ala Trp Gly Pro Pro Val Pro Pro Met Ser Leu Gly Gly Glu Gly Asp		
215	220	225
		230
aga cct tcc ctt gct tta tac agc tgt gga gga gaa ggg att gtc tta		1192
Arg Pro Ser Leu Ala Leu Tyr Ser Cys Gly Gly Glu Gly Ile Val Leu		
231	236	241
		246
cag cat aat ccc tgg aag ctt agt gga gaa gcc ttt gac atc aac aaa		1240
Gln His Asn Pro Trp Lys Leu Ser Gly Glu Ala Phe Asp Ile Asn Lys		
247	252	257
		262
ctc atc agg gac acc aat tca atc aaa tac aaa ttg cct gta cac aca		1288
Leu Ile Arg Asp Thr Asn Ser Ile Lys Tyr Lys Leu Pro Val His Thr		
263	268	273
		278
gag ata agt tgg aaa gca gat ggc aaa atc atg gct ctt ggc aat gaa		1336
Glu Ile Ser Trp Lys Ala Asp Gly Lys Ile Met Ala Leu Gly Asn Glu		
279	284	289
		294
gat gga tca ata gaa ata ttt cag att ccc aac ctg aaa ctg atc tgt		1384
Asp Gly Ser Ile Glu Ile Phe Gln Ile Pro Asn Leu Lys Leu Ile Cys		
295	300	305
		310
act atc caa cag cat cac aag ctt gtg aat acc att agc tgg cat cat		1432

Thr Ile Gln Gln His His Lys Leu Val Asn Thr Ile Ser Trp His His				
311	316	321	326	
gag cat ggc agc cag cca gaa ttg agc tat ctg atg gcc tct ggc tcc				1480
Glu His Gly Ser Gln Pro Glu Leu Ser Tyr Leu Met Ala Ser Gly Ser				
327	332	337	342	
aac aat gca gtc att tac gtg cac aac ctg aag act gtc ata gag agc				1528
Asn Asn Ala Val Ile Tyr Val His Asn Leu Lys Thr Val Ile Glu Ser				
343	348	353	358	
agc cct gag tct cca gtg acc att aca gag ccc tac cgg acc ctc tca				1576
Ser Pro Glu Ser Pro Val Thr Ile Thr Glu Pro Tyr Arg Thr Leu Ser				
359	364	369	374	
ggg cat acg gcc aag att acc agt gtg gcg tgg agc cca cat cat gat				1624
Gly His Thr Ala Lys Ile Thr Ser Val Ala Trp Ser Pro His His Asp				
375	380	385	390	
gga agg ctg gta tct gct tat gat ggt aca gcc cag gtg tgg gat				1672
Gly Arg Leu Val Ser Ala Ser Tyr Asp Gly Thr Ala Gln Val Trp Asp				
391	396	401	406	
gct ctc cg ^g gaa gag ccc ctg tgc aat ttc cga gga cat caa ggt cga				1720
Ala Leu Arg Glu Glu Pro Leu Cys Asn Phe Arg Gly His Gln Gly Arg				
407	412	417	422	
ctg ctt tgt gtg gca tgg tct cct ttg gat cca gac tgc atc tat tca				1768
Leu Leu Cys Val Ala Trp Ser Pro Leu Asp Pro Asp Cys Ile Tyr Ser				
423	428	433	438	
ggg gca gat gac ttt tgt gtg cac aag tgg ctc act tcc atg caa gat				1816
Gly Ala Asp Asp Phe Cys Val His Lys Trp Leu Thr Ser Met Gln Asp				
439	444	449	454	
cat tcc cg ^g cct cct caa ggc aaa aaa agt att gaa ttg gag aaa aaa				1864
His Ser Arg Pro Pro Gln Gly Lys Lys Ser Ile Glu Leu Glu Lys Lys				
455	460	465	470	
cg ^g ctc tct caa cct aag gca aag ccc aaa aag aag aaa aag ccc acc				1912
Arg Leu Ser Gln Pro Lys Ala Lys Pro Lys Lys Lys Lys Pro Thr				
471	476	481	486	
ttg aga act cct gta aag ctg gaa tcg att gat gga aat gaa gaa gaa				1960
Leu Arg Thr Pro Val Lys Leu Glu Ser Ile Asp Gly Asn Glu Glu Glu				
487	492	497	502	
agc atg aag gag aac tca gga cct gtt gag aat ggt gtg tca gac caa				2008
Ser Met Lys Glu Asn Ser Gly Pro Val Glu Asn Gly Val Ser Asp Gln				
503	508	513	518	
gaa ggg gag gag caa gca cg ^g gag ccg gaa tta ccc tgt ggc ctt gct				2056
Glu Gly Glu Glu Gln Ala Arg Glu Pro Glu Leu Pro Cys Gly Leu Ala				
519	524	529	534	
cca gc ^g gtt tct aga gaa cca gtt atc tgc act cca gtt tcc tca ggc				2104
Pro Ala Val Ser Arg Glu Pro Val Ile Cys Thr Pro Val Ser Ser Gly				

535	540	545	550	
ttt gaa aag tca aaa gtc acc att aat aac aaa gtc att tta ctg aaa Phe Glu Lys Ser Lys Val Thr Ile Asn Asn Lys Val Ile Leu Leu Lys 551 556 561 566				2152
aag gag cca cca aaa gag aag cca gaa acc tta atc aag aag aga aaa Lys Glu Pro Pro Lys Glu Lys Pro Glu Thr Leu Ile Lys Lys Arg Lys 567 572 577 582				2200
gct cgt tcc ttg ctt ccc ctg agt aca agc ctg gac cac aga tcc aaa Ala Arg Ser Leu Leu Pro Leu Ser Thr Ser Leu Asp His Arg Ser Lys 583 588 593 598				2248
gag gag ctt cat cag gac tgt ttg gta cta gca act gca aag cac tcc Glu Glu Leu His Gln Asp Cys Leu Val Leu Ala Thr Ala Lys His Ser 599 604 609 614				2296
aga gag ctg aat gaa gat gtg tct gct gat gtt gag gaa aga ttt cat Arg Glu Leu Asn Glu Asp Val Ser Ala Asp Val Glu Glu Arg Phe His 615 620 625 630				2344
ctg ggg ctt ttc aca gac agg gct acc ctg tat aga atg att gat att Leu Gly Leu Phe Thr Asp Arg Ala Thr Leu Tyr Arg Met Ile Asp Ile 631 636 641 646				2392
gaa gga aaa ggt cac tta gaa aat ggc cac cct gag tta ttt cac cag Glu Gly Lys Gly His Leu Glu Asn Gly His Pro Glu Leu Phe His Gln 647 652 657 662				2440
ctt atg ctt tgg aaa ggg gat ctc aaa ggt gtt ctc cag act gca gca Leu Met Leu Trp Lys Gly Asp Leu Lys Gly Val Leu Gln Thr Ala Ala 663 668 673 678				2488
gaa aga ggg gag ctg aca gac aac ctt gtg gct atg gca cca gca gct Glu Arg Gly Glu Leu Thr Asp Asn Leu Val Ala Met Ala Pro Ala Ala 679 684 689 694				2536
ggc tac cat gtg tgg cta tgg gct gtg gaa gct ttt gcc aaa cag ctg Gly Tyr His Val Trp Leu Trp Ala Val Glu Ala Phe Ala Lys Gln Leu 695 700 705 710				2584
tgt ttt cag gat cag tat gtc aag gct gct tct cac cta ctt tcc atc Cys Phe Gln Asp Gln Tyr Val Lys Ala Ala Ser His Leu Leu Ser Ile 711 716 721 726				2632
cac aaa gtg tat gaa gcg gtg gag ctg ctc aag tca aac cat ttt tac His Lys Val Tyr Glu Ala Val Glu Leu Leu Lys Ser Asn His Phe Tyr 727 732 737 742				2680
agg gaa gct att gcg att gcc aag gcc cgg ctg cgc ccg gag gac cca Arg Glu Ala Ile Ala Ile Ala Lys Ala Arg Leu Arg Pro Glu Asp Pro 743 748 753 758				2728
gtc ctg aag gac ttg tac ctc agc tgg gga acc gtc cta gaa aga gat Val Leu Lys Asp Leu Tyr Leu Ser Trp Gly Thr Val Leu Glu Arg Asp 759 764 769 774				2776 /

ggc cac tat gct gta gct gcc aaa tgc tat tta ggg gcc act tgt gct Gly His Tyr Ala Val Ala Ala Lys Cys Tyr Leu Gly Ala Thr Cys Ala 775 780 785 790	2824
tat gat gca gcc aaa gtt ttg gcc aaa aag ggg gat gcg gca tca ctt Tyr Asp Ala Ala Lys Val Leu Ala Lys Lys Gly Asp Ala Ala Ser Leu 791 796 801 806	2872
aga acg gct gca gag ttg gct gcc atc gta gga gag gat gag ttg tct Arg Thr Ala Ala Glu Leu Ala Ala Ile Val Gly Glu Asp Glu Leu Ser 807 812 817 822	2920
gct tcc ctg gct ctc aga tgt gcc caa gag ctg ctt ctg gcc aac aac Ala Ser Leu Ala Leu Arg Cys Ala Gln Glu Leu Leu Ala Asn Asn 823 828 833 838	2968
tgg gtg gga gcc cag gaa gcc ctg cag ctg cat gaa agt cta cag ggt Trp Val Gly Ala Gln Glu Ala Leu Gln Leu His Glu Ser Leu Gln Gly 839 844 849 854	3016
cag aga ttg gtg ttt tgc ctt ctg gag cta ctg tcc agg cat ctg gag Gln Arg Leu Val Phe Cys Leu Leu Glu Leu Leu Ser Arg His Leu Glu 855 860 865 870	3064
gaa aag cag ctt tca gag ggc aaa agc tcc tcc tct tac cac act tgg Glu Lys Gln Leu Ser Glu Gly Lys Ser Ser Ser Tyr His Thr Trp 871 876 881 886	3112
aac acg ggc acc gaa ggg cct ttc gtg gag agg gtg act gca gtg tgg Asn Thr Gly Thr Glu Gly Pro Phe Val Glu Arg Val Thr Ala Val Trp 887 892 897 902	3160
aag agc atc ttc agc ctt gac acc cct gag cag tat cag gaa gcc ttt Lys Ser Ile Phe Ser Leu Asp Thr Pro Glu Gln Tyr Gln Glu Ala Phe 903 908 913 918	3208
cag aag ctg cag aac atc aag tac cca tct gct aca aat aac aca cct Gln Lys Leu Gln Asn Ile Lys Tyr Pro Ser Ala Thr Asn Asn Thr Pro 919 924 929 934	3256
gcc aaa cag ctc ctg ctt cac att tgc cat gac ttg acc ctg gca gtg Ala Lys Gln Leu Leu His Ile Cys His Asp Leu Thr Leu Ala Val 935 940 945 950	3304
ctg agc caa cag atg gcc tcc tgg gac gag gct gtg cag gcg ctc ctt Leu Ser Gln Gln Met Ala Ser Trp Asp Glu Ala Val Gln Ala Leu Leu 951 956 961 966	3352
cgg gcg gtg gtc cgg agc tat gac tca ggg agc ttc acc atc atg cag Arg Ala Val Val Arg Ser Tyr Asp Ser Gly Ser Phe Thr Ile Met Gln 967 972 977 982	3400
gaa gtg tac tca gcc ttt ctc cct gat ggc tgt gac cac cta aga gac Glu Val Tyr Ser Ala Phe Leu Pro Asp Gly Cys Asp His Leu Arg Asp 983 988 993 998	3448

aag ttg ggg gac cat caa tcc cct gcc aca cca gct ttc aaa agt ttg Lys Leu Gly Asp His Gln Ser Pro Ala Thr Pro Ala Phe Lys Ser Leu	3496
999 1004 1009 1014	
 gag gcc ttt ttt ctt tat ggg cgt ctg tat gaa ttc tgg tgg tct ctc Glu Ala Phe Phe Leu Tyr Gly Arg Leu Tyr Glu Phe Trp Trp Ser Leu	3544
1015 1020 1025 1030	
 tcc aga cct tgc cca aat tcc agt gtc tgg gta agg gct ggt cac aga Ser Arg Pro Cys Pro Asn Ser Ser Val Trp Val Arg Ala Gly His Arg	3592
1031 1036 1041 1046	
 aca ctc tct gtt gag cca agc cag cag tta gac act gcc agc act gaa Thr Leu Ser Val Glu Pro Ser Gln Gln Leu Asp Thr Ala Ser Thr Glu	3640
1047 1052 1057 1062	
 gaa acg gac cct gaa act tct cag cca gag cca aac agg cct tca gaa Glu Thr Asp Pro Glu Thr Ser Gln Pro Glu Pro Asn Arg Pro Ser Glu	3688
1063 1068 1073 1078	
 cta=gac ttg aga=ctc aca=gaa gaa ggt=gag cga=atg=ctg agt=act=ttt Leu Asp Leu Arg Leu Thr Glu Glu Gly Glu Arg Met Leu Ser Thr Phe	3736
1079 1084 1089 1094	
 aag gag ctc ttt tca gaa aag cat gcc agt ctc caa aac tca cag aga Lys Glu Leu Phe Ser Glu Lys His Ala Ser Leu Gln Asn Ser Gln Arg	3784
1095 1100 1105 1110	
 act gtt gct gaa gtc caa gag acc ttg gca gaa atg atc cga caa cac Thr Val Ala Glu Val Gln Glu Thr Leu Ala Glu Met Ile Arg Gln His	3832
1111 1116 1121 1126	
 caa aag agt caa ctc tgt aaa tcc aca gca aat ggt cct gat aag aat Gln Lys Ser Gln Leu Cys Lys Ser Thr Ala Asn Gly Pro Asp Lys Asn	3880
1127 1132 1137 1142	
 gaa ccg gaa gta gaa gca gag cag ccc ctc tgc agt tct cag agc cag Glu Pro Glu Val Glu Ala Glu Gln Pro Leu Cys Ser Ser Gln Ser Gln	3928
1143 1148 1153 1158	
 tgt aaa gaa gaa aaa aat gag cca ctt tct ctg cct gag tta acc aaa Cys Lys Glu Glu Lys Asn Glu Pro Leu Ser Leu Pro Glu Leu Thr Lys	3976
1159 1164 1169 1174	
 agg ctt acc gag gca aat cag aga atg gca aaa ttt cct gag agc att Arg Leu Thr Glu Ala Asn Gln Arg Met Ala Lys Phe Pro Glu Ser Ile	4024
1175 1180 1185 1190	
 aag gcc tgg ccc ttc cca gat gtg ctg gag tgc tgc ctc gtc ctg ctt Lys Ala Trp Pro Phe Pro Asp Val Leu Glu Cys Cys Leu Val Leu Leu	4072
1191 1196 1201 1206	
 ctc atc agg tcc cac ttt cct ggc tgt ctg gcc cag gaa atg cag cag Leu Ile Arg Ser His Phe Pro Gly Cys Leu Ala Gln Glu Met Gln Gln	4120
1207 1212 1217 1222	
 cag gcc caa gag ctc ctt cag aaa tac ggc aac acg aaa act tac aga	4168

Gln	Ala	Gln	Glu	Leu	Leu	Gln	Lys	Tyr	Gly	Asn	Thr	Lys	Thr	Tyr	Arg
1223				1228				1233				1238			
aga	cac	tgc	cag	acc	ttc	tgt	atg	tga	attt	cacacac	ttt	gaagaa	actg		4220
Arg	His	Cys	Gln	Thr	Phe	Cys	Met	*							
1239				1244											
ccaaattgaa	aatgttgac	atcttcacc	tctgcagtta	tgcctcacca	gacattcact										4280
ctggcccta	gatgttttg	cagtaatcca	aaagaataca	aacaaggatt	aagtttgaat										4340
caaccctgcc	tacccataga	caacggtgga	tctgactta	gactcaattg	tggtctccta										4400
ctggagggaa	gatcatgaaa	agcccacagt	agttattcag	aactaacacc	tgcagagtgt										4460
tggtcatctc	tacagcctta	ggcaggttc	acccaaagag	gagaaacttc	tgtcgtcacc										4520
caaagtgtta	catgctaaa	acacaagcta	cctttgtaaa	tacttcatct	gatcagaagt										4580
gtgtcatgct	tgttttagat	ggagttgctg	catttttagga	ctattgatac	ctttttttaa										4640
ttgttttat	aatatttaat	ttgaaagagg	agacccttct	ctctctactc	tttcatagac										4700
tgaagtttga	atatgaaata	ggcctaacc	atcatgttga	ctctcctgtc	agaattttag										4760
gttggaaatt	tggtttatt	cttcatgta	attgcttatt	tgaacagatc	acttactaaa										4820
gctttagaag	aagtgattca	aatgtgtgtt	ttcccttcag	ttttataaca	aatggattga										4880
tggcagtcaa	atagctcagg	aataaattac	tgttcaatg	gttcttaaac	tttcttggat										4940
cataggatcc	ttttgagaat	cagattaaag	ccaaagatac	tctttggaga	aaaatgcata										5000
ttcctaattt	tgcatacatg	acctttggat	tattggactc	tgactattgg	gaccctaaat										5060
actatttaat	tataaatctt	tctttctcc	tc												5092

<210> 154
 <211> 2274
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (116)..(460)

<400> 154

taattggag	aatactccag	ccataagatc	tgcata	gcata	ggcttctctg		60
-----------	------------	------------	--------	-------	------------	--	----

gactttgcac	acctccagga	gaagaaccca	gaaaattgat	cagttctaaa	aaacc	atg	118
						Met	
						1	

ccc	cac	ttg	ttg	gtg	act	ttc	agg	gat	gtg	gcc	att	gac	ttc	tct	cag	166
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

Pro	His	Leu	Leu	Val	Thr	Phe	Arg	Asp	Val	Ala	Ile	Asp	Phe	Ser	Gln	
2																
gag	gaa	tgg	gaa	tgc	ctg	gac	cct	gct	cag	agg	gac	ttg	tac	agg	gat	214
Glu	Glu	Trp	Glu	Cys	Leu	Asp	Pro	Ala	Gln	Arg	Asp	Leu	Tyr	Arg	Asp	
18																33
gtg	atg	ttg	gag	aac	tac	agc	aac	ctg	atc	tca	ttg	gac	ttg	gaa	tcc	262
Val	Met	Leu	Glu	Asn	Tyr	Ser	Asn	Leu	Ile	Ser	Leu	Asp	Leu	Glu	Ser	
34																49
agt	tgt	gtg	acc	aaa	aag	tta	tct	cca	gaa	aag	gaa	att	tat	gaa	atg	310
Ser	Cys	Val	Thr	Lys	Lys	Leu	Ser	Pro	Glu	Lys	Glu	Ile	Tyr	Glu	Met	
50																65
gaa	tca	ctc	cag	tgg	gag	aat	atg	ggg	aaa	cgt	atc	aac	cat	cac	ctt	358
Glu	Ser	Leu	Gln	Trp	Glu	Asn	Met	Gly	Lys	Arg	Ile	Asn	His	His	Leu	
66																81
tca	ata	caa	tgg	tct	tgg	aga	caa	tat	gga	gtg	caa	agg	caa	ctt	aga	406
Ser	Ile	Gln	Trp	Ser	Trp	Arg	Gln	Tyr	Gly	Val	Gln	Arg	Gln	Leu	Arg	
82																97
ggg	tca	agt	aag	caa	gtc	aga	agg	gct	tta	cat	gtg	tgt	caa	aat	tac	454
Gly	Ser	Ser	Lys	Gln	Val	Arg	Arg	Ala	Leu	His	Val	Cys	Gln	Asn	Tyr	
98																113
ctg	tga	agaaaaaggcc	actgaaaagtc	attcaacctc	ttctactttt											510
Leu	*															
114																
ttcctaccaa	ggaaaaattg	tcaaatgtaa	ggaatgcaga	caaggtttca	gctacctgtc											570
atgccttatt	caacatgagg	aaaatcataa	tatataaaaa	tgctctgaag	ttaataaaaca											630
caggaatacc	tttagcaaaa	agccaagcta	tatttaacat	cagagaattc	agactgggtg											690
agaaaacctt	tgagtgtatg	gaatgtggaa	aggccttgg	tcgtacttct	gatctcattc											750
aacatcagaa	aattcatact	aatgaaaaac	cttatcagtg	taacgcatgt	gggaaagctt											810
ttattcgtgg	ttcacagctc	actgaacatc	agagagttca	tacaggagag	aaaccatatg											870
attgtaaagaa	atgtggaaaa	gccttttagt	attgtcacaa	tatactcttc	atcagagaat											930
tcatagtgg	gaaaaaccct	atgaatgtaa	gattgtggaa	aggcctttat	cttggctctc											990
aacttactta	ccatcagaga	attcatagtg	gtgagaaacc	ttatgagtgt	aaggaatgtg											1050
gaaaggcctt	tattcttgg	tcacacctta	cataccatca	gagagttcat	actggtgaaa											1110
agccttacat	atgtaaagaa	tgtggaaag	cctttttatg	tgcctcccaa	ctgaatgaac											1170
atcagagaat	tcatacagga	gagaaaccct	atgaatgtaa	agaatgcggg	aagacctttt											1230
ttcgtggctc	acaacttact	taccacctga	gagttcattc	aggtgagaga	ccttataaaat											1290

gcaaagaatg tggaaaagcc tttatttcta attctaatct tattcaacat caaagaattc 1350
 ataccggaga gaagccctac aaatgttaagg aatgtggaaa ggcctttatt tgtggcaaac 1410
 aacttagtga acatcagaga attcatacag gtgagaaacc ctttgaatgt aagaatgtg 1470
 gaaaggcctt tattcgtgtt gcataatctta ctcaacatga gaaaattcat ggtgagaaac 1530
 attatgaatg taaggaatgt gggaaagacct ttgtacgtgc tacacaactt acattatcat 1590
 caaagaattc atacaggtga aaagccctac aaatgttaagg aatgtgacaa ggcctttatt 1650
 tatggctcac aatacttagt gaacatcaga gaattcacag aggtgaaaaa ccttatgaat 1710
 gtaaacagtg tggaaggctt ttattcgtgg ctcacacctt acgaacatct gagaactcat 1770
 actggagaga aaccctatga atgttaaggaa tgtggaggg ccttagtcg tggctcagaa 1830
 catactctgc atcaaaggat ccatactggt gagaaaccct atacatgtgt ccagtgtgg 1890
 aaagacttta gatgtccttc acaacttact caacatacaa ggcttcataa ttgagaaagc 1950
 cttgaatgtg attaaattta agaaaatctt catctatttc atatctataa tgaatgtaga 2010
 acatcttgct tctgctcaga actgctcatt cttagaaggc ctacttaaca tggatgcaga 2070
 ataatttcag aaaccctta aataattcct taacatctt ataaacgcta gaatataatg 2130
 ctgaattata tccttattta agcatcatct ccatttcacc atatcctaac tgaaacccta 2190
 tatatttctt gtgtgttctt ttcttattgt aaatactgtt attgttatttac atgactaaat 2250
 tatattaata ctataattcc ccgg 2274

<210> 155
 <211> 6990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (61)..(2397)

<400> 155
 gggcgccgt tccccggccc ccctcggctt tgccagcgcc gcctgcgagg cggaggcagg 60
 atg aag atg act ggg gat ttc gag gag tgt ctg aag gac tcg ccc cgc 108
 Met Lys Met Thr Gly Asp Phe Glu Glu Cys Leu Lys Asp Ser Pro Arg
 1 5 10 15
 ttc agg gca gct ttg gaa gaa gta gaa ggt gat gtg gca gaa ttg gaa 156
 Phe Arg Ala Ala Leu Glu Glu Val Glu Gly Asp Val Ala Glu Leu Glu
 17 22 27 32

ctt aaa ctt gat aag ctt gtg aaa ctt ggg att gca atg att gat act		204
Leu Lys Leu Asp Lys Leu Val Lys Leu Gly Ile Ala Met Ile Asp Thr		
33	38	43
		48
gga aaa gcc ttt tgt gtt gca aat aaa cag ttc atg aat ggg att cga		252
Gly Lys Ala Phe Cys Val Ala Asn Lys Gln Phe Met Asn Gly Ile Arg		
49	54	59
		64
gac ctg gcc cag tat tct agt aat gat gct gtc gtt gag aca agt ttg		300
Asp Leu Ala Gln Tyr Ser Ser Asn Asp Ala Val Val Glu Thr Ser Leu		
65	70	75
		80
acc aag ttt tct gac agt ctt caa gaa atg ata aat ttt cac aca atc		348
Thr Lys Phe Ser Asp Ser Leu Gln Glu Met Ile Asn Phe His Thr Ile		
81	86	91
		96
ctg ttg cca aac tca gag atc aat tta agg cac agc ttc agt aac ttt		396
Leu Leu Pro Asn Ser Glu Ile Asn Leu Arg His Ser Phe Ser Asn Phe		
97	102	107
		112
gtt aaa gaa gat ctt aga aaa ttc aaa gat=gcc aag aag caa ttt gaa		444
Val Lys Glu Asp Leu Arg Lys Phe Lys Asp Ala Lys Lys Gln Phe Glu		
113	118	123
		128
aaa gtc agt gaa gaa aaa gaa aat gcg tta gta aaa aat gcc caa gta		492
Lys Val Ser Glu Glu Lys Glu Asn Ala Leu Val Lys Asn Ala Gln Val		
129	134	139
		144
caa aga aac aaa caa cat gaa gtt gaa gaa gcc acc aac att ctg aca		540
Gln Arg Asn Lys Gln His Glu Val Glu Ala Thr Asn Ile Leu Thr		
145	150	155
		160
gca aca aga aaa tgt ttc cga cac ata gcc ctc gat tat gtg ctt cag		588
Ala Thr Arg Lys Cys Phe Arg His Ile Ala Leu Asp Tyr Val Leu Gln		
161	166	171
		176
att aat gtt ctt caa tca aaa agg aga tca gaa atc cta aaa tca atg		636
Ile Asn Val Leu Gln Ser Lys Arg Arg Ser Glu Ile Leu Lys Ser Met		
177	182	187
		192
ttg tca ttt atg tat gcc cat ttg gcc ttc ttt cat caa gga tat gat		684
Leu Ser Phe Met Tyr Ala His Leu Ala Phe Phe His Gln Gly Tyr Asp		
193	198	203
		208
ctg ttt agt gaa ctt gga ccc tac atg aag gat ctt ggt gca cag ttg		732
Leu Phe Ser Glu Leu Gly Pro Tyr Met Lys Asp Leu Gly Ala Gln Leu		
209	214	219
		224
gat cga ctg gtt gtg gat gca gca aag gag aaa aga gaa atg gag caa		780
Asp Arg Leu Val Val Asp Ala Ala Lys Glu Lys Arg Glu Met Glu Gln		
225	230	235
		240
aaa cat tcc acc att caa caa aag gat ttc tcc agt gat gat tct aag		828
Lys His Ser Thr Ile Gln Gln Lys Asp Phe Ser Ser Asp Asp Ser Lys		
241	246	251
		256
tta gaa tat aac gta gat gct gca aat ggc ata gtt atg gaa gga tat		876

Leu	Glu	Tyr	Asn	Val	Asp	Ala	Ala	Asn	Gly	Ile	Val	Met	Glu	Gly	Tyr	
257																272
ctg	tgc	aaa	cga	gcc	agc	aat	gcc	ttc	aaa	act	tgg	aac	agg	cgc	tgg	924
Leu	Phe	Lys	Arg	Ala	Ser	Asn	Ala	Phe	Lys	Thr	Trp	Asn	Arg	Arg	Trp	
273																288
ttt	tca	ata	cag	aat	aat	cag	ttg	gtt	tac	cag	aaa	aaa	ttt	aag	gat	972
Phe	Ser	Ile	Gln	Asn	Asn	Gln	Leu	Val	Tyr	Gln	Lys	Lys	Phe	Lys	Asp	
289																304
aat	ccg	act	gtg	gta	gtt	gaa	gac	ctc	agg	ctt	tgc	aca	gtg	aaa	cat	1020
Asn	Pro	Thr	Val	Val	Val	Glu	Asp	Leu	Arg	Leu	Cys	Thr	Val	Lys	His	
305																320
tgt	gaa	gac	ata	gag	cga	cga	ttc	tgc	ttt	gag	gtg	gtc	tcg	cca	aca	1068
Cys	Glu	Asp	Ile	Glu	Arg	Arg	Phe	Cys	Phe	Glu	Val	Val	Ser	Pro	Thr	
321																336
aaa	agt	tgc	atg	ctc	cag	gca	gat	tcc	gaa	aag	ctg	cgc	cag	gca	tgg	1116
Lys	Ser	Cys	Met	Leu	Gln	Ala	Asp	Ser	Glu	Lys	Leu	Arg	Gln	Ala	Trp	
337																352
att	aag	gct	gtt	cag	acc	agt	att	gct	act	gct	tat	aga	gag	aag	ggt	1164
Ile	Lys	Ala	Val	Gln	Thr	Ser	Ile	Ala	Thr	Ala	Tyr	Arg	Glu	Lys	Gly	
353																368
gat	gaa	tca	gag	aag	ctg	gat	aag	aaa	tca	tct	cca	tcc	aca	gga	agc	1212
Asp	Glu	Ser	Glu	Lys	Leu	Asp	Lys	Lys	Ser	Ser	Pro	Ser	Thr	Gly	Ser	
369																384
cta	gat	tct	gga	aat	gag	tcc	aaa	gag	aaa	tta	ttg	aaa	gga	gaa	agt	1260
Leu	Asp	Ser	Gly	Asn	Glu	Ser	Lys	Glu	Lys	Leu	Leu	Lys	Gly	Glu	Ser	
385																400
gcg	ctt	cag	cg	gtc	cag	tgt	atc	cct	ggc	aat	gcc	agc	tgt	tgt	gac	1308
Ala	Leu	Gln	Arg	Val	Gln	Cys	Ile	Pro	Gly	Asn	Ala	Ser	Cys	Cys	Asp	
401																416
tgt	ggc	ctg	gca	gat	cca	cg	tg	gg	gc	atc	aa	ctg	gg	atc	acc	1356
Cys	Gly	Leu	Ala	Asp	Pro	Arg	Trp	Ala	Ser	Ile	Asn	Leu	Gly	Ile	Thr	
417																432
ttg	tgt	atc	gag	tg	tcc	gga	att	cac	cg	agc	ctt	gg	gtt	cat	ttt	1404
Leu	Cys	Ile	Glu	Cys	Ser	Gly	Ile	His	Arg	Ser	Leu	Gly	Val	His	Phe	
433																448
tca	aaa	gta	cga	tct	tta	act	tta	gac	acc	tgg	gag	cca	gaa	ctt	tta	1452
Ser	Lys	Val	Arg	Ser	Leu	Thr	Leu	Asp	Thr	Trp	Glu	Pro	Glu	Leu	Leu	
449																464
aag	ctt	atg	tgt	gag	ttg	gg	aat	gat	gtt	ata	aat	cga	gtt	tat	gaa	1500
Lys	Leu	Met	Cys	Glu	Leu	Gly	Asn	Asp	Val	Ile	Asn	Arg	Val	Tyr	Glu	
465																480
gct	aat	gtg	gaa	aaa	atg	gga	ata	aag	aaa	ccc	caa	cca	gga	caa	aga	1548
Ala	Asn	Val	Glu	Lys	Met	Gly	Ile	Lys	Lys	Pro	Gln	Pro	Gly	Gln	Arg	

481	486	491	496	
cag gag aag gag gca tat atc aga gca aaa tat gtg gag agg aaa ttt Gln Glu Lys Glu Ala Tyr Ile Arg Ala Lys Tyr Val Glu Arg Lys Phe 497 502 507 512				1596
gtg gat aaa tat tct ata tca tta tca cct cct gag cag caa aaa aag Val Asp Lys Tyr Ser Ile Ser Leu Ser Pro Pro Glu Gln Gln Lys Lys 513 518 523 528				1644
ttt gtc tct aaa agt tct gaa gaa aag agg ctg agc att tct aaa ttt Phe Val Ser Lys Ser Ser Glu Glu Lys Arg Leu Ser Ile Ser Lys Phe 529 534 539 544				1692
ggg cca ggg gac caa gtc aga gca tct gcc caa agt tca gtc aga agt Gly Pro Gly Asp Gln Val Arg Ala Ser Ala Gln Ser Ser Val Arg Ser 545 550 555 560				1740
aat gac agt gga att cag cag agc tct gat gat gga aga gaa tct tta Asn Asp Ser Gly Ile Gln Ser Ser Asp Asp Gly Arg Glu Ser Leu 561 566 571 576				1788
ccc tcc acg gtg tca gcc aat agt tta tat gag cct gaa gga gaa agg Pro Ser Thr Val Ser Ala Asn Ser Leu Tyr Glu Pro Glu Gly Glu Arg 577 582 587 592				1836
caa gat tct tct atg ttt ctt gac tcg aaa cat ctt aat cca gga ctt Gln Asp Ser Ser Met Phe Leu Asp Ser Lys His Leu Asn Pro Gly Leu 593 598 603 608				1884
cag ctt tat agg gcg tca tat gaa aaa aac ctt cct aaa atg gct gag Gln Leu Tyr Arg Ala Ser Tyr Glu Lys Asn Leu Pro Lys Met Ala Glu 609 614 619 624				1932
gct ttg gct cat ggt gca gac gtg aac tgg gcc aat tca gag gaa aac Ala Leu Ala His Gly Ala Asp Val Asn Trp Ala Asn Ser Glu Glu Asn 625 630 635 640				1980
aaa gcg aca cca ctt att cag gct gta tta ggg ggc tct ttg gtg acg Lys Ala Thr Pro Leu Ile Gln Ala Val Leu Gly Gly Ser Leu Val Thr 641 646 651 656				2028
tgt gag ttc ctc cta cag aat ggt gct aat gtc aac caa aga gat gtc Cys Glu Phe Leu Leu Gln Asn Gly Ala Asn Val Asn Gln Arg Asp Val 657 662 667 672				2076
caa ggg cgg gga cca ttg cac cat gcc acc gtc tta ggg cac aca ggg Gln Gly Arg Gly Pro Leu His His Ala Thr Val Leu Gly His Thr Gly 673 678 683 688				2124
cag gta tgt tta ttc cta aaa cga ggt gcc aat caa cat gcc act gat Gln Val Cys Leu Phe Leu Lys Arg Gly Ala Asn Gln His Ala Thr Asp 689 694 699 704				2172
gaa gaa ggg aaa gac cct ttg agc ata gct gtg gaa gca gcc aat gct Glu Glu Gly Lys Asp Pro Leu Ser Ile Ala Val Glu Ala Ala Asn Ala 705 710 715 720				2220

gat ata gtc acc ttg tta cgt tta gca aga atg aat gaa gag atg cgg	2268
Asp Ile Val Thr Leu Leu Arg Leu Ala Arg Met Asn Glu Glu Met Arg	
721 726 731 736	
gaa tca gaa gga ctt tat gga cag cca ggt gat gaa act tat cag gac	2316
Glu Ser Glu Gly Leu Tyr Gly Gln Pro Gly Asp Glu Thr Tyr Gln Asp	
737 742 747 752	
ata ttt cgt gat ttt tcc caa atg gca tcc aat aat cca gag aaa cta	2364
Ile Phe Arg Asp Phe Ser Gln Met Ala Ser Asn Asn Pro Glu Lys Leu	
753 758 763 768	
aat cgt ttc cag caa gat tca cag aaa ttc tga atttttt aaaaatggga	2415
Asn Arg Phe Gln Gln Asp Ser Gln Lys Phe *	
769 774 779	
aaatatgaaa tctggtgacc ccotaatgtatcacagctaaa aattcacaat tttttactg	2475
<u>ctttaattct</u> <u>acttaatttt</u> <u>ggttagatatt</u> <u>gaatggcttg</u> <u>gaaaagaggt</u> <u>accattcat</u>	2535
atattttataa attaaaacat agttatctag tagtaggaga ggaacctagt ttaggacctc	2595
tttttattaaa aaagcctatt taaagggcta tttctgtaga cagaagttca gtctagattt	2655
aggccatctc tagttacaa gatgatagga gtttagacaa aagtgattct tttgccaatg	2715
ggtgtggca ttgatttttt tcctccatgc atcttgccta ggatcactca gtcaagcatg	2775
tcttcatcaa gtggaagcca actgtcctgc ctgcctcaag aatatgtgtt ttcttagct	2835
tccctgagga tttttggg ttcagaaata ggtgtgtgt ttgatgtgtt tttggtaacc	2895
tagcttcat acacataata tatgatttat tagaactaga gaatgtgtt tccccgtttg	2955
ttcataaaatg cggtcggta tacttcttag gtgacagggtt attgtccagt actttaatgt	3015
atgtatgtat aatggctgta caggtagacc ataattcagt ccttttagatt tattttatgc	3075
agcaaaaaga agctttttt ttttttaatc aaaaaaaaaa accccagttc aaaatgtgta	3135
gttcttcatt gttgggttga ttccccaaaa cttgacaga tgtatcgatg gaataaaaagt	3195
atgttttaaa ggttacttga atgtcacaaa attatggcct tcacccaaaa ctttaaaggg	3255
aaaatcaatt tataaaatca tgtaggccat ttttatattt gaaatttgc ctttaaaga	3315
tagtttgct gttgctccta gtgaaagaaa aatctctgta caaaggagaa aaagaacccc	3375
acttattctt agttaatact aaaatatata gcaataaaatt gctgtttatt ttttctacat	3435
ctatTTTGTG tacttgcata cagtgtacat tcttttaat tatatcgatg atatagctt	3495
agtattcggt tacatgattc acagacccct gaattccaaa atattatgga taaacattac	3555
catttatatg ctacaaatta gtctgattcc atctttgaaa atgtcttaaa gtataaaata	3615

attaaatgc tttttttttt tttttcccg agatggcgtc ttgctgtgtc acccaggctg 3675
gagtgcaagt gcacgatctc agctcaactgc agcctcctcc tcttgggttc aagcaattct 3735
cctgcctcag cctcccgagt agctggact acaggcaccc gccaccatc cgagctaatt 3795
tctatatttt tagtaaagac gggtttcacc atttggcca gggtggtctc gaactcctga 3855
cctcaggta tcagcctgct ttagcctccc agagtgcgtgg gattacaggc gtgagccacc 3915
gcacccagcc taatttgcct tttgattcct tcccattgtt gtcaaaaatt aagtctattc 3975
ttctttaga aattatatgt aaatgatatt attgataactc tttctaaata agaggttta 4035
aaatatataa aaactttatg atccaattat agataaattt tctaacattt cccagtcact 4095
agggtttat aagttgatta aacatcaa at cagaatctag ccaagcagga attatattga 4155
aataagttca cattacagaa aaggttccat aatttggcca aactgcattgc atgtaatgct 4215
tat tagtaa tggtcaactgt atgttagata aggataaaaa tatatttgc aattacttct 4275
gaggaaatgc taacttccac agcattgtat ttaattataa caataacagg aacattaaat 4335
ctttatctt gctgttcac ctcaaagtca tagatcatct ggcttttag gcacccctcac 4395
taaaggcaaa aatctgattt gtagtttta ttagcatgta cttgaaatt atttgaccaa 4455
gaagctcaaa gaaaagaagt acgttaaaga aaaagaaaaa acctcacttt tcctttatag 4515
tgtcccttcc tgtttaatt ctcaaagatc ctgactttta tctgaggaag tctaggtgt 4575
tttcctttt gatctggcca ttggtgcggt tttcattcag atcacctctg gaatctctgt 4635
ggtgtgaag gcaattcctt atgagactct tgcctcctgt ggcttacgtg atgaattgtt 4695
aatatggcag taattaatta gtatctactt aaatttagtg gtcagaaatg tatttgaagt 4755
gccttaaaga tgatcatggt tcagaatatc ttcagagaaa gcaaaatctt taatattgca 4815
gggagcctag caatacaa at acacattct gtggcttgat ttcttgaata tgctgagacc 4875
caatttggac tacatttggc agaaatcatg gagtaaacag caaggctta aattaaatta 4935
atagttacaa ggttagttgg ctcttaggtg aatttagcca tgtcaactaa tagctttat 4995
atggtagtgc acaaatctga attatgtt at gctgtgaatt attcagtgc ttataagaaa 5055
tcttagttaa tcatgctttt gggcttcatt agtcaatgtg attggccttt tattttctt 5115
ccataactta tctgcttta ttagttctt attccttatt attaatctgt tagcttatt 5175
tcatttagctt actaacttgc aagtttagatt aatataaaaa taagaatagc agcactatga 5235
agagttaata aaatgcaatt tcatgttgc gctagaataa aagtaattga gcagtcattt 5295
gcaaatgctt cattataaca tttatgtgct taagattct aaggtttaa aaagttacct 5355

ttaataacaat ccttagaaac tcagaaattt cctgatattc attagattat ggtgttgcc 5415
taatttatac cggtttcac tgtatattt aatgaacttt gattgggtta ctttccaga 5475
catacagatt taatttggga atatggaact ttgggtcttc atgagtgcattttt 5535
aaaaaaaaagta cacattcaga atctggccaa tttaagtttg tattttaaaa atatttatg 5595
catgttaagt atggtcgcag taaatgaaat tgtgtttaag actaaattta ctaccgtttt 5655
gaacagacat tcccagatca ttcttatattt gtcagataac acttgtgtat aatatcactt 5715
tggaccatgg acatgagctg gaaaaatgat gtattttgt agattgtatg tccagaatga 5775
ctttagaacc gcatgatacg gtgaaaggag cactggacta gtcgtcacta cccttttgg 5835
attcayggctt cttcacaatt aaaatgagtg taatgaaaca aggtgaaaat atagaagcat 5895
ccctttgtat actgtttgc tacttacagt gtacttggca ttgctttatc tcactggattt 5955
ctcatggtag gatttctgag atcttaatct aagctccaaa gttgtctact tttttgatcc 6015
tagggtgctc cttttttttt acagagcagg gtcacttgat ttgcttagctg gtggcagaat 6075
tggcaccatt acccaggtct gactgaccac cagtcagagg cactttattt gtatcatgaa 6135
atgatttgaa atcattgtaa agcagcgaag tctgataatg aatgccagct ttccttgatc 6195
tttgataaca aagactccaa atattctgga gaacctggat aaaagttga agggctagat 6255
tgggatttga agacaaaattt gtaggaaatc ttacattttt gcaataacaa acattaatga 6315
aagcaaaaca ttataaaagt aatttttaattt caccacatac ttatcaattt ctgtatgctt 6375
ccaaatgaca tctacagata tggtttggat gacatctttt tctgtttaca taaattttatc 6435
cactttaaaat gtgataatgt ggagacaaag caagatttga ttacataaaac ttttctctgc 6495
attggtcttt tcactatctt atttgctaac ttttcttattt tttcttcaac ctccccaccc 6555
tccatttttt ggatattaaa cagggaaagc ttgctacatt ataaagattt gttggcaccat 6615
ttatTTTACA caaaggctaa aggttaactt ttggaaatga tgagctactt ttatatatgt 6675
gtttactcat gctttgtat atttctggat cattccagtc ataaagactt attacatgtt 6735
ctatttcttg ctacctgtga aaaggtataat tttaaagaat gtataacaa cagtcattt 6795
actttttattt agtatgtaga ggatttggat ctaattcatg aatgttagtt tacagtagtt 6855
tgtcattgtat aatggagcaa agtacattat cttctaaaat gtacattatg taagaattgt 6915
aaatataactt aagtaattt gatgccaataaa aattacaata agtcaataaa gatctcacct 6975
ctgaaaaaaaaaaaa 6990

<210> 156
<211> 4053
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (409)..(3819)

<220>
<221> misc_feature
<222> (1)...(4053)
<223> n = a,t,c or g

<400> 156

cctaaggccc	taattgaaga	gctgttgcta	tacaagcgct	canaagatca	gatagaactg	60
aaggaaaagc	agttgtcaac	tatgagggtg	gatgtgtgca	gcacagaaac	tctcaaatgc	120
ttaaaagata	aaacaggtgg	gaagaagttc	tccaaagnat	ttgaagaggc	aagctccaag	180
ctggaagaat	tttgtgaatgg	attagatann	caggtgaaaa	acggaccctc	attaacagaa	240
gcactggaaa	atgctggaat	tttcttatgaa	gcacaataca	aagaagtaaa	agtggtggt	300
aatgcataata	aaacctttgc	taaccgagta	aacaatttaa	agaagaagtt	ggatcaattg	360
aagtcaaccc	ttccagatcc	tgaagaatca	ccagttcctt	ccccaaagc	atg gac gct	417
					Met Asp Ala	
				1		

ccc tcc ccg act ggt	tct gag tct cct ttt	cag gga atg gga ggt	gag	465
Pro Ser Pro Thr Gly	Ser Glu Ser Pro Phe	Gln Gly Met Gly Gly	Glu	
4	9	14	19	

gaa tcc cag tca cca acc atg gag agt gag aaa	tct gcc aca cct gaa	513		
Glu Ser Gln Ser Pro Thr Met Glu Ser Glu Lys Ser Ala Thr Pro Glu				
20	25	30	35	

cct gtg aca gat aat cgt gat gtg gaa gac atg gaa ctc tca gat gtg	561			
Pro Val Thr Asp Asn Arg Asp Val Glu Asp Met Glu Leu Ser Asp Val				
36	41	46	51	

gaa gat gat ggg tca aaa atc att gtc gag gac agg aag gaa aaa cct	609			
Glu Asp Asp Gly Ser Lys Ile Ile Val Glu Asp Arg Lys Glu Lys Pro				
52	57	62	67	

gca gag aag tca gct gta tcc act tct gta cct aca aag cca aca gaa	657			
Ala Glu Lys Ser Ala Val Ser Thr Ser Val Pro Thr Lys Pro Thr Glu				
68	73	78	83	

aat atc tca aag gcc tct tca tgt acc cca gtg cct gtg acc atg aca	705			
Asn Ile Ser Lys Ala Ser Ser Cys Thr Pro Val Pro Val Thr Met Thr				
84	89	94	99	

gca act cca cct ctt cca aag cct gtg aat act tct ctt tcc cct tcc		753	
Ala Thr Pro Pro Leu Pro Lys Pro Val Asn Thr Ser Leu Ser Pro Ser			
100	105	110	115
cca gca ttg gct ttg cca aac ctg gct aat gtg gat ctg gca aag atc		801	
Pro Ala Leu Ala Leu Pro Asn Leu Ala Asn Val Asp Leu Ala Lys Ile			
116	121	126	131
agt tcc atc ctt agc agt tta aca tca gtc atg aaa aat act ggg gtc		849	
Ser Ser Ile Leu Ser Ser Leu Thr Ser Val Met Lys Asn Thr Gly Val			
132	137	142	147
agt cct gca tca aga cct tct cca gga acg ccc acc agc ccc agc aac		897	
Ser Pro Ala Ser Arg Pro Ser Pro Gly Thr Pro Thr Ser Pro Ser Asn			
148	153	158	163
ctc acc agt ggc ctg aaa aca cct gca cct gcc acg aca aca tct cac		945	
Leu Thr Ser Gly Leu Lys Thr Pro Ala Pro Ala Thr Thr Ser His			
164	169	174	179
aac cct ctg gca aat atc ctc tcc aag gtg gag atc acc cca gag agc		993	
Asn Pro Leu Ala Asn Ile Leu Ser Lys Val Glu Ile Thr Pro Glu Ser			
180	185	190	195
att ctg tct gca ctt tcc aaa acc cag aca cag tca gcc cct gca ctg		1041	
Ile Leu Ser Ala Leu Ser Lys Thr Gln Thr Gln Ser Ala Pro Ala Leu			
196	201	206	211
caa ggc ctg tca tct tta ctt cag agt gtt act ggg aac cca gtt cca		1089	
Gln Gly Leu Ser Ser Leu Leu Gln Ser Val Thr Gly Asn Pro Val Pro			
212	217	222	227
gcc agt gaa gct gcc tca cag agc act tca gcc tcc cct gcc aac acc		1137	
Ala Ser Glu Ala Ala Ser Gln Ser Thr Ser Ala Ser Pro Ala Asn Thr			
228	233	238	243
aca gtc tct acc ata aag gga aga aat ctg ccc tcc agt gcc caa cct		1185	
Thr Val Ser Thr Ile Lys Gly Arg Asn Leu Pro Ser Ser Ala Gln Pro			
244	249	254	259
ttt att ccc aaa agc ttc aac tat tct cct aac tca tca act tct gaa		1233	
Phe Ile Pro Lys Ser Phe Asn Tyr Ser Pro Asn Ser Ser Thr Ser Glu			
260	265	270	275
gtc tct tca act tca gcc agc aag gcc tca att ggg caa agc cca ggg		1281	
Val Ser Ser Thr Ser Ala Ser Lys Ala Ser Ile Gly Gln Ser Pro Gly			
276	281	286	291
ctc cca agc act act ttt aaa cta cct tcc aac tct ttg ggg ttt aca		1329	
Leu Pro Ser Thr Thr Phe Lys Leu Pro Ser Asn Ser Leu Gly Phe Thr			
292	297	302	307
gct acc cac aat act agc cct gct gcc cca cct act gaa gtt acc atc		1377	
Ala Thr His Asn Thr Ser Pro Ala Ala Pro Pro Thr Glu Val Thr Ile			
308	313	318	323

tgc caa tct tca gag gtc tcc aag cca aag ctg gag tca gag tcc acc			1425
Cys Gln Ser Ser Glu Val Ser Lys Pro Lys Leu Glu Ser Glu Ser Thr			
324	329	334	339
tcc cca agc ctg gaa atg aag att cac aac ttc tta aaa ggt aat cct			1473
Ser Pro Ser Leu Glu Met Lys Ile His Asn Phe Leu Lys Gly Asn Pro			
340	345	350	355
ggt ttc agt ggc tta aac tta aac atc cca atc ctg agc agt ttg ggg			1521
Gly Phe Ser Gly Leu Asn Leu Asn Ile Pro Ile Leu Ser Ser Leu Gly			
356	361	366	371
tcc agc gcc cca tca gag agc cat ccc tca gac ttc cag cgt ggc cct			1569
Ser Ser Ala Pro Ser Glu Ser His Pro Ser Asp Phe Gln Arg Gly Pro			
372	377	382	387
act agc acc tca atc gac aac att gat gga acc cct gta cgg gat gaa			1617
Thr Ser Thr Ser Ile Asp Asn Ile Asp Gly Thr Pro Val Arg Asp Glu			
388	393	398	403
cgg agt ggg aca ccc acc cag gat gag atg atg gac aag ccc aca tcc			1665
Arg Ser Gly Thr Pro Thr Gln Asp Glu Met Met Asp Lys Pro Thr Ser			
404	409	414	419
agc agt gta gat act atg tcc ctg ctt tct aag atc att agc cct ggt			1713
Ser Ser Val Asp Thr Met Ser Leu Leu Ser Lys Ile Ile Ser Pro Gly			
420	425	430	435
tcc tca aca ccc agc agt aca aga tca cca ccc cct ggg aga gat gaa			1761
Ser Ser Thr Pro Ser Ser Thr Arg Ser Pro Pro Pro Gly Arg Asp Glu			
436	441	446	451
agc tac ccc cga gag ctc tcc aat tct gta tct aca tat cga ccc ttt			1809
Ser Tyr Pro Arg Glu Leu Ser Asn Ser Val Ser Thr Tyr Arg Pro Phe			
452	457	462	467
ggt ctg ggc agt gaa tct ccc tat aag cag cct tct gat gga atg gag			1857
Gly Leu Gly Ser Glu Ser Pro Tyr Lys Gln Pro Ser Asp Gly Met Glu			
468	473	478	483
aga cca tct tcc ctg atg gac tct tca cag gaa aag ttc tac cca gat			1905
Arg Pro Ser Ser Leu Met Asp Ser Ser Gln Glu Lys Phe Tyr Pro Asp			
484	489	494	499
act tct ttc caa gaa gat gag gat tac cga gat ttt gag tat tca ggg			1953
Thr Ser Phe Gln Glu Asp Glu Asp Tyr Arg Asp Phe Glu Tyr Ser Gly			
500	505	510	515
cct cca ccc tct gcc atg atg aac cta gag aag aaa cca gcc aaa tct			2001
Pro Pro Pro Ser Ala Met Met Asn Leu Glu Lys Lys Pro Ala Lys Ser			
516	521	526	531
atc ctg aaa tca agc aag ctg tct gat acc acc gag tac cag cca att			2049
Ile Leu Lys Ser Ser Lys Leu Ser Asp Thr Thr Glu Tyr Gln Pro Ile			
532	537	542	547
ctg tcc agt tat agc cac aga gcc caa gaa ttt ggg gta aag tct gcc			2097

Leu Ser Ser Tyr Ser His Arg Ala Gln Glu Phe Gly Val Lys Ser Ala			
548	553	558	563
ttc cct cca tct gta agg gcc ctc ctg gac tct agt gag aac tgt gac			2145
Phe Pro Pro Ser Val Arg Ala Leu Leu Asp Ser Ser Glu Asn Cys Asp			
564	569	574	579
cgt ctc tca tct tcc cct ggg cta ttt ggt gcc ttc agc gta aga ggg			2193
Arg Leu Ser Ser Pro Gly Leu Phe Gly Ala Phe Ser Val Arg Gly			
580	585	590	595
aat gaa cct ggg tct gac cgg tca cca tca ccg agt aag aat gat tca			2241
Asn Glu Pro Gly Ser Asp Arg Ser Pro Ser Pro Ser Lys Asn Asp Ser			
596	601	606	611
ttt ttc acc cct gac tcc aac cac aat agc ttg tctcaa tct acc act			2289
Phe Phe Thr Pro Asp Ser Asn His Asn Ser Leu Ser Gln Ser Thr Thr			
612	617	622	627
ggg cat ctc agt ttg cca cag aag cag tac cca gac tct cct cac cca			2337
Gly His Leu Ser Leu Pro Gln Lys Gln Tyr Pro Asp Ser Pro His Pro			
628	633	638	643
gtc cca cat cgt tcc ctt ttc tct ccg cag aac acc ctt gcc gct ccc			2385
Val Pro His Arg Ser Leu Phe Ser Pro Gln Asn Thr Leu Ala Ala Pro			
644	649	654	659
acg ggt cac cca ccc acg tca ggc gtg gag aaa gtc ctg gcc tcc acc			2433
Thr Gly His Pro Pro Thr Ser Gly Val Glu Lys Val Leu Ala Ser Thr			
660	665	670	675
att tcc acc acg tcg acg att gaa ttt aag aat atg ctt aaa aac gcc			2481
Ile Ser Thr Thr Ser Thr Ile Glu Phe Lys Asn Met Leu Lys Asn Ala			
676	681	686	691
tca cgt aag ccc tca gat gat aag cat ttt ggc cag gct ccc agc aag			2529
Ser Arg Lys Pro Ser Asp Asp Lys His Phe Gly Gln Ala Pro Ser Lys			
692	697	702	707
ggc act cca agt gat ggt gtc agt ctc tca aac ctc acc caa ccc agc			2577
Gly Thr Pro Ser Asp Gly Val Ser Leu Ser Asn Leu Thr Gln Pro Ser			
708	713	718	723
ttg acc gcc act gat cag cag caa caa gaa gag cac tac cgc ata gaa			2625
Leu Thr Ala Thr Asp Gln Gln Gln Glu His Tyr Arg Ile Glu			
724	729	734	739
acc cgc gtc tcc tcc tcc tgc tta gac ttg cct gat agc aca gaa gaa			2673
Thr Arg Val Ser Ser Cys Leu Asp Leu Pro Asp Ser Thr Glu Glu			
740	745	750	755
aag ggg gcc cct ata gaa acc ttg ggt tat cac agt gca tcc aat agg			2721
Lys Gly Ala Pro Ile Glu Thr Leu Gly Tyr His Ser Ala Ser Asn Arg			
756	761	766	771
agg atg tca ggg gag ccg atc cag acc gta gag tcc atc cga gtt cct			2769
Arg Met Ser Gly Glu Pro Ile Gln Thr Val Glu Ser Ile Arg Val Pro			

772	777	782	787	
ggg aag gga aat aga gga cat ggg cgt gag gct tca agg gtg ggt tgg Gly Lys Gly Asn Arg Gly His Gly Arg Glu Ala Ser Arg Val Gly Trp				2817
788 793		798		803
ttt gat ctg agc aca tca ggt agc tct ttt gac aat ggc cct tca agt Phe Asp Leu Ser Thr Ser Gly Ser Ser Phe Asp Asn Gly Pro Ser Ser				2865
804 809		814		819
gcc tct gag ttg gca tcc ctt ggg ggt ggg ggc agc gga ggc ctc act Ala Ser Glu Leu Ala Ser Leu Gly Gly Ser Gly Gly Leu Thr				2913
820 825		830		835
ggc ttt aaa aca gca cca tac aag gaa cgg gca cct caa ttt cag gag Gly Phe Lys Thr Ala Pro Tyr Lys Glu Arg Ala Pro Gln Phe Gln Glu				2961
836 841		846		851
agt gtc ggc cgc ttt cgt tcc aac agt ttc aac tca aca ttt gag cat Ser Val Gly Arg Phe Arg Ser Asn Ser Phe Asn Ser Thr Phe Glu His				3009
852 857		862		867
cat ctt ccc cca tcc ccc ttg gaa cat ggg aca ccc ttc cag aga gag His Leu Pro Pro Ser Pro Leu Glu His Gly Thr Pro Phe Gln Arg Glu				3057
868 873		878		883
cca gtg ggg cca tca tct gcc cca cct gtc cct cct aag gat cat ggt Pro Val Gly Pro Ser Ser Ala Pro Pro Val Pro Pro Lys Asp His Gly				3105
884 889		894		899
ggt atc ttc tct cga gat gca ccc act cat cta ccc tct gtg gat ctt Gly Ile Phe Ser Arg Asp Ala Pro Thr His Leu Pro Ser Val Asp Leu				3153
900 905		910		915
tcg aac ccc ttc aca aag gag gca gcc ctg gcc cat gct gcc cca ccc Ser Asn Pro Phe Thr Lys Glu Ala Ala Leu Ala His Ala Ala Pro Pro				3201
916 921		926		931
cct cct cct gga gag cac agt gga att cct ttc cct acc cca cct cct Pro Pro Pro Gly Glu His Ser Gly Ile Pro Phe Pro Thr Pro Pro Pro				3249
932 937		942		947
cct ccc cct cct ggg gaa cat agc agc agt ggt ggg agt ggt gtc ccc Pro Pro Pro Pro Gly Glu His Ser Ser Ser Gly Gly Ser Gly Val Pro				3297
948 953		958		963
ttt tct act cca ccc cct cct cca ccc cct gtt gac cac tct gga gtt Phe Ser Thr Pro Pro Pro Pro Pro Val Asp His Ser Gly Val				3345
964 969		974		979
gta ccc ttc cca gcc cca cca ctg gca gag cac gga gtg gca ggg gct Val Pro Phe Pro Ala Pro Pro Leu Ala Glu His Gly Val Ala Gly Ala				3393
980 985		990		995
gtg gca gta ttt ccc aag gac cat agt tcc ctc ctt caa ggg acc ctg Val Ala Val Phe Pro Lys Asp His Ser Ser Leu Leu Gln Gly Thr Leu				3441
996 1001		1006		1011

gct gag cat ttt ggg gta ctc cca gga ccc agg gac cac ggg ggc ccc Ala Glu His Phe Gly Val Leu Pro Gly Pro Arg Asp His Gly Gly Pro	3489
1012 1017 1022 1027	
 acc caa cg ^g gac ctc aac gg ^c cct gg ^c ctt agc cgt gta cga gag agc Thr Gln Arg Asp Leu Asn Gly Pro Gly Leu Ser Arg Val Arg Glu Ser	3537
1028 1033 1038 1043	
 ctc acc cta ccc tcc cat tct ctg gaa cac ctg gg ^c cca ccc cat gga Leu Thr Leu Pro Ser His Ser Leu Glu His Leu Gly Pro Pro His Gly	3585
1044 1049 1054 1059	
 gg ^a gg ^a gg ^t gg ^g gg ^a gg ^c agc aac agc agc agt gg ^c ccc ccc ttg gg ^t Gly Gly Gly Gly Ser Asn Ser Ser Gly Pro Pro Leu Gly	3633
1060 1065 1070 1075	
 ccc tca cac aga gac acc atc agc cg ^g agt gg ^t ata atc tta cg ^g agt Pro Ser His Arg Asp Thr Ile Ser Arg Ser Gly Ile Ile Leu Arg Ser	3681
1076 1081 1086 1091	
 ccc cg ^g cca gac ttt cg ^g cct agg gaa cct ttt ctc agc aga gac cca Pro Arg Pro Asp Phe Arg Pro Arg Glu Pro Phe Leu Ser Arg Asp Pro	3729
1092 1097 1102 1107	
 ttt cac agt tta aag aga ccc agg cca cct ttt gct agg gg ^c cct cc ^g Phe His Ser Leu Lys Arg Pro Arg Pro Pro Phe Ala Arg Gly Pro Pro	3777
1108 1113 1118 1123	
 ttc ttt gca cca aaa cg ^c cca ttc ttc cct ccc agg tac tga tg ^g aaac Phe Phe Ala Pro Lys Arg Pro Phe Pro Pro Arg Tyr *	3826
1124 1129 1134	
 caagggaaaag gcattttgaa cagtcttagag aacattggaa gttaggagttt gg ^t ttattgt	3886
tg ^t ttgtttt atttgtttc tctttctcg ^a tttttttttt attataacaa agggcctctc	3946
 ttccaaagta agaaatcaca tacgcttacg ttttactatt caattcaatc ctccctccca	4006
 ttgcacttat ctaccttccc caagttttt gtataaaaaa aaaaaaaaa	4053

<210> 157
<211> 1091
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (112)..(927)

 <400> 157 gctataggag acccaagctg gctagcg ^t ttt aaacttaagc ttgg ^t accga gctcg ^g atcc	60
actagtccag tgtggggaa ttgcgg ^t cg gtagtgccgc gctgtttaaa g atg gcg	117

Met Ala
1

gag gag gaa cct cag cag cag aag cag gag ccg ctg ggc agc gac tcc 165
Ala Glu Glu Pro Gln Gln Lys Gln Glu Pro Leu Gly Ser Asp Ser
3 8 13 18

gaa ggt gtt aac tgt ctg gcc tat gat gaa gcc atc atg gct cag cag 213
Glu Gly Val Asn Cys Leu Ala Tyr Asp Glu Ala Ile Met Ala Gln Gln
19 24 29 34

gac cga att cag caa gag att gct gtg cag aac cct ctg gtg tca gag 261
Asp Arg Ile Gln Gln Glu Ile Ala Val Gln Asn Pro Leu Val Ser Glu
35 40 45 50

cgg ctg gag ctc tcg gtc cta tac aag gag tat gct gaa gat gac aac 309
Arg Leu Glu Leu Ser Val Leu Tyr Lys Glu Tyr Ala Glu Asp Asp Asn
51 56 61 66

atc tat caa cag aag atc aag gac ctc cac aaa aag tac tcg tac atc 357
Ile Tyr Gln Gln Lys Ile Lys Asp Leu His Lys Lys Tyr Ser Tyr Ile
67 72 77 82

cgc aag acc agg cct gac ggc aac tgt ttc tat cgg gct ttc gga ttc 405
Arg Lys Thr Arg Pro Asp Gly Asn Cys Phe Tyr Arg Ala Phe Gly Phe
83 88 93 98

tcc cac ttg gag gca ctg ctg gat gac agc aag gag ttg cag cgg ttc 453
Ser His Leu Glu Ala Leu Leu Asp Asp Ser Lys Glu Leu Gln Arg Phe
99 104 109 114

aag gct gtg tct gcc aag agc aag gaa gac ctg gtg tcc cag ggc ttc 501
Lys Ala Val Ser Ala Lys Ser Lys Glu Asp Leu Val Ser Gln Gly Phe
115 120 125 130

act gaa ttc aca att gag gat ttc cac aac acg ttc atg gac ctg att 549
Thr Glu Phe Thr Ile Glu Asp Phe His Asn Thr Phe Met Asp Leu Ile
131 136 141 146

gag cag gtg gag aag cag acc tct gtc gcc gac ctg ctg gcc tcc ttc 597
Glu Gln Val Glu Lys Gln Thr Ser Val Ala Asp Leu Leu Ala Ser Phe
147 152 157 162

aat gac cag agc acc tcc gac tac ctt gtg gtc tac ctg cgg ctg ctc 645
Asn Asp Gln Ser Thr Ser Asp Tyr Leu Val Val Tyr Leu Arg Leu Leu
163 168 173 178

acc tcg ggc tac ctg cag cgc gag agc aag ttc ttc gag cac ttc atc 693
Thr Ser Gly Tyr Leu Gln Arg Glu Ser Lys Phe Phe Glu His Phe Ile
179 184 189 194

gag ggt gga cgg act gtc aag gag ttc tgc cag cag gag gtg gag ccc 741
Glu Gly Gly Arg Thr Val Lys Glu Phe Cys Gln Gln Glu Val Glu Pro
195 200 205 210

atg tgc aag gag agc gac cac atc cac att gcg ctg gcc cag gcc 789
Met Cys Lys Glu Ser Asp His Ile His Ile Ala Leu Ala Gln Ala

211	216	221	226													
ctc	agc	gtg	tcc	atc	cag	gtg	gag	tac	atg	gac	cgc	ggc	gag	ggc	ggc	837
Leu	Ser	Val	Ser	Ile	Gln	Val	Glu	Tyr	Met	Asp	Arg	Gly	Glu	Gly	Gly	
227															242	
acc	acc	aat	ccg	cac	atc	ttc	cct	gag	ggc	tcc	gag	ccc	aag	gtc	tac	885
Thr	Thr	Asn	Pro	His	Ile	Phe	Pro	Glu	Gly	Ser	Glu	Pro	Lys	Val	Tyr	
243															258	
ctt	ctc	tac	cg	cct	gga	cac	tac	gat	atc	ctc	tac	aaa	tag	ggctggc	934	
Leu	Leu	Tyr	Arg	Pro	Gly	His	Tyr	Asp	Ile	Leu	Tyr	Lys	*			
259														269		
tccagccccgc	tgctgccctg	ctgccccct	ctgccaggcg	ctagacatgt	acagaggttt											994
ttctgtggtt	gtaaatggtc	ctatttcacc	cccttcttcc	tgtcacatga	cccccccccc											1054
atgttttattt	aaagggggtg	ctggtgtga	aaaaaaaa													1091
<hr/>																
<210>	158															
<211>	2418															
<212>	DNA															
<213>	Homo sapiens															
<220>																
<221>	CDS															
<222>	(467)..(2026)															
<400>	158															
gcbcacgtaa	gcttggatcc	tctagagcg	ccgcaataca	tttggctt	gttttca	cacta										60
cttttaagtt	actatcaa	at	ctatacatct	atctcg	tttgc	atgttttta	aatttttattt									120
ttaaaaaacat	ttagtgg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	180
gttagaggaac	ttaaaatgg	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	240
agaaaaca	ac	cg	ca	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	300
aacattccca	gttca	catcac	caac	cc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	360
catccccgaa	cg	gac	cg	gg	ac	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	420
aactgcagac	ttt	aaactcc	tttca	acat	gt	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	tttgc	475
Met	Thr	Cys														
1																
cca	gac	aag	ccg	ggg	cag	ctc	ata	aac	tgg	ttc	atc	tgc	tcc	ctg	tgc	523
Pro	Asp	Lys	Pro	Gly	Gln	Leu	Ile	Asn	Trp	Phe	Ile	Cys	Ser	Leu	Cys	
4	/														19	
9																
gtc	ccg	cg	gt	cg	tg	aa	ctc	tg	ag	ac	cg	cc	ag	ac	cg	571
Val	Pro	Arg	Val	Arg	Lys	Leu	Trp	Ser	Ser	Arg	Arg	Pro	Arg	Thr	Arg	

20	25	30	35	
aga aac ctt ctg ctg ggc act gcg tgt gcc atc tac ttg ggc ttc ctg Arg Asn Leu Leu Leu Gly Thr Ala Cys Ala Ile Tyr Leu Gly Phe Leu	36	41	46	619
gtg agc cag gtg ggg agg gcc tct ctc cag cat gga cag gcg gct gag Val Ser Gln Val Gly Arg Ala Ser Leu Gln His Gly Gln Ala Ala Glu	52	57	62	667
aag ggg cca cat cgc agc cgc gac acc gcc gag cca tcc ttc cct gag Lys Gly Pro His Arg Ser Arg Asp Thr Ala Glu Pro Ser Phe Pro Glu	68	73	78	715
ata ccc ctg gat ggt acc ctg gcc cct cca gag tcc cag ggc aat ggg Ile Pro Leu Asp Gly Thr Leu Ala Pro Pro Glu Ser Gln Gly Asn Gly	84	89	94	763
tcc act ctg cag ccc aat gtg gtg tac att acc cta cgc tcc aag cgc Ser Thr Leu Gln Pro Asn Val Val Tyr Ile Thr Leu Arg Ser Lys Arg	100	105	110	811
agc aag ccg gcc aat atc cgt ggc acc gtg aag ccc aag cgc agg aaa Ser Lys Pro Ala Asn Ile Arg Gly Thr Val Lys Pro Lys Arg Arg Lys	116	121	126	859
aag cat gca gtg gca tcg gct gcc cca ggg cag gag gct ttg gtc gga Lys His Ala Val Ala Ser Ala Ala Pro Gly Gln Glu Ala Leu Val Gly	132	137	142	907
cca tcc ctt cag ccg cag gaa gcg gca agg gaa gct gat gct gta gca Pro Ser Leu Gln Pro Gln Glu Ala Ala Arg Glu Ala Asp Ala Val Ala	148	153	158	955
cct ggg tac gct cag gga gca aac ctg gtt aag att gga gag cga ccc Pro Gly Tyr Ala Gln Gly Ala Asn Leu Val Lys Ile Gly Glu Arg Pro	164	169	174	1003
tgg agg ttg gtg cgg ggt ccg gga gtg cga gcc ggg ggc cca gac ttc Trp Arg Leu Val Arg Gly Pro Gly Val Arg Ala Gly Gly Pro Asp Phe	180	185	190	1051
ctg cag ccc agc tcc agg gag agc aac att agg atc tac agc gag agc Leu Gln Pro Ser Ser Arg Glu Ser Asn Ile Arg Ile Tyr Ser Glu Ser	196	201	206	1099
gcc ccc tcc tgg ctg agc aaa gat gac atc cga aga atg cga ctc ttg Ala Pro Ser Trp Leu Ser Lys Asp Asp Ile Arg Arg Met Arg Leu Leu	212	217	222	1147
gcg gac agc gca gtg gca ggg ctc cgg cct gtg tcc tct agg agc gga Ala Asp Ser Ala Val Ala Gly Leu Arg Pro Val Ser Ser Arg Ser Gly	228	233	238	1195
gcc cgt ttg ctg gtg ctg gag ggg ggc gca cct ggc gct gtg ctc cgc Ala Arg Leu Leu Val Leu Glu Gly Ala Pro Gly Ala Val Leu Arg	244	249	254	1243
				259

tgt ggc cct agc ccc tgt ggg ctt ctc aag cag ccc ttg gac atg agt Cys Gly Pro Ser Pro Cys Gly Leu Leu Lys Gln Pro Leu Asp Met Ser 260 265 270 275	1291
gag gtg ttt gcc ttc cac cta gac agg atc ctg ggg ctc aac agg acc Glu Val Phe Ala Phe His Leu Asp Arg Ile Leu Gly Leu Asn Arg Thr 276 281 286 291	1339
ctg ccg tct gtg agc agg aaa gca gag ttc atc caa gat ggc cgc cca Leu Pro Ser Val Ser Arg Lys Ala Glu Phe Ile Gln Asp Gly Arg Pro 292 297 302 307	1387
tgc ccc atc att ctt tgg gat gca tct tta tct tca gca agt aat gac Cys Pro Ile Ile Leu Trp Asp Ala Ser Leu Ser Ser Ala Ser Asn Asp 308 313 318 323	1435
acc cat tct tct gtt aag ctc acc tgg gga act tat cag cag ttg ctg Thr His Ser Ser Val Lys Leu Thr Trp Gly Thr Tyr Gln Gln Leu Leu 324 329 334 339	1483
aaa cag aaa tgc tgg cag aat ggc cga gta ccc aag cct gaa tca ggt Lys Gln Lys Cys Trp Gln Asn Gly Arg Val Pro Lys Pro Glu Ser Gly 340 345 350 355	1531
tgt act gaa ata cat cat gag tgg tcc aag atg gca ctc ttt gat Cys Thr Glu Ile His His Glu Trp Ser Lys Met Ala Leu Phe Asp 356 361 366 371	1579
ttt ttg tta cag att tat aat cgc tta gat aca aat tgc tgt gga ttc Phe Leu Leu Gln Ile Tyr Asn Arg Leu Asp Thr Asn Cys Cys Gly Phe 372 377 382 387	1627
aga cct cgc aag gaa gat gcc tgt gta cag aat gga ttg agg cca aaa Arg Pro Arg Lys Glu Asp Ala Cys Val Gln Asn Gly Leu Arg Pro Lys 388 393 398 403	1675
tgt gat gac caa ggt tct gcg gct cta gca cac att atc cag cga aag Cys Asp Asp Gln Gly Ser Ala Ala Leu Ala His Ile Ile Gln Arg Lys 404 409 414 419	1723
cat gac cca agg cat ttg gtt ttt ata gac aac aag ggt ttc ttt gac His Asp Pro Arg His Leu Val Phe Ile Asp Asn Lys Gly Phe Phe Asp 420 425 430 435	1771
agg agt gaa gat aac tta aac ttc aaa ttg tta gaa ggc atc aaa gag Arg Ser Glu Asp Asn Leu Asn Phe Lys Leu Leu Glu Gly Ile Lys Glu 436 441 446 451	1819
ttt cca gct tct gca gtt tct ttg aag agc cag cac tta cgg cag Phe Pro Ala Ser Ala Val Ser Val Leu Lys Ser Gln His Leu Arg Gln 452 457 462 467	1867
aaa ctt ctt cag tct ctg ttt ctt gat aaa gtg tat ttg gaa agt caa Lys Leu Leu Gln Ser Leu Phe Leu Asp Lys Val Tyr Trp Glu Ser Gln 468 473 478 483	1915

cctgggttag tctggctgta gcagtgacgc tgccggccca agggctgggg acttggggca	660
ggg atg agg ggg agt agg atg tcc cag ccc ccg cag tgt ctc cgc aga Met Arg Gly Ser Arg Met Ser Gln Pro Pro Gln Cys Leu Arg Arg	708
1 5 10	
gcc caa agc agc tgc tgc cat ttc atg gtg aag ctc ttg gat gat ggg Ala Gln Ser Ser Cys Cys His Phe Met Val Lys Leu Leu Asp Asp Gly	756
16 21 26 31	
act ttc atg atc ccc ggg gag aag gtg gcc cac acc tcg ctg gac gcc Thr Phe Met Ile Pro Gly Glu Lys Val Ala His Thr Ser Leu Asp Ala	804
32 37 42 47	
ctg gtc acc ttc cac cag cag aag cca att gag ccg cgc agg gag ctg Leu Val Thr Phe His Gln Gln Lys Pro Ile Glu Pro Arg Arg Glu Leu	852
48 53 58 63	
ctg aca cag ccc tgc agg cag aag gat ccc gca aac gtg gat tac gag Leu Thr Gln Pro Cys Arg Gln Lys Asp Pro Ala Asn Val Asp Tyr Glu	900
64 69 74 79	
gat ctc ttc ctc tac tcc aac gca gtg gcc gag gaa gct gcc tgc ccg Asp Leu Phe Leu Tyr Ser Asn Ala Val Ala Glu Glu Ala Ala Cys Pro	948
80 85 90 95	
gtg tct gcc cct gag gag gcc tcc cca aag cca gtc ctg tgt cac caa Val Ser Ala Pro Glu Glu Ala Ser Pro Lys Pro Val Leu Cys His Gln	996
96 101 106 111	
tca aag gaa agg aag ccg tca gca gag atg aac aga ata acc acc aag Ser Lys Glu Arg Lys Pro Ser Ala Glu Met Asn Arg Ile Thr Thr Lys	1044
112 117 122 127	
gaa gcc act tcc tcc tgc ccc cca aaa tcc cct ctt gga gag acc cgc Glu Ala Thr Ser Ser Cys Pro Pro Lys Ser Pro Leu Gly Glu Thr Arg	1092
128 133 138 143	
cag aaa ctc tgg agg agc ctc aaa atg ctc ccc gag aga ggc cag agg Gln Lys Leu Trp Arg Ser Leu Lys Met Leu Pro Glu Arg Gly Gln Arg	1140
144 149 154 159	
gtc cgg cag cag cta aaa agc cac ctc gcc act gtg aac ttg tcg tca Val Arg Gln Gln Leu Lys Ser His Leu Ala Thr Val Asn Leu Ser Ser	1188
160 165 170 175	
ctc ttg gat gtc cgg aga tcc acg gtg atc tca ggc cct ggg acc gga Leu Leu Asp Val Arg Arg Ser Thr Val Ile Ser Gly Pro Gly Thr Gly	1236
176 181 186 191	
aaa ggc agc caa gat cac tca ggg gat ccc acc tcg ggg gac aga ggc Lys Gly Ser Gln Asp His Ser Gly Asp Pro Thr Ser Gly Asp Arg Gly	1284
192 197 202 207	
tac acg gat ccc tgt gtg gcc aca tct ctc aaa agc ccc tca cag ccc Tyr Thr Asp Pro Cys Val Ala Thr Ser Leu Lys Ser Pro Ser Gln Pro	1332
208 213 218 223	

cag gca cca aaa gac aga aag gtc ccc acc agg aag gcc gag agg tcg		1380
Gln Ala Pro Lys Asp Arg Lys Val Pro Thr Arg Lys Ala Glu Arg Ser		
224	229	234
gtc agc tgc att gag gtg acc cca ggg gac agg agt tgg cac caa atg		1428
Val Ser Cys Ile Glu Val Thr Pro Gly Asp Arg Ser Trp His Gln Met		
240	245	250
255		
gta gtg aga gcc cta tcc tcc cag gag tcc aag cca gag cac cag ggc		1476
Val Val Arg Ala Leu Ser Ser Gln Glu Ser Lys Pro Glu His Gln Gly		
256	261	266
271		
ttg gca gag cct gag aac gac cag ctc ccg gag gag tac caa caa ccg		1524
Leu Ala Glu Pro Glu Asn Asp Gln Leu Pro Glu Glu Tyr Gln Gln Pro		
272	277	282
287		
cca ccc ttt gcc cct ggg tac tgc tag agaac aggtccaccc tggctctggg		1576
Pro Pro Phe Ala Pro Gly Tyr Cys *		
288	293	
actcgctgcc aggggctgcc acactcctga atgccttaac atttcttcca tggccccaca		1636
ccatggcattc cgggggtctt cgggaaccccg ggaaatggaa taaagatgtt tttggggtct		1696
aaaaaaaaaaa aaaaa		1711

<210> 160
<211> 2487
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (235)..(2469)

<400> 160		
gcacgagtaa ggacagaaaa gtgaaatgca gtaggtgaa gaggataccc tgaatatgta		60
tgaagacatg ctgttgtgag acggagttgt gaaacagagg ccacagaagc tggtgtgaag		120
gcagagcagc atctgctgaa gagacagaaa ccagccccag aggtgtcaca ggaaggcacc		180
agcaaggaca ttggtctttg atttgattca gcagtcctgt caagtataaa tgtg atg		237
Met		
1		
gct gtg ctg cct ggc cct ctg cag ctg gga gtg ctg ctt acc att		285
Ala Val Leu Pro Gly Pro Leu Gln Leu Leu Gly Val Leu Leu Thr Ile		
2	7	12
17		
tcc ctg agt tcc atc agg ctc att cag gct ggt gcc tac tat ggg atc		333
Ser Leu Ser Ser Ile Arg Leu Ile Gln Ala Gly Ala Tyr Tyr Gly Ile		
18	23	28
33		

aag ccg ctg cca cct caa att cct cct cag atg cca cca caa att cca		381
Lys Pro Leu Pro Pro Gln Ile Pro Pro Gln Met Pro Pro Gln Ile Pro		
34	39	44
49		
caa tac cag ccc ctg ggt cag caa gta cct cac atg cct ttg gcc aaa		429
Gln Tyr Gln Pro Leu Gly Gln Gln Val Pro His Met Pro Leu Ala Lys		
50	55	60
65		
gat ggc ctc gcc atg ggc aag gag atg ccc cac ttg cag tat ggc aaa		477
Asp Gly Leu Ala Met Gly Lys Glu Met Pro His Leu Gln Tyr Gly Lys		
66	71	76
81		
gag tat cca cac cta ccc caa tat atg aag gaa att caa ccc ggc cca		525
Glu Tyr Pro His Leu Pro Gln Tyr Met Lys Glu Ile Gln Pro Ala Pro		
82	87	92
97		
aga atg ggc aag gaa gcc gtt ccc aag aaa ggc aaa gaa ata cca tta		573
Arg Met Gly Lys Glu Ala Val Pro Lys Lys Gly Lys Glu Ile Pro Leu		
98	103	108
113		
gcc agt tta cga ggg gaa caa ggt ccc cgt gga gag cct ggc cca aga		621
Ala Ser Leu Arg Gly Glu Gln Gly Pro Arg Gly Glu Pro Gly Pro Arg		
114	119	124
129		
gga cca cct ggg ccc cct ggt tta cca ggt cat ggg ata cct gga att		669
Gly Pro Pro Gly Pro Pro Gly Leu Pro Gly His Gly Ile Pro Gly Ile		
130	135	140
145		
aaa gga aaa cca ggg cca cag gga tat cca gga gtt gga aag cca ggt		717
Lys Gly Lys Pro Gly Pro Gln Gly Tyr Pro Gly Val Gly Lys Pro Gly		
146	151	156
161		
atg cct gga atg cca ggg aag cca gga gcc atg ggc atg cct ggg gca		765
Met Pro Gly Met Pro Gly Lys Pro Gly Ala Met Gly Met Pro Gly Ala		
162	167	172
177		
aaa gga gaa att gga cag aaa ggg gaa att ggg cct atg ggg atc cca		813
Lys Gly Glu Ile Gly Gln Lys Gly Glu Ile Gly Pro Met Gly Ile Pro		
178	183	188
193		
gga cca caa gga cct cca ggg cct cat gga ctt cct ggc att ggg aag		861
Gly Pro Gln Gly Pro Pro Gly Pro His Gly Leu Pro Gly Ile Gly Lys		
194	199	204
209		
cca ggt ggg cca ggg tta cca ggg caa cca gga cca aag ggt gat cga		909
Pro Gly Gly Pro Gly Leu Pro Gly Gln Pro Gly Pro Lys Gly Asp Arg		
210	215	220
225		
gga ccc aaa gga cta cca gga cct caa ggc ctt cgg ggt cct aaa gga		957
Gly Pro Lys Gly Leu Pro Gly Pro Gln Gly Leu Arg Gly Pro Lys Gly		
226	231	236
241		
gac aag ggc ttc ggg atg cca ggt gcg cca ggt gta aag ggg cct cca		1005
Asp Lys Gly Phe Gly Met Pro Gly Ala Pro Gly Val Lys Gly Pro Pro		
242	247	252
257		

ggg atg cac ggc cct ccc ggc cct gtt gga ctg cca gga gtg ggc aaa		1053
Gly Met His Gly Pro Pro Gly Pro Val Gly Leu Pro Gly Val Gly Lys		
258	263	268
268		273
cca gga gtg aca ggc ttc cct ggg ccc cag ggc ccc ctg gga aag cca		1101
Pro Gly Val Thr Gly Phe Pro Gly Pro Gln Gly Pro Leu Gly Lys Pro		
274	279	284
284		289
ggg gct cca gga gaa cct ggg cca caa ggc cct att ggg gta ccc ggg		1149
Gly Ala Pro Gly Glu Pro Gly Pro Gln Gly Pro Ile Gly Val Pro Gly		
290	295	300
300		305
gtt caa gga cct cct ggg ata ccc gga att gga aag cca ggc cag gat		1197
Val Gln Gly Pro Pro Gly Ile Pro Gly Ile Gly Lys Pro Gly Gln Asp		
306	311	316
316		321
ggg atc cca ggc cag cca gga ttt cca ggt ggc aaa ggg gag caa gga		1245
Gly Ile Pro Gly Gln Pro Gly Phe Pro Gly Gly Lys Gly Glu Gln Gly		
322	327	332
332		337
ctg cca ggg cta cca gga ccc cca ggc ctt cca ggg att ggg aaa cca		1293
Leu Pro Gly Leu Pro Gly Pro Pro Gly Leu Pro Gly Ile Gly Lys Pro		
338	343	348
348		353
ggc ttc cca gga ccc aaa ggt gac cgg ggc atg gga ggt gtt cct ggg		1341
Gly Phe Pro Gly Pro Lys Gly Asp Arg Gly Met Gly Gly Val Pro Gly		
354	359	364
364		369
gct ctt gga cca aga ggg gag aaa gga cca ata ggt gcc cca gga ata		1389
Ala Leu Gly Pro Arg Gly Glu Lys Gly Pro Ile Gly Ala Pro Gly Ile		
370	375	380
380		385
ggg ggt cct cca gga gag cca ggc ctg cct gga atc cca ggt cct atg		1437
Gly Gly Pro Pro Gly Glu Pro Gly Leu Pro Gly Ile Pro Gly Pro Met		
386	391	396
396		401
ggc cct cca ggt gct att ggt ttt cct gga ccc aaa gga gaa ggt ggg		1485
Gly Pro Pro Gly Ala Ile Gly Phe Pro Gly Pro Lys Gly Glu Gly Gly		
402	407	412
412		417
att gta ggg cca cag ggg cca cca ggt ccc aag ggt gag cca ggg ctt		1533
Ile Val Gly Pro Gln Gly Pro Pro Gly Pro Lys Gly Glu Pro Gly Leu		
418	423	428
428		433
caa ggc ttc cca gga aag cca ggt ttc ctt ggt gaa gta ggg cct cct		1581
Gln Gly Phe Pro Gly Lys Pro Gly Phe Leu Gly Glu Val Gly Pro Pro		
434	439	444
444		449
ggc atg agg ggt ttc cca ggt ccc ata ggc ccc aag ggg gaa cat ggg		1629
Gly Met Arg Gly Phe Pro Gly Pro Ile Gly Pro Lys Gly Glu His Gly		
450	455	460
460		465
caa aaa ggt gta cca gga ctc cct ggt gtt cca ggg ctt ctc gga cct		1677
Gln Lys Gly Val Pro Gly Leu Pro Gly Val Pro Gly Leu Leu Gly Pro		
466	471	476
476		481
aag gga gaa cca gga atc cca ggg gat cag ggt tta cag ggc ccc cca		1725

Lys	Gly	Glu	Pro	Gly	Ile	Pro	Gly	Asp	Gln	Gly	Leu	Gln	Gly	Pro	Pro
482				487					492					497	
ggt atc cca ggg att ggg ggc cct agt ggc ccc att gga cca cct ggg															1773
Gly	Ile	Pro	Gly	Ile	Gly	Gly	Pro	Ser	Gly	Pro	Ile	Gly	Pro	Pro	Gly
498					503				508					513	
att cca ggc ccc aaa ggg gag cct ggc ctc cca ggg ccc cct ggg ttc															1821
Ile	Pro	Gly	Pro	Lys	Gly	Glu	Pro	Gly	Leu	Pro	Gly	Pro	Pro	Gly	Phe
514					519				524					529	
cct ggt ata ggg aaa ccc gga gtg gca gga ctt cat ggc ccc cca ggg															1869
Pro	Gly	Ile	Gly	Lys	Pro	Gly	Val	Ala	Gly	Leu	His	Gly	Pro	Pro	Gly
530					535				540					545	
aag cct ggt gcc ctt ggt cct caa ggc cag cct ggc ctt cca gga ccc															1917
Lys	Pro	Gly	Ala	Leu	Gly	Pro	Gln	Gly	Gln	Pro	Gly	Leu	Pro	Gly	Pro
546					551				556					561	
cca ggc cct cca gga cct cca gga ccc cca gct gtg atg ccc cct aca															1965
Pro	Gly	Pro	Gly	Pro	Gly	Pro	Gly	Pro	Pro	Ala	Val	Met	Pro	Pro	Thr
562					567				572					577	
cca cca ccc cag gga gag tat ctg cca gat atg ggg ctg gga att gat															2013
Pro	Pro	Pro	Gln	Gly	Tyr	Leu	Pro	Asp	Met	Gly	Leu	Gly	Ile	Asp	
578					583				588					593	
ggc gtg aaa ccc ccc cat gcc tac ggg gct aag aaa ggc aag aat gga															2061
Gly	Val	Lys	Pro	Pro	His	Ala	Tyr	Gly	Ala	Lys	Lys	Gly	Lys	Asn	Gly
594					599				604					609	
ggg cca gcc tat gag atg cct gca ttt acc gcc gag cta acc gca cct															2109
Gly	Pro	Ala	Tyr	Glu	Met	Pro	Ala	Phe	Thr	Ala	Glu	Leu	Thr	Ala	Pro
610					615				620					625	
ttc cca ccg gtg ggg gcc cca gtg aag ttt aac aaa ctg ctg tat aac															2157
Phe	Pro	Pro	Val	Gly	Ala	Pro	Val	Lys	Phe	Asn	Lys	Leu	Leu	Tyr	Asn
626					631				636					641	
ggc aga cag aac tac aac ccg cag aca ggc atc ttc acc tgt gag gtc															2205
Gly	Arg	Gln	Asn	Tyr	Asn	Pro	Gln	Thr	Gly	Ile	Phe	Thr	Cys	Glu	Val
642					647				652					657	
cct ggt gtc tac tac ttt gca tac cac gtt cac tgc aag ggg ggc aac															2253
Pro	Gly	Val	Tyr	Tyr	Phe	Ala	Tyr	His	Val	His	Cys	Lys	Gly	Gly	Asn
658					663				668					673	
gtg tgg gtt gct cta ttc aag aac gag ccc gtg atg tac acg tac															2301
Val	Trp	Val	Ala	Leu	Phe	Lys	Asn	Asn	Glu	Pro	Val	Met	Tyr	Thr	Tyr
674					679				684					689	
gac gag tac aaa aag ggc ttc ctg gac cag gca tct ggg agt gca gtg															2349
Asp	Glu	Tyr	Lys	Lys	Gly	Phe	Leu	Asp	Gln	Ala	Ser	Gly	Ser	Ala	Val
690					695				700					705	
ctg ctg ctc agg ccc gga gac cgg gtg ttc ctc cag atg ccc tca gaa															2397
Leu	Leu	Leu	Arg	Pro	Gly	Asp	Arg	Val	Phe	Leu	Gln	Met	Pro	Ser	Glu

706	711	716	721	
cag gct gca gga ctg tat gcc ggg cag tat gtc cac tcc tcc ttt tca Gln Ala Ala Gly Leu Tyr Ala Gly Gln Tyr Val His Ser Ser Phe Ser				2445
722	727	732	737	
gga tat tta ttg tat ccc atg taa aaacaaaaaaaaaaaaaaa Gly Tyr Leu Leu Tyr Pro Met *				2487
738	743			
<210> 161				
<211> 1718				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (258)..(1697)				
<400> 161				
ttgaacgcct tagtaccgg tccggaattc ccgggtcgac ccacgcgtcc ggtttgccaa				60
tgttggagcc gtctgcaaag tgtccccggc aagaagaggc tgcctaccac aaggacttta				120
gcttacttt taaagattga agaaaaaaaaaa gaagacagaa aaagaagaac tcaaagatac				180
acaaagtaat ttgaaccaag gtcagaagt ttttggagcc gtgagggata cagcagttt				240
gtcaatattt tcttaac atg ctt caa ata aat cag atg ttc tca gtg cag Met Leu Gln Ile Asn Gln Met Phe Ser Val Gln				290
1	5			
ctg agt ctt ggt gag cag aca tgg gaa tcc gaa ggc agc agt ata aag Leu Ser Leu Gly Glu Gln Thr Trp Glu Ser Glu Gly Ser Ser Ile Lys				338
12	17	22	27	
aag gct cag cag gct gtt gcc aat aaa gct ttg act gaa tct acg ctt Lys Ala Gln Gln Ala Val Ala Asn Lys Ala Leu Thr Glu Ser Thr Leu				386
28	33	38	43	
ccc aaa cca gtt cag aag cca ccc aaa agt aat gtt aac aat aac cca Pro Lys Pro Val Gln Lys Pro Pro Lys Ser Asn Val Asn Asn Asn Pro				434
44	49	54	59	
ggc agt ata act cca act gtg gaa ctg aat ggg ctt gct atg aaa agg Gly Ser Ile Thr Pro Thr Val Glu Leu Asn Gly Leu Ala Met Lys Arg				482
60	65	70	75	
gga gag cct gcc atc tac agg cca tta gat cca aag cca ttc cca aat Gly Glu Pro Ala Ile Tyr Arg Pro Leu Asp Pro Lys Pro Phe Pro Asn				530
76	81	86	91	
tat aga gct aat tac aac ttt cgg ggc atg tac aat cag agg tat cat				578

Tyr	Arg	Ala	Asn	Tyr	Asn	Phe	Arg	Gly	Met	Tyr	Asn	Gln	Arg	Tyr	His	
92				97					102				107			
tgc	cca	gtg	cct	aag	atc	ttt	tat	gtt	cag	ctc	act	gta	gga	aat	aat	626
Cys	Pro	Val	Pro	Lys	Ile	Phe	Tyr	Val	Gln	Leu	Thr	Val	Gly	Asn	Asn	
108				113					118				123			
gaa	ttt	ttt	ggg	gaa	gga	aag	act	cga	caa	gct	gct	aga	cac	aat	gct	674
Glu	Phe	Phe	Gly	Glu	Gly	Lys	Thr	Arg	Gln	Ala	Ala	Arg	His	Asn	Ala	
124			129						134				139			
gca	atg	aaa	gcc	ctc	caa	gca	ctg	cag	aat	gaa	cct	att	cca	gaa	aga	722
Ala	Met	Lys	Ala	Leu	Gln	Ala	Leu	Gln	Asn	Glu	Pro	Ile	Pro	Glu	Arg	
140				145					150				155			
tct	cct	cag	aat	ggt	gaa	tca	gga	aag	gat	atg	gat	gat	gac	aaa	gat	770
Ser	Pro	Gln	Asn	Gly	Glu	Ser	Gly	Lys	Asp	Met	Asp	Asp	Asp	Lys	Asp	
156				161					166				171			
gca	aat	aag	tct	gag	atc	agc	tta	gtg	ttt	gaa	att	gct	ctg	aag	cga	818
Ala	Asn	Lys	Ser	Glu	Ile	Ser	Leu	Val	Phe	Glu	Ile	Ala	Leu	Lys	Arg	
172				177					182				187			
aat	atg	cct	gtc	agt	ttt	gag	gtt	att	aaa	gaa	agt	gga	cca	cca	cat	866
Asn	Met	Pro	Val	Ser	Phe	Glu	Val	Ile	Lys	Glu	Ser	Gly	Pro	Pro	His	
188				193					198				203			
atg	aaa	agc	ttt	gtt	act	cga	gtg	tca	gta	gga	gag	ttc	tct	gca	gaa	914
Met	Lys	Ser	Phe	Val	Thr	Arg	Val	Ser	Val	Gly	Glu	Phe	Ser	Ala	Glu	
204				209					214				219			
gga	gaa	gga	aat	agc	aaa	aaa	ctc	tcc	aag	aag	cgc	gct	gcg	acc	acc	962
Gly	Glu	Gly	Asn	Ser	Lys	Lys	Leu	Ser	Lys	Lys	Arg	Ala	Ala	Thr	Thr	
220				225					230				235			
gtc	tta	cag	gag	ctt	aaa	aaa	ctt	cca	cct	ctt	cct	gtg	gtg	gaa	aag	1010
Val	Leu	Gln	Glu	Leu	Lys	Lys	Leu	Pro	Pro	Leu	Pro	Val	Val	Glu	Lys	
236				241					246				251			
cca	aaa	cta	ttt	ttt	aaa	aaa	cgc	cct	aaa	aca	ata	gta	aag	gcc	gga	1058
Pro	Lys	Leu	Phe	Phe	Lys	Lys	Arg	Pro	Lys	Thr	Ile	Val	Lys	Ala	Gly	
252				257					262				267			
cca	gaa	tat	ggc	caa	ggg	atg	aac	cct	att	agc	cgc	ctg	gcg	caa	att	1106
Pro	Glu	Tyr	Gly	Gln	Gly	Met	Asn	Pro	Ile	Ser	Arg	Leu	Ala	Gln	Ile	
268				273					278				283			
caa	cag	gcc	aaa	aag	gaa	aag	gag	ccg	gat	tat	gtt	ttg	ctt	tca	gaa	1154
Gln	Gln	Ala	Lys	Lys	Glu	Lys	Glu	Pro	Asp	Tyr	Val	Leu	Lys	Glu		
284				289					294				299			
aga	gga	atg	cct	cga	cgt	cga	gaa	ttt	gtg	atg	cag	gtg	aag	gta	ggc	1202
Arg	Gly	Met	Pro	Arg	Arg	Arg	Glu	Phe	Val	Met	Gln	Val	Lys	Val	Gly	
300				305					310				315			
aat	gaa	gtt	gct	aca	gga	aca	gga	cct	aat	aaa	aag	ata	gcc	aaa	aaa	1250
Asn	Glu	Val	Ala	Thr	Gly	Thr	Gly	Pro	Asn	Lys	Lys	Ile	Ala	Lys	Lys	

316	321	326	331	
aat gct gca gaa gca atg ctg tta caa ctt ggt tat aaa gca tcc act Asn Ala Ala Glu Ala Met Leu Leu Gln Leu Gly Tyr Lys Ala Ser Thr 332	337	342	347	1298
aat ctt cag gat caa ctt gag aag aca ggg gaa aac aaa gga tgg agt Asn Leu Gln Asp Gln Leu Glu Lys Thr Gly Glu Asn Lys Gly Trp Ser 348	353	358	363	1346
ggt cca aag cct ggg ttt cct gaa cca aca aat aat act cca aaa gga Gly Pro Lys Pro Gly Phe Pro Glu Pro Thr Asn Asn Thr Pro Lys Gly 364	369	374	379	1394
att ctt cat ttg tct cct gat gtt tat caa gag atg gaa gcc agc cgc Ile Leu His Leu Ser Pro Asp Val Tyr Gln Glu Met Glu Ala Ser Arg 380	385	390	395	1442
cac aaa gta atc tct ggc act act cta ggc tat ttg tca ccc aaa gat His Lys Val Ile Ser Gly Thr Thr Leu Gly Tyr Leu Ser Pro Lys Asp 396	401	406	411	1490
atg aac caa cct tca agc tct ttc ttc agt ata tct ccc aca tcg aat Met Asn Gln Pro Ser Ser Phe Phe Ser Ile Ser Pro Thr Ser Asn 412	417	422	427	1538
agt tca gct aca att gcc agg gaa ctc ctt atg aat gga aca tct tct Ser Ser Ala Thr Ile Ala Arg Glu Leu Leu Met Asn Gly Thr Ser Ser 428	433	438	443	1586
aca gct gaa gcc ata ggt tta aaa gga agt tct cct act ccc cct tgt Thr Ala Glu Ala Ile Gly Leu Lys Gly Ser Ser Pro Thr Pro Pro Cys 444	449	454	459	1634
tct cca gta caa cct tca aaa caa ctg gaa tat tta gca agg att caa Ser Pro Val Gln Pro Ser Lys Gln Leu Glu Tyr Leu Ala Arg Ile Gln 460	465	470	475	1682
ggc ttt cag gta tga attaaaagca aaaaaaaaaa a Gly Phe Gln Val *				1718
476				

<210> 162
 <211> 1221
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (263)..(862)

<400> 162

ccgcgcggca attccccgggt cgaccccacgc gtccgggcgc cgagagtaga gaaaaaggggc

60

ctctggtgac cgcccattacc tggcatccct ctaaccagg aggagcgtgg ggaaaggggc	120
tgtgggcctc tcggggagcg agctgcgggt agcggcgcac tgggtacagg cgcgcttg	180
gctgtcgctt ctgccgtgt gtttggagg actcgaactg gcgccaggaa atattaggaa	240
gctgtgattt tcaaagctaa tt atg aaa aca ttt atc att gga atc agt ggt Met Lys Thr Phe Ile Ile Gly Ile Ser Gly	292
1 5	
gtg aca aac agt ggc aaa aca aca ctg gct aag aat ttg cag aaa cac Val Thr Asn Ser Gly Lys Thr Thr Leu Ala Lys Asn Leu Gln Lys His	340
11 16 21 26	
ctc cca aat tgc agt gtc ata tct cag gat gat ttc ttc aag cca gag Leu Pro Asn Cys Ser Val Ile Ser Gln Asp Asp Phe Phe Lys Pro Glu	388
27 32 37 42	
tct gag ata gag aca gat aaa aat gga ttt ttg cag tac gat gtg ctt Ser Glu Ile Glu Thr Asp Lys Asn Gly Phe Leu Gln Tyr Asp Val Leu	436
43 48 53 58	
gaa gca ctt aac atg gaa aaa atg atg tca gcc att tcc tgc tgg atg Glu Ala Leu Asn Met Glu Lys Met Ser Ala Ile Ser Cys Trp Met	484
59 64 69 74	
gaa agc gca aga cac tct gtg gta tca aca gac cag gaa agt gct gag Glu Ser Ala Arg His Ser Val Val Ser Thr Asp Gln Glu Ser Ala Glu	532
75 80 85 90	
gaa att ccc att tta atc atc gaa ggt ttt ctt ctt ttt aat tat aag Glu Ile Pro Ile Leu Ile Ile Glu Gly Phe Leu Leu Phe Asn Tyr Lys	580
91 96 101 106	
ccc ctt gac act ata tgg aat aga agc tat ttc ctg act att cca tat Pro Leu Asp Thr Ile Trp Asn Arg Ser Tyr Phe Leu Thr Ile Pro Tyr	628
107 112 117 122	
gaa gaa tgt aaa agg agg agg agt aca agg gtc tat cag cct cca gac Glu Glu Cys Lys Arg Arg Ser Thr Arg Val Tyr Gln Pro Pro Asp	676
123 128 133 138	
tct ccg gga tac ttt gat ggc cat gtg tgg ccc atg tat cta aag tac Ser Pro Gly Tyr Phe Asp Gly His Val Trp Pro Met Tyr Leu Lys Tyr	724
139 144 149 154	
aga caa gaa atg cag gac atc aca tgg gaa gtt gtg tac ctg gat gga Arg Gln Glu Met Gln Asp Ile Thr Trp Glu Val Val Tyr Leu Asp Gly	772
155 160 165 170	
aca aaa tct gaa gag gac ctc ttt ttg caa gta tat gaa gat cta ata Thr Lys Ser Glu Glu Asp Leu Phe Leu Gln Val Tyr Glu Asp Leu Ile	820
171 176 181 186	
caa gaa cta gca aag caa aag tgt ttg caa gtg aca gca taa agacgga Gln Glu Leu Ala Lys Gln Lys Cys Leu Gln Val Thr Ala *	869

187	192	197		
acacaacaaa	tccttcctga	agtgaattag	gaaactccaa ggagtaattt aagaaccttc	929
accaagatac	aatgtatact	gtggtacaat	gacagccatt gtttcataatg tttgatTTT	989
attgcacatg	gtttcccaa	catgtggAAC	aataaatatc catgccaatg gacaggactg	1049
taccttagca	agttgctccc	tctccaggGA	gcgcataGAT acagcAGAGC tcacAGTgag	1109
tcagaaagtc	tccactttct	gaacataGCT	ctataacaat gattgtcaaa ctTTTctaAC	1169
tggagctcaG	agtaagaaat	aaAGATTACA	tcacaatCCA aaaaaaaaaaa aa	1221

<210> 163
 <211> 2925
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (178)..(2433)

<400> 163				
ttgcttgtcc	accttcCAGC	tttaacgctc	tgcaacaggg tagacaacct cagcgtgttG	60
cagattccct	gcaaggGGGAG	ttagacatct	gagtccTAGA ccgagataacc agctgaagga	120
acgctgcctg	gcgaaccctg	gtgttcaagt	tccagAGGAA cgggatgAGC tccttag	177
atg gaa gat	ctg tcc tct	cca gac tcc acc ctt ctc caa	ggg gga cat	225
Met Glu Asp Leu Ser Ser Pro Asp Ser Thr Leu Leu Gln Gly His				
1	5	10	15	
aat cta ctc tca tca gcc agt ttt cag gaa gCG gtG act ttc aag gat				273
Asn Leu Leu Ser Ser Ala Ser Phe Gln Glu Ala Val Thr Phe Lys Asp	17	22	27	32
gtg ata gtg gac ttt acc cag gaa gaa tgg aaa cag ctg gac cct ggc				321
Val Ile Val Asp Phe Thr Gln Glu Glu Trp Lys Gln Leu Asp Pro Gly	33	38	43	48
cag aga gat ttG ttc agg gat gtG aca ttG gaa aat tat aca cac ctG				369
Gln Arg Asp Leu Phe Arg Asp Val Thr Leu Glu Asn Tyr Thr His Leu	49	54	59	64
gtc tct ata gga ctc caa gtt tct aaa cct gat gtG att tcc cag tta				417
Val Ser Ile Gly Leu Gln Val Ser Lys Pro Asp Val Ile Ser Gln Leu	65	70	75	80
gag caa ggg aca gag cca tgg atc atG gag cca agc att cca gta ggt				465
Glu Gln Gly Thr Glu Pro Trp Ile Met Glu Pro Ser Ile Pro Val Gly	81	86	91	96
acc tgt gca gac tgg gag aca aga ctt gaa aat agt gtG tca gcc cca				513

Thr	Cys	Ala	Asp	Trp	Glu	Thr	Arg	Leu	Glu	Asn	Ser	Val	Ser	Ala	Pro
97				102					107					112	
gag cct gac att tct gaa gaa gag cta tct cca gag gta ata gtg gaa															561
Glu	Pro	Asp	Ile	Ser	Glu	Glu	Glu	Leu	Ser	Pro	Glu	Val	Ile	Val	Glu
113				118					123					128	
aaa cac aaa aga gat gat tct tgg agt tcc aac ttg cta gaa agt tgg															609
Lys	His	Lys	Arg	Asp	Asp	Ser	Trp	Ser	Ser	Asn	Leu	Leu	Glu	Ser	Trp
129				134					139					144	
gaa tat gaa ggc agt tta gag aga cag cag gca aac caa cag aca ctg															657
Glu	Tyr	Glu	Gly	Ser	Leu	Glu	Arg	Gln	Gln	Ala	Asn	Gln	Gln	Thr	Leu
145				150					155					160	
cca aag gaa ata aag gta acc gaa aag aca ata ccc agt tgg gaa aaa															705
Pro	Lys	Glu	Ile	Lys	Val	Thr	Glu	Lys	Thr	Ile	Pro	Ser	Trp	Glu	Lys
161				166					171					176	
ggc cct gta aat aat gaa ttt ggg aaa agt gtc aat gtg agt tca aac															753
Gly	Pro	Val	Asn	Asn	Glu	Phe	Gly	Lys	Ser	Val	Asn	Val	Ser	Ser	Asn
177				182					187					192	
ctt gta aca caa gaa cca tct cca gaa gag acc tct act aaa aga agc															801
Leu	Val	Thr	Gln	Glu	Pro	Ser	Pro	Glu	Glu	Thr	Ser	Thr	Lys	Arg	Ser
193				198					203					208	
atc aaa cag aat tca aac cca gtt aaa aaa gag aaa tct tgt aag tgc															849
Ile	Lys	Gln	Asn	Ser	Asn	Pro	Val	Lys	Lys	Glu	Lys	Ser	Cys	Lys	Cys
209				214					219					224	
aat gaa tgt ggg aaa gcc ttt agt tat tgt tca gct ctt att cgc cat															897
Asn	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Tyr	Cys	Ser	Ala	Leu	Ile	Arg	His
225				230					235					240	
cag aga aca cat act gga gaa aaa ccc tac aaa tgt aat gaa tgt gaa															945
Gln	Arg	Thr	His	Thr	Gly	Glu	Lys	Pro	Tyr	Lys	Cys	Asn	Glu	Cys	Glu
241				246					251					256	
aaa gcc ttc agc cggt gat gaa aac ctt ata aac cat caa aga att cat															993
Lys	Ala	Phe	Ser	Arg	Ser	Glu	Asn	Leu	Ile	Asn	His	Gln	Arg	Ile	His
257				262					267					272	
act gga gat aaa cca tat aaa tgt gat cag tgt gga aaa ggc ttc att															1041
Thr	Gly	Asp	Lys	Pro	Tyr	Lys	Cys	Asp	Gln	Cys	Gly	Lys	Gly	Phe	Ile
273				278					283					288	
gag ggt cca tct ctt act caa cat caa aga att cat act gga gaa aaa															1089
Glu	Gly	Pro	Ser	Leu	Thr	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys
289				294					299					304	
cca tat aaa tgt gat gaa tgt ggg aaa gcc ttt agt cag agg acc cat															1137
Pro	Tyr	Lys	Cys	Asp	Glu	Cys	Gly	Lys	Ala	Phe	Ser	Gln	Arg	Thr	His
305				310					315					320	
ctt gtt cag cat cag aga att cat act ggc gag aag cca tac act tgt															1185
Leu	Val	Gln	His	Gln	Arg	Ile	His	Thr	Gly	Glu	Lys	Pro	Tyr	Thr	Cys

321	326	331	336	
aat gag tgt gga aaa gcc ttt agc cag aga ggc cac ttt atg gaa cat Asn Glu Cys Gly Lys Ala Phe Ser Gln Arg Gly His Phe Met Glu His				1233
337	342	347	352	
cag aaa att cat acg gga gaa aaa cct ttt aaa tgt gat gaa tgt gat Gln Lys Ile His Thr Gly Glu Lys Pro Phe Lys Cys Asp Glu Cys Asp				1281
353	358	363	368	
aaa acc ttc acc agg agc aca cac ctt actcaa cat caa aaa att cat Lys Thr Phe Thr Arg Ser Thr His Leu Thr Gln His Gln Lys Ile His				1329
369	374	379	384	
act gga gaa aaa acc tat aaa tgt aat gaa tgt gga aag gcc ttc aac Thr Gly Glu Lys Thr Tyr Lys Cys Asn Glu Cys Gly Lys Ala Phe Asn				1377
385	390	395	400	
ggg ccc tca act ttt atc cgt cat cat atg att cat act ggt gaa aaa Gly Pro Ser Thr Phe Ile Arg His His Met Ile His Thr Gly Glu Lys				1425
401	406	411	416	
ccg tac gaa tgc aat gaa tgt ggg aaa gcc ttc agc cag cac tca aac Pro Tyr Glu Cys Asn Glu Cys Gly Lys Ala Phe Ser Gln His Ser Asn				1473
417	422	427	432	
ctc act cag cat caa aaa act cat act ggg gag aaa ccc tat gat tgt Leu Thr Gln His Gln Lys Thr His Thr Gly Glu Lys Pro Tyr Asp Cys				1521
433	438	443	448	
gca gaa tgt gga aaa tct ttt agt tac tgg tca tcc ctt gct caa cac Ala Glu Cys Gly Lys Ser Phe Ser Tyr Trp Ser Ser Leu Ala Gln His				1569
449	454	459	464	
ctg aaa att cat act gga gaa aaa cct tac aaa tgc aat gaa tgt gga Leu Lys Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Asn Glu Cys Gly				1617
465	470	475	480	
aag gcc ttc agt tac tgc tca tcc ctt act caa cat cgg aga att cac Lys Ala Phe Ser Tyr Cys Ser Ser Leu Thr Gln His Arg Arg Ile His				1665
481	486	491	496	
acg aga gaa aag ccc ttt gaa tgc agt gaa tgt gga aag gct ttc agt Thr Arg Glu Lys Pro Phe Glu Cys Ser Glu Cys Gly Lys Ala Phe Ser				1713
497	502	507	512	
tat ctc tca aac ctt aat cag cat cag aaa act cat act caa gag aaa Tyr Leu Ser Asn Leu Asn Gln His Gln Lys Thr His Thr Gln Glu Lys				1761
513	518	523	528	
gct tat gaa tgt aaa gaa tgt ggg aaa gct ttt att cgg agt tca tct Ala Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Ile Arg Ser Ser Ser				1809
529	534	539	544	
ctt gct aag cat gaa aga att cat act gga gag aaa ccc tat cag tgt Leu Ala Lys His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Gln Cys				1857
545	550	555	560	

cat gaa tgt ggg aaa acc ttc agt tat ggt tca tcc ctt att cag cat His Glu Cys Gly Lys Thr Phe Ser Tyr Gly Ser Ser Leu Ile Gln His 561 566 571 576	1905
agg aag atc cat act gga gaa cga cct tac aag tgt aat gag tgt ggg Arg Lys Ile His Thr Gly Glu Arg Pro Tyr Lys Cys Asn Glu Cys Gly 577 582 587 592	1953
aga gca ttc aac cag aac ata cac ctt aca cag cat aag aga att cat Arg Ala Phe Asn Gln Asn Ile His Leu Thr Gln His Lys Arg Ile His 593 598 603 608	2001
aca gga gcc aag cct tat gag tgt gct gag tgt ggt aaa gcc ttt cga Thr Gly Ala Lys Pro Tyr Glu Cys Ala Glu Cys Gly Lys Ala Phe Arg 609 614 619 624	2049
cat tgt tca tct ctt gct caa cat caa aaa act cac aca gaa gaa aaa His Cys Ser Ser Leu Ala Gln His Gln Lys Thr His Thr Glu Glu Lys 625 630 635 640	2097
ccc tac cag tgt aat aaa tgt gaa aag acc ttt agc cag agc tcc cat Pro Tyr Gln Cys Asn Lys Cys Glu Lys Thr Phe Ser Gln Ser Ser His 641 646 651 656	2145
cta act cag cat caa cga att cac act ggg gag aag ccc tat aag tgc Leu Thr Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Lys Cys 657 662 667 672	2193
aat gaa tgt gac aaa gcc ttt agc cgg agc act cat ctg act gaa cat Asn Glu Cys Asp Lys Ala Phe Ser Arg Ser Thr His Leu Thr Glu His 673 678 683 688	2241
cag aat act cat act gga gag aaa cct tat aac tgt aat gaa tgc aga Gln Asn Thr His Thr Gly Glu Lys Pro Tyr Asn Cys Asn Glu Cys Arg 689 694 699 704	2289
aag act ttt agc cag agc aca tat ctc att cag cac cag aga att cat Lys Thr Phe Ser Gln Ser Thr Tyr Leu Ile Gln His Gln Arg Ile His 705 710 715 720	2337
tca gga gag aag cct ttt gga tgt aat gat tgt gga aaa tcc ttc aga Ser Gly Glu Lys Pro Phe Gly Cys Asn Asp Cys Gly Lys Ser Phe Arg 721 726 731 736	2385
tat cgc tct gct ctc aac aaa cat cag aga ctg cat cct ggc ata tga Tyr Arg Ser Ala Leu Asn Lys His Gln Arg Leu His Pro Gly Ile *737 742 747 752	2433
caattctagg aacatcataa attagggga gatatttact ttagttgtc ctttgttaa gtactgaaga atcagagtgg attagaaac tgccttgaaa tcttttaat ttctactatc	2493 2553
atgttatgga atggaaagta cattgggctg aactaatcca attgttattt agccactctg	2613
tgacattaga aaactctact gtttaagct ttagttcct ttatggaatg aaggcttgg	2673

agtagattat ttcaaaggta gtttggagtt ttataatcag ttttgtatat ttacaatatt	2733
ttcttgaatg ggtttactat acatcagcat tttgctgtgt tgcacatctaga atgtgtatgt	2793
ttatgcgtgt tttgccaata gaatttgc ttcagtaact agatcgaaaa tctagatgc	2853
tcctggtcta atgcatttac attgtttagg taactggttc ctaataaaaa gaattataaa	2913
ataaaaaaaaaa aa	2925

<210> 164
 <211> 4631
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (184) .. (3003)

<400> 164

aaggatcctt aattgacttt atccccgccc tcgtatgcgg cgctgggacc ctgaggcggc	60
cgtggtagg cggctccccc gcggctcctc cgcggcggtg acggcgaccg cactccccgc	120
ttcccgctcc ccgcgctcct ccgccccgggt ccgccagccg aggccgctcc cgagcgtcgg	180
aag atg ccg gcc gtg tcc aag ggg gac ggg atg cgg ggc ctg gcg gtc	228
Met Pro Ala Val Ser Lys Gly Asp Gly Met Arg Gly Leu Ala Val	
1 5 10	

ttc atc tcg gat atc cgc aac tgt aaa agt aaa gaa gca gaa ata aaa	276
Phe Ile Ser Asp Ile Arg Asn Cys Lys Ser Lys Glu Ala Glu Ile Lys	
16 21 26 31	

agg ata aac aag gaa ctg gca aat atc aga tca aaa ttt aaa ggt gac	324
Arg Ile Asn Lys Glu Leu Ala Asn Ile Arg Ser Lys Phe Lys Gly Asp	
32 37 42 47	

aag gct ctt gat ggc tat agt aaa aaa aag tac gtc tgc aag ttg ctc	372
Lys Ala Leu Asp Gly Tyr Ser Lys Lys Tyr Val Cys Lys Leu Leu	
48 53 58 63	

ttc atc ttt ctc ctt ggt cat gac att gac ttt gga cac atg gag gct	420
Phe Ile Phe Leu Leu Gly His Asp Ile Asp Phe Gly His Met Glu Ala	
64 69 74 79	

gtg aac ctg ctg agt tca aac aga tac acg gaa aag cag atc ggc tac	468
Val Asn Leu Leu Ser Ser Asn Arg Tyr Thr Glu Lys Gln Ile Gly Tyr	
80 85 90 95	

ctt ttc atc tct gtg ttg gtg aac tca aac agt gag ctg atc cgc ctg	516
Leu Phe Ile Ser Val Leu Val Asn Ser Asn Ser Glu Leu Ile Arg Leu	
96 101 106 111	

atc aac aac gcc atc aag aat gac ctg gcc agc cgc aac ccc acc ttc Ile Asn Asn Ala Ile Lys Asn Asp Leu Ala Ser Arg Asn Pro Thr Phe 112 117 122 127	564
atg ggc ctg gcc ctg cac tgc atc gcc agc gtg ggc agc cgg gag atg Met Gly Leu Ala Leu His Cys Ile Ala Ser Val Gly Ser Arg Glu Met 128 133 138 143	612
gcc gag gcc ttc gcc ggg gag atc cct aag gtc ctc gta gcc gga gac Ala Glu Ala Phe Ala Gly Glu Ile Pro Lys Val Leu Val Ala Gly Asp 144 149 154 159	660
act atg gac agc gtg aag cag agc gcg gcc ctg tgc ttg ctg cgc ctg Thr Met Asp Ser Val Lys Gln Ser Ala Ala Leu Cys Leu Leu Arg Leu 160 165 170 175	708
tac agg acg tcc ccc gat ctt gtc ccc atg ggc gac tgg aca tcc cga Tyr Arg Thr Ser Pro Asp Leu Val Pro Met Gly Asp Trp Thr Ser Arg 176 181 186 191	756
gtg gtg cac ctg ctc aat gac cag cac ttg ggt gtg gta act gca gcc Val Val His Leu Leu Asn Asp Gln His Leu Gly Val Val Thr Ala Ala 192 197 202 207	804
aca agt ctg atc acc act tta gca cag aag aac cca gaa gag ttt aaa Thr Ser Leu Ile Thr Thr Leu Ala Gln Lys Asn Pro Glu Glu Phe Lys 208 213 218 223	852
acc tcc gtg tct ctg gct gtc tct agg cta agc aga atc gtg acg tct Thr Ser Val Ser Leu Ala Val Ser Arg Leu Ser Arg Ile Val Thr Ser 224 229 234 239	900
gca tcc aca gat ctc cag gat tac act tac tat ttt gtc ccg gct ccc Ala Ser Thr Asp Leu Gln Asp Tyr Thr Tyr Tyr Phe Val Pro Ala Pro 240 245 250 255	948
tgg ctg tct gtc aaa ctg ctg aga ctg ctg cag tgc tac cca ccc cca Trp Leu Ser Val Lys Leu Leu Arg Leu Leu Gln Cys Tyr Pro Pro Pro 256 261 266 271	996
gac cct gca gtg cga ggc cgc ctg act gag tgc ctg gag acc atc ctg Asp Pro Ala Val Arg Gly Arg Leu Thr Glu Cys Leu Glu Thr Ile Leu 272 277 282 287	1044
aac aaa gcc caa gaa ccg ccc aag tcg aag aag gtc cag cac tcc aac Asn Lys Ala Gln Glu Pro Pro Lys Ser Lys Lys Val Gln His Ser Asn 288 293 298 303	1092
gcg aag aat gcc gtg ctc ttc gag gcc atc agc tta atc att cac cat Ala Lys Asn Ala Val Leu Phe Glu Ala Ile Ser Leu Ile Ile His His 304 309 314 319	1140
gac agt gag ccg aac ctg ctc gtc cgt gcc tgc aac cag ttg ggc cag Asp Ser Glu Pro Asn Leu Leu Val Arg Ala Cys Asn Gln Leu Gly Gln 320 325 330 335	1188
ttt ctg cag cac cgc gag acc aac ctg cgc tac ctg gcc ctg gag agc	1236

Phe	Leu	Gln	His	Arg	Glu	Thr	Asn	Leu	Arg	Tyr	Leu	Ala	Leu	Glu	Ser		
336																351	
atg	tgc	acg	ctg	gcc	agc	tct	gag	ttc	tcc	cat	gag	gct	gtc	aag	acg	1284	
Met	Cys	Thr	Leu	Ala	Ser	Ser	Glu	Phe	Ser	His	Glu	Ala	Val	Lys	Thr		
352																367	
cac	atc	gag	acg	gtc	atc	aac	gcc	ctg	aag	act	gag	cg	gac	gtg	agc	1332	
His	Ile	Glu	Thr	Val	Ile	Asn	Ala	Leu	Lys	Thr	Glu	Arg	Asp	Val	Ser		
368																383	
gtg	cgg	cag	cg	gcc	gtg	gac	ctc	ctc	tac	gcc	atg	tgc	gac	cg	agc	1380	
Val	Arg	Gln	Arg	Ala	Val	Asp	Leu	Leu	Tyr	Ala	Met	Cys	Asp	Arg	Ser		
384																399	
aac	gcc	cca	cag	atc	gtg	gcc	gag	atg	ctg	agc	tat	ctg	gag	aca	gct	1428	
Asn	Ala	Pro	Gln	Ile	Val	Ala	Glu	Met	Leu	Ser	Tyr	Leu	Glu	Thr	Ala		
400																415	
gac	tac	tcc	atc	cga	gaa	gag	att	gtg	ctg	aag	gtc	gcc	atc	ctg	gct	1476	
Asp	Tyr	Ser	Ile	Arg	Glu	Glu	Ile	Val	Leu	Lys	Val	Ala	Ile	Leu	Ala		
416																431	
gag	aag	tac	g	cg	gt	g	ac	acc	tgg	tat	gt	g	at	cc	tt	1524	
Glu	Lys	Tyr	Ala	Val	Asp	Tyr	Thr	Trp	Tyr	Val	Asp	Thr	Ile	Leu	Asn		
432																447	
ttg	atc	cga	att	gct	ggt	gat	tac	gt	ag	gaa	gag	gt	tg	ta	c	1572	
Leu	Ile	Arg	Ile	Ala	Gly	Asp	Tyr	Val	Ser	Glu	Glu	Val	Trp	Tyr	Arg		
448																463	
gtc	att	cag	atc	gtc	atc	aac	cg	gac	gt	cag	gg	tc	ac	cg	cc	1620	
Val	Ile	Gln	Ile	Val	Ile	Asn	Arg	Asp	Asp	Val	Gln	Gly	Tyr	Ala	Ala		
464																479	
aag	act	gt	tt	g	ag	g	c	tt	c	g	cc	g	tc	ca	ct	1668	
Lys	Thr	Val	Phe	Glu	Ala	Leu	Gln	Ala	Pro	Ala	Cys	His	Glu	Asn	Leu		
480																495	
gtc	aaa	gt	gg	gc	ta	tc	ct	gg	g	ttt	gg	aa	cc	tt	at	g	1716
Val	Lys	Val	Gly	Gly	Tyr	Ile	Leu	Gly	Phe	Gly	Asn	Leu	Ile	Ala			
496																511	
gga	gac	ccg	aga	tcc	agc	ccg	ctg	atc	cag	ttc	cac	ctg	ctg	cac	tcc	1764	
Gly	Asp	Pro	Arg	Ser	Ser	Pro	Leu	Ile	Gln	Phe	His	Leu	Leu	His	Ser		
512																527	
aag	ttc	cac	ctg	tg	agc	cc	cc	cc	cg	cg	ct	ct	ct	cc	cc	1812	
Lys	Phe	His	Leu	Cys	Ser	Val	Pro	Thr	Arg	Ala	Leu	Leu	Leu	Ser	Thr		
528																543	
tac	atc	aag	ttc	gt	aa	cc	ttc	cc	g	ag	cc	cc	ac	atc	c	1860	
Tyr	Ile	Lys	Phe	Val	Asn	Leu	Phe	Pro	Glu	Val	Lys	Pro	Thr	Ile	Gln		
544																559	
gac	gt	ct	cg	ag	gc	ag	ct	ag	aa	gc	g	tc	g	ag	ct	1908	
Asp	Val	Leu	Arg	Ser	Asp	Ser	Gln	Leu	Arg	Asn	Ala	Asp	Val	Glu	Leu		

560	565	570	575	
cag cag cgt gct gtg gag tac ctg cg ^g ctc agc acc gtg gcc agc acc Gln Gln Arg Ala Val Glu Tyr Leu Arg Leu Ser Thr Val Ala Ser Thr 576 581 586 591				1956
gac att ctg gc ^g acc gtg ctg gag gag atg ccc cca ttc cc ^g gag cg ^g Asp Ile Leu Ala Thr Val Leu Glu Glu Met Pro Pro Phe Pro Glu Arg 592 597 602 607				2004
gag tcc tcc atc ttg gca aag ctc aag aag aag aag gg ^g ccc agc acg Glu Ser Ser Ile Leu Ala Lys Leu Lys Lys Lys Gly Pro Ser Thr 608 613 618 623				2052
gtg aca gac ctg gag gac acc aag cg ^g gac agg agt gtg gac gtg aac Val Thr Asp Leu Glu Asp Thr Lys Arg Asp Arg Ser Val Asp Val Asn 624 629 634 639				2100
gg ^g ggt cct gag cct gcc cca agt acc agc gg ^g tct acg cct Gly Gly Pro Glu Pro Ala Pro Ala Ser Thr Ser Ala Val Ser Thr Pro 640 645 650 655				2148
tct ccg tcg gca gac ctg ctg ggt ctc gg ^g gct gcc ccc cct gcc ccc Ser Pro Ser Ala Asp Leu Leu Gly Leu Gly Ala Ala Pro Pro Ala Pro 656 661 666 671				2196
g ^g gc ^g ccc cca ccc tcc tcc gg ^g gg ^g agc gg ^g ctg ctc gtg gac gtg Ala Gly Pro Pro Pro Ser Ser Gly Gly Ser Gly Leu Leu Val Asp Val 672 677 682 687				2244
t ^g tc ^g tca gac tcg gcc tct gtg gtc gg ^g cct ctc gct cct gg ^g tcc gaa Phe Ser Asp Ser Ala Ser Val Val Ala Pro Leu Ala Pro Gly Ser Glu 688 693 698 703				2292
gac aac ttt gcc agg ttt gtt tgt aaa aac aat ggt gtg ttg ttt gaa Asp Asn Phe Ala Arg Phe Val Cys Lys Asn Asn Gly Val Leu Phe Glu 704 709 714 719				2340
aac cag ctg ctt caa att gga ctt aag tct gaa ttt cg ^g cag aat tta Asn Gln Leu Leu Gln Ile Gly Leu Lys Ser Glu Phe Arg Gln Asn Leu 720 725 730 735				2388
ggt cg ^g atg ttt atc ttt tat ggt aat aag acc tcc acg cag ttc cta Gly Arg Met Phe Ile Phe Tyr Gly Asn Lys Thr Ser Thr Gln Phe Leu 736 741 746 751				2436
aac ttt acc cca aca cta atc tgt tca gac gac ctt cag cct aac ctg Asn Phe Thr Pro Thr Leu Ile Cys Ser Asp Asp Leu Gln Pro Asn Leu 752 757 762 767				2484
aac ctg cag acc aag ccc gtg gac ccg acc gtg gag gg ^g gg ^g gc ^g cag Asn Leu Gln Thr Lys Pro Val Asp Pro Thr Val Glu Gly Gly Ala Gln 768 773 778 783				2532
gtg cag cag gtg gtc aac ata gag tgc gtg tcc gac tt ^g acg gag gc ^g Val Gln Gln Val Val Asn Ile Glu Cys Val Ser Asp Phe Thr Glu Ala 784 789 794 799				2580

cca gtc ctc aac att cag ttc agg tat ggg ggc acc ttc cag aac gtg Pro Val Leu Asn Ile Gln Phe Arg Tyr Gly Thr Phe Gln Asn Val 800 805 810 815	2628
tct gtg cag ctg ccc atc act ctc aac aaa ttc ttc cag ccg aca gaa Ser Val Gln Leu Pro Ile Thr Leu Asn Lys Phe Phe Gln Pro Thr Glu 816 821 826 831	2676
atg gct tct cag gat ttc ttt caa cgt tgg aag cag ttg agc aat cca Met Ala Ser Gln Asp Phe Phe Gln Arg Trp Lys Gln Leu Ser Asn Pro 832 837 842 847	2724
cag cag gaa gtg cag aac atc ttc aaa gca aag cac cca atg gac aca Gln Gln Glu Val Gln Asn Ile Phe Lys Ala Lys His Pro Met Asp Thr 848 853 858 863	2772
gaa gtc acc aaa gcc aag atc att gga ttt ggt tct gca ctt ctt gaa Glu Val Thr Lys Ala Lys Ile Ile Gly Phe Gly Ser Ala Leu Leu Glu 864 869 874 879	2820
gaa gtt gat cct aat cct gcg aat ttc gtg gga gct gga atc atc cac Glu Val Asp Pro Asn Pro Ala Asn Phe Val Gly Ala Gly Ile Ile His 880 885 890 895	2868
acg aaa acc acc cag att gga tgc ctg ctg cgc ttg gag ccg aac ctg Thr Lys Thr Thr Gln Ile Gly Cys Leu Leu Arg Leu Glu Pro Asn Leu 896 901 906 911	2916
caa gcc cag atg tac cgg ctc acg ctg cgc aca agt aag gaa gcc gtt Gln Ala Gln Met Tyr Arg Leu Thr Leu Arg Thr Ser Lys Glu Ala Val 912 917 922 927	2964
tct cag aga tta tgt gaa ttg ctc tca gcg cag ttt tag tcctgaggat Ser Gln Arg Leu Cys Glu Leu Leu Ser Ala Gln Phe *928 933 938	3013
ggaagaccag gctcggtgt cttgttgtt cttcgctgtt gcccgtttgtc ttctggctta tcctgcagat gagcaccgtg tccagtgcc a cgcacaagg cgcctccccg cccacccgccc ccacacctct cccctttggg ctggacggga acacacgtgt gtggctcagg aggaaaagct cagcctggac tgtggcagcc acggcagaag gtggatcttg ggatcaattt ttataaaaat cgagacagtt ctgtggtaa atctacaaat taaaggaaaa tttagaagttt gcgtgaacgt ggcgtttggc ggagtgtcac tgagatggcc cgtgctgccg cccacccgc ctcggagcct ctgggagcag cagtgccact gtgcattggcg tggctgagc cttgggtgtt ggccgtcctg gtggctgcac acctggcgac gtcctgggcc cttgggagga gcacagctga ccctggttt gctgcagtcc cagctggact gtttccag gcaggattt aatctagaat tttagaaacat ttgtatgtt aatgacttct ggcaaaagca cgtgtcctgg ccggatgtaa ctgttctcct	3073 3133 3193 3253 3313 3373 3433 3493 3553 3613

L
B
D
M
S
E
P
R

ttcccagctc ctgttgtga agggcgtctg ttatgctcct gcagtcgccg aggcccttggaa	3673
tgtcagcca ggggaggagc gtcctgccgg cccccgcaggg cccccaggac tccagggtaa	3733
agtgtgggcc ggtggcgcaa gactcagagg tgtgctcgta tccttcctgt cagagtggc	3793
gtccccaggc cacggtgcag gcctgagtcc ttccaccggc cccgtccagt cgcccttggaa	3853
ggggctgtgg aggaaggacg cctctgtgtg gtcaggaagt gaagggggca ttggccgcat	3913
gccatgtgcc acctgcggct tgtgtctcac ctgtcatctg gactcagcac ccaggctgca	3973
cgtctgacac ctgagaggcg agagagtggg gccggcctag gagccaaggc tggttttttg	4033
cgctctgtcc ccaggatggt ggccttgttt gtcctaaaca cacccagcac aggttctggc	4093
ttcctgacat gctgtggagg cagggagggt ggggtggccac atgtgttttga gggttttac	4153
cctggccctc agttgcctgc tgtgcgggtc cctggggcag ctgcagggc tcatggaccc	4213
atcagggtct ccacagctcc cctgcagtgt gtgcacccca caatgtctgc ggcttttctt	4273
ccggcgtgtc gggctttgat cacagcatag ccacgtcagt ggcgtgcgcc tctcgacag	4333
gccattctgg gtctgggtgt gccaggtgcc gtgacacgcc gtgctggct tgtgtgcag	4393
ctgggtgggt tgccctcat tctcatgttc cagctgctgg cagtgctct gcctgtgtgc	4453
tgcgcctgca ggctgcgtgt gctgccgtgg atctcctgca tcccttgacc cctccgcaca	4513
tcagaggaaa ggctgcgtccc cgaggcaccc cttccctgtg cggcgctgca gagggggccct	4573
cagtgtggca ctccctcgta aagaaaaata aaggctagaa ctgccaaaaa aaaaaaaaa	4631

<210> 165
<211> 3292
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118) .. (2313)

<220>
<221> misc_feature
<222> (1) .. (3292)
<223> n = a,t,c or g

<400> 165

tgaaacaann nnnttgatn gcctttgatg ggcgatccag ctggctagcg tttaaactta	60
agctcgggac cgagctcgga tccactagtc cagtgtggtg gaattccaga tccctgc	117
atg tca ctg agt cca cca tgc ttt aca gaa gaa gac aga ttt agt ctg	165
Met Ser Leu Ser Pro Pro Cys Phe Thr Glu Glu Asp Arg Phe Ser Leu	

1	5	10	15	
gaa gct ctt caa aca ata cat aaa caa atg gat gat gac aaa gat ggt Glu Ala Leu Gln Thr Ile His Lys Gln Met Asp Asp Asp Lys Asp Gly				213
17 22 27 32				
gga att gaa gta gag gaa agt gat gaa ttc atc aga gaa gat atg aaa Gly Ile Glu Val Glu Glu Ser Asp Glu Phe Ile Arg Glu Asp Met Lys				261
33 38 43 48				
tat aaa gat gct act aat aaa cac agc cat ctg cac aga gaa gat aaa Tyr Lys Asp Ala Thr Asn Lys His Ser His Leu His Arg Glu Asp Lys				309
49 54 59 64				
cat ata acg att gag gat tta tgg aaa cga tgg aaa aca tca gaa gtt His Ile Thr Ile Glu Asp Leu Trp Lys Arg Trp Lys Thr Ser Glu Val				357
65 70 75 80				
cat aat tgg acc ctt gaa gac act ctt cag tgg ttg ata gag ttt gtt His Asn Trp Thr Leu Glu Asp Thr Leu Gln Trp Leu Ile Glu Phe Val				405
81 86 91 96				
gaa cta ccc caa tat gag aag aat ttt aga gac aac aat gtc aaa gga Glu Leu Pro Gln Tyr Glu Lys Asn Phe Arg Asp Asn Asn Val Lys Gly				453
97 102 107 112				
acg aca ctt ccc agg ata gca gtg cac gaa cct tca ttt atg atc tcc Thr Thr Leu Pro Arg Ile Ala Val His Glu Pro Ser Phe Met Ile Ser				501
113 118 123 128				
cag ttg aaa atc agt gac cgg agt cac aga caa aaa ctt cag ctc aag Gln Leu Lys Ile Ser Asp Arg Ser His Arg Gln Lys Leu Gln Leu Lys				549
129 134 139 144				
gca ttg gat gtg gtt ttg gga cct cta aca cgc cca cct cat aac Ala Leu Asp Val Val Leu Phe Gly Pro Leu Thr Arg Pro Pro His Asn				597
145 150 155 160				
tgg atg aaa gat ttt atc ctc aca gtt tct ata gta att ggt gtt gga Trp Met Lys Asp Phe Ile Leu Thr Val Ser Ile Val Ile Gly Val Gly				645
161 166 171 176				
ggc tgc tgg ttt gct tat acg cag aat aag aca tca aaa gaa cat gtt Gly Cys Trp Phe Ala Tyr Thr Gln Asn Lys Thr Ser Lys Glu His Val				693
177 182 187 192				
gca aaa atg atg aaa gat tta gag agc tta caa act gca gag caa agt Ala Lys Met Met Lys Asp Leu Glu Ser Leu Gln Thr Ala Glu Gln Ser				741
193 198 203 208				
cta atg gac tta caa gag agg ctt gaa aag gca cag gaa gaa aac aga Leu Met Asp Leu Gln Glu Arg Leu Glu Lys Ala Gln Glu Glu Asn Arg				789
209 214 219 224				
aat gtt gct gta gaa aag caa aat tta gag cgc aaa atg atg gat gaa Asn Val Ala Val Glu Lys Gln Asn Leu Glu Arg Lys Met Met Asp Glu				837
225 230 235 240				

atc aat tat gca aag gag gag gct tgt cgg ctg aga gag cta agg gag Ile Asn Tyr Ala Lys Glu Glu Ala Cys Arg Leu Arg Glu Leu Arg Glu	885
241 246 251 256	
gga gct gaa tgt gaa ttg agt aga cgt cag tat gca gaa cag gaa ttg Gly Ala Glu Cys Glu Leu Ser Arg Arg Gln Tyr Ala Glu Gln Glu Leu	933
257 262 267 272	
gaa cag gtt cgc atg gct ctg aaa aag gcc gaa aaa gaa ttt gaa ctg Glu Gln Val Arg Met Ala Leu Lys Ala Glu Lys Glu Phe Glu Leu	981
273 278 283 288	
aga agc agt tgg tct gtt cca gat gca ctt cag aaa tgg ctt cag tta Arg Ser Ser Trp Ser Val Pro Asp Ala Leu Gln Lys Trp Leu Gln Leu	1029
289 294 299 304	
aca cat gaa gta gaa gtg caa tac tac aat att aaa aga caa aac gct Thr His Glu Val Glu Val Gln Tyr Tyr Asn Ile Lys Arg Gln Asn Ala	1077
305 310 315 320	
gaa atg cag cta gct att gct aaa gat gag gca gaa aaa att aaa aag Glu Met Gln Leu Ala Ile Ala Lys Asp Glu Ala Glu Lys Ile Lys Lys	1125
321 326 331 336	
aag aga agc aca gtc ttt ggg act ctg cac gtt gca cac agc tcc tcc Lys Arg Ser Thr Val Phe Gly Thr Leu His Val Ala His Ser Ser Ser	1173
337 342 347 352	
cta gat gag gta gac cac aaa att ctg gaa gca aag aaa gct ctc tct Leu Asp Glu Val Asp His Lys Ile Leu Glu Ala Lys Lys Ala Leu Ser	1221
353 358 363 368	
gag ttg aca act tgt tta cga gaa cga ctt ttt cgc tgg caa caa att Glu Leu Thr Thr Cys Leu Arg Glu Arg Leu Phe Arg Trp Gln Gln Ile	1269
369 374 379 384	
gag aag atc tgt ggc ttt cag ata gcc cat aac tca gga ctc ccc agc Glu Lys Ile Cys Gly Phe Gln Ile Ala His Asn Ser Gly Leu Pro Ser	1317
385 390 395 400	
ctg acc tct tcc ctt tat tct gat cac agc tgg gtg gtg atg ccc aga Leu Thr Ser Ser Leu Tyr Ser Asp His Ser Trp Val Val Met Pro Arg	1365
401 406 411 416	
gtc tcc att cca ccc tat cca att gct gga gga gtt gat gac tta gat Val Ser Ile Pro Pro Tyr Pro Ile Ala Gly Gly Val Asp Asp Leu Asp	1413
417 422 427 432	
gaa gac aca ccc cca ata gtg tca caa ttt ccc ggg acc atg gct aaa Glu Asp Thr Pro Pro Ile Val Ser Gln Phe Pro Gly Thr Met Ala Lys	1461
433 438 443 448	
cct cct gga tca tta gcc aga agc agc agc ctg tgc cgt tca cgc cgc Pro Pro Gly Ser Leu Ala Arg Ser Ser Ser Leu Cys Arg Ser Arg Arg	1509
449 454 459 464	

agc att gtg ccg tcc tcg cct cag cct cag cga gct cag ctt gct cca Ser Ile Val Pro Ser Ser Pro Gln Pro Gln Arg Ala Gln Leu Ala Pro	465	470	475	480	1557
cac gcc ccc cac ccg tca cac cct cgg cac cct cac cac ccg caa cac His Ala Pro His Pro Ser His Pro Arg His Pro His His Pro Gln His	481	486	491	496	1605
aca cca cac tcc ttg cct tcc cct gat cca gat atc ctc tca gtg tca Thr Pro His Ser Leu Pro Ser Pro Asp Pro Asp Ile Leu Ser Val Ser	497	502	507	512	1653
agt tgc cct gcg ctt tat cga aat gaa gag gag gaa gag gcc att tac Ser Cys Pro Ala Leu Tyr Arg Asn Glu Glu Glu Glu Ala Ile Tyr	513	518	523	528	1701
ttc tct gct gaa aag caa tgg aac aca agg gag tgt gca gtt gga gac Phe Ser Ala Glu Lys Gln Trp Asn Thr Arg Glu Cys Ala Val Gly Asp	529	534	539	544	1749
agc cag gga cca cat gta cac ggc ctg gta cgc ttt gac aag gac ttt Ser Gln Gly Pro His Val His Gly Leu Val Arg Phe Asp Lys Asp Phe	545	550	555	560	1797
gga tct tac tct gag tat gag aga aag cac tgg gaa gtt tca atg cca Gly Ser Tyr Ser Glu Tyr Glu Arg Lys His Trp Glu Val Ser Met Pro	561	566	571	576	1845
gac aca gct tca gaa tgt gac tcc tta aat tct tcc att gga agg aaa Asp Thr Ala Ser Glu Cys Asp Ser Leu Asn Ser Ser Ile Gly Arg Lys	577	582	587	592	1893
cag tct cct cct tta agc ctc gag ata tac caa aca tta tct ccg cga Gln Ser Pro Pro Leu Ser Leu Glu Ile Tyr Gln Thr Leu Ser Pro Arg	593	598	603	608	1941
aag ata tca aga gat gag gtg tcc cta gag gat tcc tcc cga ggg gat Lys Ile Ser Arg Asp Glu Val Ser Leu Glu Asp Ser Ser Arg Gly Asp	609	614	619	624	1989
tcg cct gta act gtg gat gtg tct tgg ggt tct ccc gac tgt gta ggt Ser Pro Val Thr Val Asp Val Ser Trp Gly Ser Pro Asp Cys Val Gly	625	630	635	640	2037
ctg aca gaa act aag agt atg atc ttc agt cct gca agc aaa gtg tac Leu Thr Glu Thr Lys Ser Met Ile Phe Ser Pro Ala Ser Lys Val Tyr	641	646	651	656	2085
aat ggc att ttg gag aaa tcc tgt agc atg aac cag ctt tcc agt ggc Asn Gly Ile Leu Glu Lys Ser Cys Ser Met Asn Gln Leu Ser Ser Gly	657	662	667	672	2133
atc ccg gtg cct aaa cct cgc cac aca tca tgt tcc tca gct ggc aac Ile Pro Val Pro Lys Pro Arg His Thr Ser Cys Ser Ser Ala Gly Asn	673	678	683	688	2181
gac agt aaa cca gtt cag gaa gcc cca agt gtt gcc aga ata agc agc					2229

Asp Ser Lys Pro Val Gln Glu Ala Pro Ser Val Ala Arg Ile Ser Ser			
689	694	699	704
atc cca cat gac ctt tgt cat aat gga gag aaa agc aaa aag cca tca Ile Pro His Asp Leu Cys His Asn Gly Glu Lys Ser Lys Lys Pro Ser			2277
705	710	715	720
aaa atc aaa agc ctt ttt aag aag aaa tct aag tga actg gctgacttga Lys Ile Lys Ser Leu Phe Lys Lys Ser Lys *			2327
721	726	731	
tggaatcatg ttcaagtggc atctgtaaac tattatcccc caccctccac tccccacctt			2387
ttttttgggt taatttttagg aatgttaactc cattggggct ttccaggccg gatgccatag			2447
tggaacatcc cagaagggca actgtctact gtctgcttat ttaagtgact atatataatc			2507
aattcatcaa gccagttatt actgaaaaat cattgaaatg agacagttt cagtcatttc			2567
tgcctattta tttctgcttt gttctcagtg atgtatatgc aacattttgt tgaaagccac			2627
gatggactta caagcttaa tggactcgta agccagcatg ggcttgcaaa aatttcttgt			2687
ttaccagagc atcttcttat cttccacag agctattac atcctggact atataactta			2747
aaagaagtaa aacgtaattt cactactgtt ttccagactg gaaaaaaaaaaa aaaaatctct			2807
gcaagtgaaa ctgtatagag ttataaaaat gactatggat aggggactgt tttcactttt			2867
agatcaaaaat gggtttttaa gttagaaccta gggtttctaa ttgacttgat ttctggaaat			2927
gaaaacccgc gcttttatta tggaaagctt cttgaactgc atttactatt gtgaagttc			2987
aagtcccgct gtaaagatca tggatgtttt gtttccccag ggcttccct gtgatttact			3047
gcattgcagg ctgtatgata aaaccccat aatttaaaga gagaaggctc ttgattcctt			3107
atgcaagtgg aaaagttgaa acttgattga aggactaaa acattcccac ccttaagccg			3167
aggtgggggg atatggggat tcaggcagg ttttacccccc tttgaataac tgcaaaggat			3227
ttacggtttg tgaaaaatgt gtactgtgga aaagataata aattgaagcc cttaaaaaaaaaa			3287
aaaaaa			3292

```

<210> 166
<211> 2306
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(2232)

```

<400> 166

atg ctc cac ttt aac cga tgt cat cat ctg aaa aag ata aca cag aaa Met Leu His Phe Asn Arg Cys His His Leu Lys Lys Ile Thr Gln Lys	48
1 5 10	
tgt ttt tct agt ata cat gtt aaa acg gat aaa cat gca cag cga ttt Cys Phe Ser Ser Ile His Val Lys Thr Asp Lys His Ala Gln Arg Phe	96
17 22 27 32	
ctt tca aga acc ttt gca ctt gcg gaa ttg agg aag tca tgg tat tca Leu Ser Arg Thr Phe Ala Leu Ala Glu Leu Arg Lys Ser Trp Tyr Ser	144
33 38 43 48	
acc cac tct ctt gtt gga gac aaa aat att atc ctg atg gga cct cct Thr His Ser Leu Val Gly Asp Lys Asn Ile Ile Leu Met Gly Pro Pro	192
49 54 59 64	
ggt gct ggg aaa aca aca gta ggc aga ata ata ggt cag aaa cta ggt Gly Ala Gly Lys Thr Val Gly Arg Ile Ile Gly Gln Lys Leu Gly	240
65 70 75 80	
tgt tgt gtc ata gat gtg gat gat gat atc ctt gaa aaa acc tgg aat Cys Cys Val Ile Asp Val Asp Asp Asp Ile Leu Glu Lys Thr Trp Asn	288
81 86 91 96	
atg agt gtg tct gaa aaa tta cag gat gtt ggt aat gag caa ttt tta Met Ser Val Ser Glu Lys Leu Gln Asp Val Gly Asn Glu Gln Phe Leu	336
97 102 107 112	
gaa gag gaa gga aaa gct gtg tta aac ttc tct gca tct gga agt gtg Glu Glu Glu Gly Lys Ala Val Leu Asn Phe Ser Ala Ser Gly Ser Val	384
113 118 123 128	
att tcc ctt act ggg tcc aat cca atg cat gat gct agc atg tgg cat Ile Ser Leu Thr Gly Ser Asn Pro Met His Asp Ala Ser Met Trp His	432
129 134 139 144	
ctg aag aaa aat gga ata att gta tac ctg gat gta cct cta cta aat Leu Lys Lys Asn Gly Ile Ile Val Tyr Leu Asp Val Pro Leu Leu Asn	480
145 150 155 160	
cta att tgt cgt cta aaa tta atg aag aca gat agg att gta ggt cag Leu Ile Cys Arg Leu Lys Leu Met Lys Thr Asp Arg Ile Val Gly Gln	528
161 166 171 176	
aat tct gga aca tct atg aaa gac tta ctt aaa ttt aga aga cag tat Asn Ser Gly Thr Ser Met Lys Asp Leu Leu Lys Phe Arg Arg Gln Tyr	576
177 182 187 192	
tat aag aag tgg tat gat gct cgt gtt ttc tgt gaa agt ggg gct tcc Tyr Lys Lys Trp Tyr Asp Ala Arg Val Phe Cys Glu Ser Gly Ala Ser	624
193 198 203 208	
cca gag gag gta gct gac aaa gtg ctg aat gca att aaa aga tac caa Pro Glu Glu Val Ala Asp Lys Val Leu Asn Ala Ile Lys Arg Tyr Gln	672
209 214 219 224	

gat gtg gac tcg gaa aca ttc att tca aca aga cac gtt tgg cct gaa		720
Asp Val Asp Ser Glu Thr Phe Ile Ser Thr Arg His Val Trp Pro Glu		
225 230 235 240		
gac tgt gaa cag aag gtt tca gca aaa ttc ttt agt gaa gct gta att		768
Asp Cys Glu Gln Lys Val Ser Ala Lys Phe Phe Ser Glu Ala Val Ile		
241 246 251 256		
gag ggg ttg gct tct gat ggt ggc ctc ttt gtt cct gca aag gag ttt		816
Glu Gly Leu Ala Ser Asp Gly Gly Leu Phe Val Pro Ala Lys Glu Phe		
257 262 267 272		
cca aaa tta agc tgc ggg gag tgg aaa agc cta gta gga gca acc tac		864
Pro Lys Leu Ser Cys Gly Glu Trp Lys Ser Leu Val Gly Ala Thr Tyr		
273 278 283 288		
gta gaa aga gca cag ata ctg ttg gaa aga tgt atc cat cct gca gac		912
Val Glu Arg Ala Gln Ile Leu Leu Glu Arg Cys Ile His Pro Ala Asp		
289 294 299 304		
ata cct gct gcc agg ttg gga gaa atg att gaa act gct tat ggg gaa		960
Ile Pro Ala Ala Arg Leu Gly Glu Met Ile Glu Thr Ala Tyr Gly Glu		
305 310 315 320		
aac ttt gcc tgc tca aaa att gct cct gtc agg cac ctt tca ggc aac		1008
Asn Phe Ala Cys Ser Lys Ile Ala Pro Val Arg His Leu Ser Gly Asn		
321 326 331 336		
cag ttc atc ctg gag ttg ttt cat gga cca aca gga tca ttt aaa gat		1056
Gln Phe Ile Leu Glu Leu Phe His Gly Pro Thr Gly Ser Phe Lys Asp		
337 342 347 352		
ttg tct tta cag ctt atg cct cat att ttt gca cac tgt atc cca cca		1104
Leu Ser Leu Gln Leu Met Pro His Ile Phe Ala His Cys Ile Pro Pro		
353 358 363 368		
agt tgc aat tat atg ata ctt gta gct act tca gga gac aca ggg agt		1152
Ser Cys Asn Tyr Met Ile Leu Val Ala Thr Ser Gly Asp Thr Gly Ser		
369 374 379 384		
gca gtc tta aat ggt ttt agt cgt cta aat aag aat gat aag caa agg		1200
Ala Val Leu Asn Gly Phe Ser Arg Leu Asn Lys Asn Asp Lys Gln Arg		
385 390 395 400		
ata gct gtg gtt gca ttt ttt cct gag aat gga gta agt gat ttt caa		1248
Ile Ala Val Val Ala Phe Phe Pro Glu Asn Gly Val Ser Asp Phe Gln		
401 406 411 416		
aaa gca caa ata att ggc agt cag aga gaa aat gga tgg gca gtg ggt		1296
Lys Ala Gln Ile Ile Gly Ser Gln Arg Glu Asn Gly Trp Ala Val Gly		
417 422 427 432		
gtt gag tca gat ttt gat ttt tgc cag aca gct ata aaa aga att ttt		1344
Val Glu Ser Asp Phe Asp Phe Cys Gln Thr Ala Ile Lys Arg Ile Phe		
433 438 443 448		
aat gat tct gat ttt act ggc ttt ctt act gtg gaa tat gga aca atc		1392

Asn Asp Ser Asp Phe Thr Gly Phe Leu Thr Val Glu Tyr Gly Thr Ile				
449	454	459	464	
tta agt tcg gct aac tcc ata aac tgg ggc cga cta ctt ccg cag gta				1440
Leu Ser Ser Ala Asn Ser Ile Asn Trp Gly Arg Leu Leu Pro Gln Val				
465	470	475	480	
gtt tat cat gct tcc gca tat ctt gat ctt gtt agt caa gga ttt att				1488
Val Tyr His Ala Ser Ala Tyr Leu Asp Leu Val Ser Gln Gly Phe Ile				
481	486	491	496	
tct ttt gga agc cca gtc gat gtc tgt att ccc aca gga aac ttt ggt				1536
Ser Phe Gly Ser Pro Val Asp Val Cys Ile Pro Thr Gly Asn Phe Gly				
497	502	507	512	
aac att tta gca gca gtg tat gcc aaa atg atg gga atc ccg att cga				1584
Asn Ile Leu Ala Ala Val Tyr Ala Lys Met Met Gly Ile Pro Ile Arg				
513	518	523	528	
aaa ttt atc tgt gcc tct aat cag aac cat gtt ttg act gat ttt ata				1632
Lys Phe Ile Cys Ala Ser Asn Gln Asn His Val Leu Thr Asp Phe Ile				
529	534	539	544	
aaa aca gga cat tat gat cta agg gaa aga aaa tta gca caa acc ttt				1680
Lys Thr Gly His Tyr Asp Leu Arg Glu Arg Lys Leu Ala Gln Thr Phe				
545	550	555	560	
tca ccg tca ata gat att ctc aaa tct tca aac cta gaa cga cat tta				1728
Ser Pro Ser Ile Asp Ile Leu Lys Ser Ser Asn Leu Glu Arg His Leu				
561	566	571	576	
cac ttg atg gct aat aaa gat gga cag cta atg aca gaa tta ttt aat				1776
His Leu Met Ala Asn Lys Asp Gly Gln Leu Met Thr Glu Leu Phe Asn				
577	582	587	592	
cga tta gaa agt cag cat cat ttc cag ata gaa aag gct cta gtt gag				1824
Arg Leu Glu Ser Gln His His Phe Gln Ile Glu Lys Ala Leu Val Glu				
593	598	603	608	
aaa ctt cag cag gat ttt gta gct gac tgg tgc tct gag gga gag tgc				1872
Lys Leu Gln Gln Asp Phe Val Ala Asp Trp Cys Ser Glu Gly Glu Cys				
609	614	619	624	
cta gca gct att aac tcc acc tat aat act tca ggg tat att ttg gat				1920
Leu Ala Ala Ile Asn Ser Thr Tyr Asn Thr Ser Gly Tyr Ile Leu Asp				
625	630	635	640	
cca cac act gct gtt gca aaa gtg gtt gca gat agg gtg caa gac aaa				1968
Pro His Thr Ala Val Ala Lys Val Val Ala Asp Arg Val Gln Asp Lys				
641	646	651	656	
act tgc cct gtg att atc tca tct aca gcc cat tac tca aag ttt gca				2016
Thr Cys Pro Val Ile Ile Ser Ser Thr Ala His Tyr Ser Lys Phe Ala				
657	662	667	672	
cct gct atc atg cag gct tta aag att aaa gaa atc aat gag act tca				2064
Pro Ala Ile Met Gln Ala Leu Lys Ile Lys Glu Ile Asn Glu Thr Ser				

673	678	683	688	
tca agt cag ctc tat ttg ctg ggt tca tac aat gca tta cct cca ctg Ser Ser Gln Leu Tyr Leu Leu Gly Ser Tyr Asn Ala Leu Pro Pro Leu 689	694	699	704	2112
cat gag gct tta tta gag aga aca aaa cag caa gag aag atg gag tac His Glu Ala Leu Leu Glu Arg Thr Lys Gln Gln Glu Lys Met Glu Tyr 705	710	715	720	2160
cag gtc tgt gca gct gat atg aat gtc ttg aag agt cat gtg gaa caa Gln Val Cys Ala Ala Asp Met Asn Val Leu Lys Ser His Val Glu Gln 721	726	731	736	2208
ctt gtc caa aat caa ttc ata tga aagcttcag agtaaaatttt tttttctagc Leu Val Gln Asn Gln Phe Ile *	737	742		2262
tataaggatg caataataaa tctcaaacac tgaaaaaaaaaaa aaaa				2306
 Annotations:				
<210> 167				
<211> 3454				
<212> DNA				
<213> Homo sapiens				
<220>				
<221> CDS				
<222> (340)..(2055)				
 Sequence:				
<400> 167				
atttggccct cgaggccaag aattcgac gaggagctgg ctcagggcgt ccgcgttggct cgacgacct gctgagcctc ccaaaccgct tccataaggc tttgccttgc caacttcagc				60
tacagtgtta gctaagtttg gaaagaagga aaaaagaaaa tccctgggcc cctttcttt tgttcttgc caaagtgcgtc gttgtgtct tttgccccaa ggctgttgc ttttagagg				120
tgctatctcc agttcccttgc actcctgtta acaagcacct cagcgagagc agcagcagcg atagcagccg cagaagagcc agcggttcg cctagtgtc	atg acc agg gcg gga Met Thr Arg Ala Gly 1			180
gat cac aac cgc cag aga gga tgc tgt gga tcc ttg gcc gac tac ctg Asp His Asn Arg Gln Arg Gly Cys Cys Gly Ser Leu Ala Asp Tyr Leu 6	11	16	21	240
acc tct gca aaa ttc ctt ctc tac ctt ggt cat tct ctc tct act tgg Thr Ser Ala Lys Phe Leu Leu Tyr Leu Gly His Ser Leu Ser Thr Trp 22	27	32	37	300
gga gat cgg atg tgg cac ttt gcg gtg tct gtg ttt ctg gta gag ctc Gly Asp Arg Met Trp His Phe Ala Val Ser Val Phe Leu Val Glu Leu				354
				402
				450
				498

38	43	48	53	
tat gga aac agc ctc ctt ttg aca gca gtc tac ggg ctg gtg gtg gca Tyr Gly Asn Ser Leu Leu Leu Thr Ala Val Tyr Gly Leu Val Val Ala				546
54	59	64	69	
ggg tct gtt ctg gtc ctg gga gcc atc atc ggt gac tgg gtg gac aag Gly Ser Val Leu Val Leu Gly Ala Ile Ile Gly Asp Trp Val Asp Lys				594
70	75	80	85	
aat gct aga ctt aaa gtg gcc cag acc tcg ctg gtg gta cag aat gtt Asn Ala Arg Leu Lys Val Ala Gln Thr Ser Leu Val Val Gln Asn Val				642
86	91	96	101	
tca gtc atc ctg tgt gga atc atc ctg atg atg gtt ttc tta cat aaa Ser Val Ile Leu Cys Gly Ile Ile Leu Met Met Val Phe Leu His Lys				690
102	107	112	117	
cat gag ctt ctg acc atg tac cat gga tgg gtt ctc act tcc tgc tat His Glu Leu Leu Thr Met Tyr His Gly Trp Val Leu Thr Ser Cys Tyr				738
118	123	128	133	
atc ctg atc atc act att gca aat att gca aat ttg gcc agt act gct Ile Leu Ile Ile Thr Ile Ala Asn Ile Ala Asn Leu Ala Ser Thr Ala				786
134	139	144	149	
act gca atc aca atc caa agg gat tgg att gtt gtt gca gga gaa Thr Ala Ile Thr Ile Gln Arg Asp Trp Ile Val Val Val Ala Gly Glu				834
150	155	160	165	
gac aga agc aaa cta gca aat atg aat gcc aca ata cga agg att gac Asp Arg Ser Lys Leu Ala Asn Met Asn Ala Thr Ile Arg Arg Ile Asp				882
166	171	176	181	
cag tta acc aac atc tta gcc ccc atg gct gtt ggc cag att atg aca Gln Leu Thr Asn Ile Leu Ala Pro Met Ala Val Gly Gln Ile Met Thr				930
182	187	192	197	
ttt ggc tcc cca gtc atc ggc tgt ggc ttt att tcg gga tgg aac ttg Phe Gly Ser Pro Val Ile Gly Cys Gly Phe Ile Ser Gly Trp Asn Leu				978
198	203	208	213	
gta tcc atg tgc gtg gag tac gtt ctg ctc tgg aag gtt tac cag aaa Val Ser Met Cys Val Glu Tyr Val Leu Leu Trp Lys Val Tyr Gln Lys				1026
214	219	224	229	
acc cca gct cta gct gtg aaa gct ggt ctt aaa gaa gag gaa act gaa Thr Pro Ala Leu Ala Val Lys Ala Gly Leu Lys Glu Glu Glu Thr Glu				1074
230	235	240	245	
ttg aaa cag ctg aat tta cac aaa gat act gag cca aaa ccc ctg gag Leu Lys Gln Leu Asn Leu His Lys Asp Thr Glu Pro Lys Pro Leu Glu				1122
246	251	256	261	
gga act cat cta atg ggt gtg aaa gac tct aac atc cat gag ctt gaa Gly Thr His Leu Met Gly Val Lys Asp Ser Asn Ile His Glu Leu Glu				1170
262	267	272	277	

cat gag caa gag cct act tgt gcc tcc cag atg gct gag ccc ttc cgt			1218
His Glu Gln Glu Pro Thr Cys Ala Ser Gln Met Ala Glu Pro Phe Arg			
278	283	288	293
acc ttc cga gat gga tgg gtc tcc tac tac aac cag cct gtg ttt ctg			1266
Thr Phe Arg Asp Gly Trp Val Ser Tyr Tyr Asn Gln Pro Val Phe Leu			
294	299	304	309
gct ggc atg ggt ctt gct ttc ctt tat atg act gtc ctg ggc ttt gac			1314
Ala Gly Met Gly Leu Ala Phe Leu Tyr Met Thr Val Leu Gly Phe Asp			
310	315	320	325
tgc atc acc aca ggg tac gcc tac act cag gga ctg agt ggt tcc atc			1362
Cys Ile Thr Thr Gly Tyr Ala Tyr Thr Gln Gly Leu Ser Gly Ser Ile			
326	331	336	341
ctc agt att ttg atg gga gca tca gct ata act gga ata atg gga act			1410
Leu Ser Ile Leu Met Gly Ala Ser Ala Ile Thr Gly Ile Met Gly Thr			
342	347	352	357
gta gct ttt act tgg cta cgt cga aaa tgt ggt ttg gtt cgg aca ggt			1458
Val Ala Phe Thr Trp Leu Arg Arg Lys Cys Gly Leu Val Arg Thr Gly			
358	363	368	373
ctg atc tca gga ttg gca cag ctt tcc tgt ttg atc ttg tgt gtg atc			1506
Leu Ile Ser Gly Leu Ala Gln Leu Ser Cys Leu Ile Leu Cys Val Ile			
374	379	384	389
tct gta ttc atg cct gga agc ccc ctg gac ttg tcc gtt tct cct ttt			1554
Ser Val Phe Met Pro Gly Ser Pro Leu Asp Leu Ser Val Ser Pro Phe			
390	395	400	405
gaa gat atc cga tca agg ttc att caa gga gag tca att aca cct acc			1602
Glu Asp Ile Arg Ser Arg Phe Ile Gln Gly Glu Ser Ile Thr Pro Thr			
406	411	416	421
aag ata cct gaa att aca act gaa ata tac atg tct aat ggg tct aat			1650
Lys Ile Pro Glu Ile Thr Thr Glu Ile Tyr Met Ser Asn Gly Ser Asn			
422	427	432	437
tct gct aat att gtc ccg gag aca agt cct gaa tct gtg ccc ata atc			1698
Ser Ala Asn Ile Val Pro Glu Thr Ser Pro Glu Ser Val Pro Ile Ile			
438	443	448	453
tct gtc agt ctg ctg ttt gca ggc gtc att gct gct aga atc ggt ctt			1746
Ser Val Ser Leu Leu Phe Ala Gly Val Ile Ala Ala Arg Ile Gly Leu			
454	459	464	469
tgg tcc ttt gat tta act gtg aca cag ttg ctg caa gaa aat gta att			1794
Trp Ser Phe Asp Leu Thr Val Thr Gln Leu Leu Gln Glu Asn Val Ile			
470	475	480	485
gaa tct gaa aga ggc att ata aat ggt gta cag aac tcc atg aac tat			1842
Glu Ser Glu Arg Gly Ile Ile Asn Gly Val Gln Asn Ser Met Asn Tyr			
486	491	496	501

ctt ctt gat ctt ctg cat ttc atc atg gtc atc ctg gct cca aat cct		1890		
Leu Leu Asp Leu Leu His Phe Ile Met Val Ile Leu Ala Pro Asn Pro				
502	507	512	517	
gaa gct ttt ggc ttg ctc gta ttg att tca gtc tcc ttt gtg gca atg		1938		
Glu Ala Phe Gly Leu Leu Val Leu Ile Ser Val Ser Phe Val Ala Met				
518	523	528	533	
ggc cac att atg tat ttc cga ttt gcc caa aat act ctg gga aac aag		1986		
Gly His Ile Met Tyr Phe Arg Phe Ala Gln Asn Thr Leu Gly Asn Lys				
534	539	544	549	
ctc ttt gct tgc ggt cct gat gca aaa gaa gtt agg aag gaa aat caa		2034		
Leu Phe Ala Cys Gly Pro Asp Ala Lys Glu Val Arg Lys Glu Asn Gln				
550	555	560	565	
gca aat aca tct gtt gtt tga ga cagtttaact gttgctatcc tgttactaga		2087		
Ala Asn Thr Ser Val Val *				
566	571			
ttatatatagag cacatgtgct tattttgtac tgcagaattc caataaatgg ctgggtgttt		2147		
tgctctgttt ttaccacagc tgtgccttga gaactaaaag ctgttttagga aacctaagtc		2207		
agcagaaaatt aactgattaa tttcccttat gttgaggcat ggaaaaaaaaa ttggaaaaga		2267		
aaaactcagt ttaaatacgg agactataat gataaacactg aattccccata tttctcatga		2327		
gtagatacaa tcttacgtaa aagagtgggt agtcacgtga attcagttat catttgacag		2387		
attcttatct gtactagaat tcagatatgt cagtttctg caaaactcac tcttgttcaa		2447		
gactagctaa tttatTTTT tgcatcttag ttatTTTaa aaacaattc ttcaagtatg		2507		
aagactaaat tttgataact aatattatcc ttattgatcc tattgatctt aaggatTTA		2567		
catgtatgtg gaaaaacaaa acacttaact agaattctct aataaggTTT atggTTtagc		2627		
ttaaagagca cctttgtatt tttattatca gatggggcaa catattgtat gaagcatatg		2687		
tagcaTTca cagcatggTT atcatgtaa ctgcaggtag aagcaaaagct gtAAAGTAGA		2747		
tttacacac aatgactgca tacagacttc aaatatgtca atagTTGTT catagaacct		2807		
agaagccaaa agccacacag aaggcaaga atcccattt aactcatgtt atcatcatta		2867		
gtgatctgtg ttgtagaaca tgagggtgta agcTTcagc ctggcaagtt acatgtagaa		2927		
agcccacact tgtgaaggTT ttgtttaca aatcacttga ttAAACACAC tcaggtagaa		2987		
tatTTTatt tttactgttt tataccaga agttatttct acattgttct acagcaagaa		3047		
tattcataaa agtacccTTT tcaaATGCCT ttgagaagaa tagaagaaaa aaagTTGTa		3107		
tatTTTaa aaaattgttt taaaagtcaG tttgcaacat gtctgtacca agatggTact		3167		
ttgcTTtaac cgTTTatATG cactttcatg gagactgcaa tacgttgcta tgagcactt		3227		

ctttatcctt ggagttaat ccttgcttc atcttctac agtatgacat aatgattgc	3287
tatgttgtaa aatctttgta aaaaatttct atataaaaat attttgaaaa tctcaaaaaa	3347
 aagtcgacgc ggccgcgaat tcggatcctc gagagatctc ttttttggg tttggtgggg	3407
tatcttcatc atcgaataga tagttatata catcagcctg tctaattg	3454

<210> 168
 <211> 1197
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (96)..(548)

<400> 168	
atggagatag ggcccggaat tgcgggcgtc actctgctcc tgcgacctag ccaggcgtga	60
gggagtgaca gcagcgcatt cgccggacga gagcgt atg agt gag aac gcc gca	113
Met Ser Glu Asn Ala Ala	
1	
cca ggt ctg atc tca gag ctg aag ctg gct gtg ccc tgg ggc cac atc	161
Pro Gly Leu Ile Ser Glu Leu Lys Leu Ala Val Pro Trp Gly His Ile	
7 12 17 22	
gca gcc aaa gcc tgg ggc tcc ctg cag ggc cct cca gtt ctc tgc ctg	209
Ala Ala Lys Ala Trp Gly Ser Leu Gln Gly Pro Pro Val Leu Cys Leu	
23 28 33 38	
cac ggc tgg ctg gac aat gcc aac tcc ttc gac aga ctc atc cct ctt	257
His Gly Trp Leu Asp Asn Ala Asn Ser Phe Asp Arg Leu Ile Pro Leu	
39 44 49 54	
ctc ccg caa gac ttt tat tac gtt gcc atg gat ttc gga ggt cat ggg	305
Leu Pro Gln Asp Phe Tyr Tyr Val Ala Met Asp Phe Gly Gly His Gly	
55 60 65 70	
ctc tcg tcc cat tac agc cca ggt gtc cca tat tac ctc cag act ttt	353
Leu Ser Ser His Tyr Ser Pro Gly Val Pro Tyr Tyr Leu Gln Thr Phe	
71 76 81 86	
gtg agt gag atc cga aga gtt gtg gca ggt aag aaa cag agt gtg tat	401
Val Ser Glu Ile Arg Arg Val Val Ala Gly Lys Lys Gln Ser Val Tyr	
87 92 97 102	
ttt cgg cgg tgt ggg ggg tgc tct agg gca ccc cct ctt atc act gga	449
Phe Arg Arg Cys Gly Gly Cys Ser Arg Ala Pro Pro Leu Ile Thr Gly	
103 108 113 118	
ggc ggg gta gga tcc agg aag cag cgc tgg cct gag agt ggg gcc tgg	497

Gly Gly Val Gly Ser Arg Lys Gln Arg Trp Pro Glu Ser Gly Ala Trp
119 124 129 134

gct ctg gcc cca ggt ctg cca gca att cac ggg aga tct tgg gaa agt 545
Ala Leu Ala Pro Gly Leu Pro Ala Ile His Gly Arg Ser Trp Glu Ser
135 140 145 150

tga agag ttcgcttcct ccagtgggtc ccccaagcta gtctcctggg tggacacccc 602
*
151

agatgctggg aaggatttc ctgagcctgg ggactagaag caagatcgta ggctgagcct 662
gtgcccgcc ggaccttctg gtccttgca ttccagcct tgaaatggaa tcgattctcc 722
attctgggcc acagttcgg tgagtacagt ggccaggagc tgaccgggcc cggagtaggg 782
ctgggaggga aggataggag ctgctgcccc accccttcc cctgcactta tgagatctgc 842
aaagagagat gagagggta gtcagaggtt gaccactgta ccctctgacc tcaggcaact 902
gcccgaaggg acacagggat gagggaaatg tggcttttg agtggtcagg tctgtatgaag 962
gggacatcat ggcggccatg ctgagcccc agccacccat atggtgcccc cccccaact 1022
ggtgggaaga agcttttaggg tatgcagctg gggagggagt gaggaaatgt caccacagc 1082
tctttgtcc cccaggtggc gtcgtggacg gaatggtgag tagatggctt tgtctggcca 1142
actggggctc cttgggtgg agtggggagg ggagcacgaa ttccgccaca gtgaa 1197

<210> 169
<211> 2046
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (325)..(1320)

<400> 169

caaggagcac aggtcctcgt tcaggacgt gtaatccttg ccatcgtaag caagctggtg 60
atacccgccg agtaggcgcc cgtccgaccc cacgtcgacg acagacatcc tctagatggg 120
tgtgagaccc tggcccccgc cccgcggcca gccccgcca ccgagccccg ccctcgccag 180
gaccaacctc gcggggattt tggctgaaaa taaaacgggg taacggctcc tgggcctctc 240
ccgggtcaag ggtctccagg tcccgctgcc tcggcgtgga tctcggaccc agagactcgg 300
ggagacccgg gcgggtccgtg gggg atg tgg agg ggt agt gac ctg cgc ccc 351
Met Trp Arg Gly Ser Asp Leu Arg Pro

cg ^g cc ^g gt ^g t ^c a ^t c ^t a ^c g ^g c ^t c ^t a ^c ct ^g g ^t t ^t g ^t a ^g t ^a g ^c c ^g c ^t a ^g	399
Arg Pro Val Ser Leu Thr Gly Leu Thr Leu Val Val Val Ala Ala Gln	
10 15 20 25	
gg ^t cc ^g ca ^g gt ^t ca ^c tc ^g g ^t a ^{aa} ct ^g t ^g c ^{tt} g ^g c ^{tt} g ^g c ^g g ^g t ^{cc}	447
Gly Pro Gln Val His Ser Val Lys Leu Cys Phe Gly Leu Gly Gly Pro	
26 31 36 41	
t ^g t ^c c ^t c ^t t ^t c ^c a ^t a ^t t ^t c ^g c ^{cc} c ^t c ^t c ^t c ^t c ^t a ^t c ^{ca} c ^g c ^g	495
Cys Leu Leu Phe Pro Ile Phe Arg Pro Leu Leu His Pro Arg Arg	
42 47 52 57	
cc ^g cg ^g c ^t c ^t c ^t g ^{gg} a ^c c ^{gt} g ^{gc} g ^t c ^{gt} g ^{ag} c ^{cg} c ^{ac} g ^{ca}	543
Pro Arg Leu His Pro Gly Thr Arg Gly Val Ala Val Glu Pro His Ala	
58 63 68 73	
ct ^g c ^{gt} g ^{tc} c ^{ac} g ^{tc} g ^{cc} c ^{ac} g ^{ga} g ^{ag} g ^a g ^{cg} g ^{gg} a ^t c ^{cg} c ^g	591
Leu Arg Val Val His Val Ala His Gly Glu Ala Gly Ile Arg Ala	
74 79 84 89	
g ^{cc} g ^{gg} c ^{cc} g ^{ga} c ^{at} g ^{gt} g ^{gt} g ^{aa} a ^t a ^t c ^c t ^c a ^a g ^{ga} g ^t a ^{ag} c ^{tg}	639
Ala Gly Pro Gly His Gly Gly Val Glu Ile Pro Gln Gly Val Ser Leu	
90 95 100 105	
g ^{ga} g ^{ca} a ^{gg} a ^{gg} g ^{gg} ct ^g a ^{ga} c ^{cc} t ^c c ^{ga} c ^{cc} t ^c c ^{cc} t ^c c ^{gg} c ^{ac} c ^{gc}	687
Gly Ala Arg Arg Gly Leu Arg Pro Ser Arg Pro Ser Ser Arg His Arg	
106 111 116 121	
a ^{ac} c ^{gg} g ^{tt} c ^c t ^g c ^{cc} c ^{cc} c ^{gg} a ^{gg} c ^{cc} c ^{ta} g ^{ct} a ^c t ^{cc} c ^{ac}	735
Asn Arg Val Pro Ala Pro Pro Gly Arg Pro Leu Ala Thr Pro His	
122 127 132 137	
a ^{ga} c ^{gc} c ^{gt} t ^{tc} c ^c t ^c g ^{ac} c ^{cc} g ^{ca} c ^t c ^t a ^{cc} t ^{gc} c ^{ca} g ^{gt} c ^{tg} g ^{gt}	783
Arg Arg Arg Phe Pro Pro Asp Pro Ala Leu Thr Cys Pro Gly Leu Gly	
138 143 148 153	
c ^{ag} g ^{ac} c ^{ag} g ^{gc} c ^{cc} c ^{ga} g ^{ag} c ^{ag} c ^{ag} a ^{ag} c ^{ag} g ^{gt} t ^{cg} g ^{gg} c ^{gc} c ^{at}	831
Gln Asp Gln Gly Pro Arg Glu Gln Gln Lys Gln Gly Ser Gly Arg His	
154 159 164 169	
g ^{ac} a ^{cc} a ^{tc} c ^t g ^{gc} g ^{ac} t ^{gg} g ^{aa} g ^{aa} t ^{cg} g ^{ag} t ^{cc} c ^{gg} t ^{gg} g ^{tg} c ^{gt}	879
Asp Thr Ile Leu Gly Asp Trp Glu Glu Ser Glu Ser Arg Trp Val Arg	
170 175 180 185	
g ^{gg} a ^{ac} t ^{tt} a ^{ga} a ^{cc} g ^{gg} a ^{cc} g ^{cg} g ^{ct} a ^{ca} t ^{tg} a ^{tt} g ^{gc} t ^{tc} t ^{ct} a ^{ga}	927
Gly Asn Phe Arg Thr Gly Thr Ala Ala Thr Leu Ile Gly Phe Ser Arg	
186 191 196 201	
a ^{ac} c ^{cg} a ^{ca} c ^t a ^{at} g ^{gg} a ^{gt} g ^{ag} a ^{ac} t ^{gg} g ^{gc} a ^{gc} c ^{cg} g ^{tg} a ^{gt} a ^{cc}	975
Asn Pro Thr Leu Asn Gly Ser Glu Asn Trp Gly Ser Pro Val Ser Thr	
202 207 212 217	
c ^{ag} g ^a a ^{aa} g ^{ga} c ^{cc} g ^{ac} a ^{ca} g ^{gt} t ^{gg} g ^{ag} a ^{gg} a ^{ag} a ^{ga} a ^{ac} c ^{ct}	1023
Gln Glu Glu Gly Pro Asp Thr Gly Trp Glu Arg Glu Lys Arg Asn Pro	
218 223 228 233	

gca aag atg ggg aat gcc cag cgc tgg gcc tcc cca atc cat aca ccg Ala Lys Met Gly Asn Ala Gln Arg Trp Ala Ser Pro Ile His Thr Pro 234 . 239 244 249	1071
cct ttg ggg cct gag atc ctg aga gcc acg cct gag gcc ctg gga ctt Pro Leu Gly Pro Glu Ile Leu Arg Ala Thr Pro Glu Ala Leu Gly Leu 250 255 260 265	1119
cgc cct gac ccc gct act tct gtg cca agc gct ctg tct caa tgt ttc Arg Pro Asp Pro Ala Thr Ser Val Pro Ser Ala Leu Ser Gln Cys Phe 266 271 276 281	1167
cct gag tct tgg ccc agg agc tgt ctg aga aac cag gga gaa acc ctc Pro Glu Ser Trp Pro Arg Ser Cys Leu Arg Asn Gln Gly Glu Thr Leu 282 287 292 297	1215
gga atg ggc ccc gtc cct ctc tct tca ctt tgc atc acg gaa tcc ccg Gly Met Gly Pro Val Pro Leu Ser Ser Leu Cys Ile Thr Glu Ser Pro 298 303 308 313	1263
tcc cag aac tgg act ccc tgc ctc cta ctc ctt acc tgt ccc cgt gga Ser Gln Asn Trp Thr Pro Cys Leu Leu Leu Thr Cys Pro Arg Gly 314 319 324 329	1311
ctc ttc tag aagaaaa atcacccccag ggagcttgtt gccagagagt gagcttgccc Leu Phe * 330	1367
tggaaatgga ggtgttagaga cagggttttt tggtgttgtt gtttgttgt ttttaaatc	1427
tggaaaagtt gtgcctgagt gcatgagata gaatagagac cagtttgctt tttgtttatt	1487
aactacagtg gtagcagaa tcggtaac tcctaattgtat caggaatcta atcgccaaa	1547
aatgtgactt tggcccttg acatataat gtgtctaaaa gcattacaac aggaatcaca	1607
aagctcctaa gtttacactt cccagacaat gtatctgtga ctcccgcttg tagtatttt	1667
aatttacctt cattccatag ccctgagttt ctgtgtgagt ccaggacatc tcctaataca	1727
aggtagccac tggttacta tatgttgtaa ccaggagcca gtacggactt tattcatctc	1787
acagtggcaa gcaactaatg cagtcacaat gcccctcacc agtgctcatg cactgcctgt	1847
tttttaggaag tatccacttc taagtgttgtt gtatattttat tatgaacact tagtatttt	1907
taaacctgat taacataaaa aaatttagttt ttaggcagac coacataagg tattaaaggc	1967
caactgcaaa gatcaccctg caaggctctg tagattgatg tattaaaata tataaaacaa	2027
tgtgtttaaa aaaaaaaaaa	2046

<210> 170
<211> 2062

<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (785)..(994)

<400> 170

tgcacgaccg	gtccggatt	cccggtcga	cccacgcgtc	cgggcggaac	ggaaatagtt	60
ttcaacgtct	atttcattcc	ctgcttcaga	ggacctctt	aatcttgat	tttggccct	120
gtttctaaga	aaagcaactg	aaaaggtcgt	aataccgccc	ctgagaaaaa	aggagcagcg	180
ctaaataatc	gagaaaatgc	ctcctttga	aacggatata	gagatggaaa	caagatataa	240
gaaggattga	gaatcatata	atacaggagc	ttaaacacct	atgcgcgtg	ataaagaggg	300
tactattaga	gcgcttgaa	aataccagga	agttgagaga	gttaacagaa	gggcgcacgc	360
<u>tggattggcc</u>	<u>acaaaatcga</u>	<u>attactgaag</u>	<u>taagtgc当地</u>	<u>acgacaaaatt</u>	<u>gtcacagaat</u>	420
acagagaaaa	ggggaaaaga	aattaagagg	agaaaaagag	agatctagag	ggccggtcca	480
ggagatacaa	tctatgcata	ataggaatac	ctgaaactga	ggacagagca	agtggagctg	540
aaacaataaa	ggatctactt	gaaaaaattt	tccagaattt	aagaacgaac	tagatctaca	600
aatggaaaag	gctcatagga	tacctttaaa	gtttaatgaa	aagaaagcag	catctagaca	660
tatccgggtg	acgaaaaatcga	atttcaaaga	cgaaacattt	tacaagcatc	cagtcagaga	720
aagcaggtta	cttacaaagg	ggcaaaagtc	aggctgacct	cagattttc	tcctgcaatt	780
ctaa atg cca gaa gac agt gga aca ata tct aga gtg tta agg gaa aat	Met Pro Glu Asp Ser Gly Thr Ile Ser Arg Val Leu Arg Glu Asn					829
1	5	10				
aat ttt gag cca aga att ata tac tct gcc aag tta tca ttt ctt tac						877
Asn Phe Glu Pro Arg Ile Ile Tyr Ser Ala Lys Leu Ser Phe Leu Tyr						
16	21	26				31
aaa gga aac tgg aag aca ttc tta gat ata cag ggg tta gga aag tat						925
Lys Gly Asn Trp Lys Thr Phe Leu Asp Ile Gln Gly Leu Gly Lys Tyr						
32	37	42				47
atc aac caa gaa ctt tcc ctg aaa att ttg ctg aag gat tta ctg cag						973
Ile Asn Gln Glu Leu Ser Leu Lys Ile Leu Leu Lys Asp Leu Leu Gln						
48	53	58				63
cta aca gag aac ctg aat taa aa taagaatagg gaggaattt tatgaaagaa						1026
Leu Thr Glu Asn Leu Asn *						
64	69					
ctgatggtat	gcattaaaac	tagttaagga	gcattaagtt	taaattgtta	tgtatagggc	1086
ataaaaacta	aataaaaaaa	tagaaacata	agctgggtgt	aaaatttcag	tttacgttta	1146

aactggaagg	gcataccaca	tgttcaatat	attggacaaa	tactgtttta	tttttagcat	1206
gtagtattgt	agatacaaat	acgcacgttc	ttaagctaaa	cctaagtaaa	agggctttgt	1266
caactgttagat	ttgacaaata	acattctaaa	tgtcaaatac	gacaattgga	aaacagtaca	1326
gttttatttc	ccttattttt	aagtatagca	ggaaaaaaat	aacaagtttgc	tccatgttac	1386
tactgatact	gtaaagaaac	ttccaaatca	ctggtttggg	agggggtgga	tacatcctca	1446
ttttctgtac	atgatgcac	gggaaaaaca	gtagttactg	catcatatag	ttccaagtaa	1506
atcatatagt	tccaaagtaaa	tttgacatgg	aaataagtgt	taactacaaa	aatagaatat	1566
atacattcca	atgtttggaa	aagaagtgg	aaaaagaaaa	atagcaaaaa	gacactaaaa	1626
tttagcaaaaa	gtagattgac	agtacagatg	acctataaac	tggtaaata	gcccttattac	1686
aattgaaatt	gggtcaaaaa	tcaatctcta	acctgagata	catttgtata	aaacaaatga	1746
tcaaagagtt	taaagataat	ggaaactata	aatcatagaa	atagcaacat	ttttcttaaa	1806
atctaaacat	aagacatttt	atgtaaaaca	tacaatata	gatgtacat	ttaacaaact	1866
atatggtaaa	taatatgaca	ttaatata	aaatataatgt	tccagatctt	gatgtgggtg	1926
atagttttac	ttatgtacat	cgatatacat	ctattaaaa	acatgtacat	ttaaattgtt	1986
gcattttatg	tattaaaaat	ttattgagta	atccttctgt	atgtattatt	aaagagaata	2046
tagcaaaaaa	aaaaaaa					2062

<210> 171
 <211> 2809
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1936)..(2364)

<400> 171

tcccgggtcg	acccacgcgt	ccgctgggga	cgctaggttc	cggAACCTGA	cctgagctgg	60
ggcctgtgct	tccagcgggt	ggggggggc	ctgggtgtgct	ggcatcaagt	aagccgacta	120
cctcggcaaa	ggcttaggga	caagagacca	gcagcctgaa	ctggctgggg	catccggaag	180
gcttagatct	tgtggccaag	agttcagacc	gtggcgaagt	ggagagtgac	atgcagttgg	240
atggcgggtga	ctgcgtggtc	ctgcaaccct	ggttccagtc	tggcaagcat	tgttagacactg	300
gctgctgaag	actgacgggg	cccagggtcc	gctgccccca	ccgccatcac	cacctcgaa	360

cccagggtaa	cgctgtcagt	ctttggacca	acctcgctgt	gcctaacaag	aattccagaa	420							
gtcacccatc	cgaaaggcac	tggcccatga	cactctccac	ttccaatctt	aatctttta	480							
cttcataacct	tgtctcagat	cttcctggt	acccttccc	cacgccccta	gataatccat	540							
ctcaattcct	catgctaatt	gaggagctat	ggctgcaagg	cacttccag	gatttcacac	600							
ctacacaat	ctccttttc	tcctttgcc	ttctctgctt	atggatatt	ctgagtc	660							
acccccaaatc	actgacagct	gggccccctt	catcagcctc	acacaccacg	tattaagtca	720							
gtcacaatct	ccctctcct	ctaactgctg	gatttgtctt	tctacacaca	cccaatgatt	780							
cacggctctt	ccggctgacc	tacttacatg	gacacagtcc	aacgtgagct	tacacatttc	840							
ttacttggt	ataccattct	tggctgattc	attcctgaaa	ccggttcata	acctggaaac	900							
tcagctaaac	acctttcctt	caaactcagc	tctctcagca	tggttcagg	taggctgtt	960							
gcgccttc	acctaatacg	ttctggacta	acatccatac	aaaccaacac	agcatcatct	1020							
aaaccaccaa	tatggggta	ccatttctac	tcaaacttcc	ttcatatccc	cacccccc	1080							
atgtctcagc	cgaacctacc	ctaattccagc	ccacgcccaca	atgggtggac	aggccccca	1140							
gtccctatgt	ggtcttattt	ttacccttgc	actccctgta	gaccatcaat	tctacaccct	1200							
aattacaaaa	tcatatccac	ctctgcctgg	cagaaggtgt	tatgctttc	tggctcgct	1260							
accatccaca	cattccatac	cctcaccacc	ggatcctctt	ttctttcctt	ccatccaatt	1320							
cctggcttcc	ccgctgccaa	ctctgctctc	tatgtctcca	gtttaaaggt	gccccctgga	1380							
aaaaatgtaa	caattccctc	acctgtgact	ggtacctgac	agccaccaca	ccggggcagc	1440							
aatggctaac	ggttgacaaa	gacaatttct	ttctctctcc	aaaaccaaac	agccttcatc	1500							
aactccctag	ccaaagactcc	ctatcaggcc	cttacaggtg	ccgctctggc	tggcagttac	1560							
ccaaatttggg	aaaacgaaaa	taccctatca	tggctaccta	ccttcaccta	caacttctgc	1620							
ctgtccaccc	ccagtcctt	cttttgtgt	gatacaaact	gatatcttg	cctaccagcc	1680							
aactggtcag	gaacttgcac	cctggctttt	caggctccaa	ccatcaacat	cctacccct	1740							
aaccaaacta	ttctaatttc	tgttagaagcc	tctatctcct	cttcacccat	aagaataaaa	1800							
tgggctctac	atctcatcac	cctgctaaca	ggattaggca	tcactgctgc	acttggcact	1860							
ggaatagcag	gcataaccac	ctcaatcacc	tcataccaaa	cactattcac	aaccctttct	1920							
aacaccgtag	aagat	atg	cac	act	tcc	att	acc	agt	ctc	caa	cga	caa	tta
	Met	His	Thr	Ser	Ile	Thr	Ser	Leu	Gln	Arg	Gln	Leu	

gac ttc ctc gtg gga gtc atc ctt caa aac tgg aga gtc ctg gac ctc Asp Phe Leu Val Gly Val Ile Leu Gln Asn Trp Arg Val Leu Asp Leu 13 18 23 28	2019
cta acc act gag aaa ggg ggt acc tgc ata tac ctc cag gaa gaa tgc Leu Thr Thr Glu Lys Gly Gly Thr Cys Ile Tyr Leu Gln Glu Glu Cys 29 34 39 44	2067
tgt ttc tgt gtt aat gaa tct ggc att gtt cat atc gca gtt cgt agg Cys Phe Cys Val Asn Glu Ser Gly Ile Val His Ile Ala Val Arg Arg 45 50 55 60	2115
ctt cat gac agg gct gca gag ctt aga cat caa gtc gct gac tcc tgg Leu His Asp Arg Ala Ala Glu Leu Arg His Gln Val Ala Asp Ser Trp 61 66 71 76	2163
tgg caa gga tca tcc ctt cta aga tgg ata ccc tgg gtt gcc ccc ttc Trp Gln Gly Ser Ser Leu Leu Arg Trp Ile Pro Trp Val Ala Pro Phe 77 82 87 92	2211
cta gga ccc ctg atc ttc ctc ttc ctg tta cta atg att ggg cca tgc Leu Gly Pro Leu Ile Phe Leu Phe Leu Leu Leu Met Ile Gly Pro Cys 93 98 103 108	2259
ata ttt aac ctt gta tcc cgc ttc att tcc caa agg ctg aat tgt ttt Ile Phe Asn Leu Val Ser Arg Phe Ile Ser Gln Arg Leu Asn Cys Phe 109 114 119 124	2307
atc cag gca agc atg caa aaa cac att gat aat ata ttt cac ctt tgc Ile Gln Ala Ser Met Gln Lys His Ile Asp Asn Ile Phe His Leu Cys 125 130 135 140	2355
cac gtc taa taccaga gcctacgagg aaaccattcg gaagctccag aaccaggccc His Val *	2411
141	
cta atcaca cccccctatc cagcaggaag cagccagatg atcaacgacg cccttttcc	2471
ttttatact aaagtaagaa ataagaatgt tagcccaa ac tgcactattt tgcagacccc	2531
taccat tta caaactggtc agagtggaaa attccaccag ggcctgagct gtgagaaaca	2591
tcctgtcagg caggtcccag gcctaacccc tggctgcact aaattccttc attatcagca	2651
gccaaacaca ccccccac cccat ttca caacaatccc agaccttcc tgccgggac	2711
tgttaactggt ccagcctgta agcgggaagg gggctctggc actagctggt acccccttc	2771
cgcagg tctt tctcccaata aatctgtgtt gccattga	2809

<210> 172
 <211> 1882
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (181)..(1194)

<400> 172

ctccggcagg	cgtgatgtat	ataactatct	attcgatgat	gaagatacc	caccaaacc	60
aaaaaaaagag	atctctcgag	gatccgaatt	cgcgccgcg	tcgactttta	aaagaataga	120
tagacgttga	attattgata	ttctccctct	ctctctctag	gatacttaca	gagagctaca	180
atg gaa aag tcc tgg atg ctg tgg aac ttt gtt gaa aga tgg cta ata						228
Met Glu Lys Ser Trp Met Leu Trp Asn Phe Val Glu Arg Trp Leu Ile						
1	5	10	15			
gcc ttg gct tca tgg tct tgg gct ctc tgc cgt att tct ctt tta cct						276
Ala Leu Ala Ser Trp Ser Trp Ala Leu Cys Arg Ile Ser Leu Leu Pro						
17	22	27	32			
tta ata gtg act ttt cat ctg tat gga ggc att atc tta ctt ttg tta						324
Leu Ile Val Thr Phe His Leu Tyr Gly Gly Ile Ile Leu Leu Leu Leu						
33	38	43	48			
ata ttc ata tca ata gca ggt att ctg tat aaa ttc cag gat gta ttg						372
Ile Phe Ile Ser Ile Ala Gly Ile Leu Tyr Lys Phe Gln Asp Val Leu						
49	54	59	64			
ctt tat ttt cca gaa cag cca tcc tct tca cgt ctt tat gtt ccc atg						420
Leu Tyr Phe Pro Glu Gln Pro Ser Ser Arg Leu Tyr Val Pro Met						
65	70	75	80			
ccc act ggc att cca cat gaa aac att ttc atc aga acc aaa gat gga						468
Pro Thr Gly Ile Pro His Glu Asn Ile Phe Ile Arg Thr Lys Asp Gly						
81	86	91	96			
ata cgt ctg aat ctt att ttg ata cga tac act gga gac aat tca ccc						516
Ile Arg Leu Asn Leu Ile Leu Ile Arg Tyr Thr Gly Asp Asn Ser Pro						
97	102	107	112			
tat tcc cca act ata att tat ttt cat ggg aat gca ggc aac ata ggt						564
Tyr Ser Pro Thr Ile Ile Tyr Phe His Gly Asn Ala Gly Asn Ile Gly						
113	118	123	128			
cac agg ttg cca aat gca tta ctt atg ttg gtt aac ctc aaa gtt aac						612
His Arg Leu Pro Asn Ala Leu Leu Met Leu Val Asn Leu Lys Val Asn						
129	134	139	144			
ctt ttg ctg gtt gat tat cga gga tat gga aaa agt gaa gga gaa gca						660
Leu Leu Leu Val Asp Tyr Arg Gly Tyr Gly Lys Ser Glu Gly Glu Ala						
145	150	155	160			
agt gaa gaa gga ctc tac tta gat tct gaa gct gtg tta gac tac gtg						708
Ser Glu Glu Gly Leu Tyr Leu Asp Ser Glu Ala Val Leu Asp Tyr Val						
161	166	171	176			
atg act agc cct gac ctt gat aaa aca aaa att ttt ctt ttt ggc cgt						756

Met	Thr	Ser	Pro	Asp	Leu	Asp	Lys	Thr	Lys	Ile	Phe	Leu	Phe	Gly	Arg	
177				182					187					192		
tcc	ttg	ggt	gga	gca	gtg	gct	att	cat	ttg	gct	tct	gaa	aat	tca	cat	804
Ser	Leu	Gly	Gly	Ala	Val	Ala	Ile	His	Leu	Ala	Ser	Glu	Asn	Ser	His	
193				198					203					208		
agg	att	tca	gcc	att	atg	gtg	gag	aac	aca	ttt	tta	agc	ata	cca	cat	852
Arg	Ile	Ser	Ala	Ile	Met	Val	Glu	Asn	Thr	Phe	Leu	Ser	Ile	Pro	His	
209				214					219					224		
atg	gcc	agc	act	tta	ttt	tca	ttc	ttt	ccg	atg	cgt	tac	ctt	cct	tta	900
Met	Ala	Ser	Thr	Leu	Phe	Ser	Phe	Phe	Pro	Met	Arg	Tyr	Leu	Pro	Leu	
225				230					235					240		
tgg	tgc	tac	aaa	aat	aaa	ttt	ttg	tcc	tac	aga	aaa	atc	tct	cag	tgt	948
Trp	Cys	Tyr	Lys	Asn	Lys	Phe	Leu	Ser	Tyr	Arg	Lys	Ile	Ser	Gln	Cys	
241				246					251					256		
aga	atg	cct	tca	ctt	ttc	atc	tct	gga	ctc	tca	gat	caa	tta	att	cca	996
Arg	Met	Pro	Ser	Leu	Phe	Ile	Ser	Gly	Leu	Ser	Asp	Gln	Leu	Ile	Pro	
257				262					267					272		
cca	gta	atg	atg	aaa	caa	ctt	tat	gaa	ctc	tcc	cca	tct	cg	act	aag	1044
Pro	Val	Met	Met	Lys	Gln	Leu	Tyr	Glu	Leu	Ser	Pro	Ser	Arg	Thr	Lys	
273				278					283					288		
aga	tta	gcc	att	ttt	cca	gat	ggg	act	cac	aat	gac	aca	tgg	cag	tgc	1092
Arg	Leu	Ala	Ile	Phe	Pro	Asp	Gly	Thr	His	Asn	Asp	Thr	Trp	Gln	Cys	
289				294					299					304		
caa	ggc	tat	ttc	act	gca	ctt	gaa	cag	ttc	atc	aaa	gaa	gtc	gta	aag	1140
Gln	Gly	Tyr	Phe	Thr	Ala	Leu	Glu	Gln	Phe	Ile	Lys	Glu	Val	Val	Lys	
305				310					315					320		
agc	cat	tct	cct	gaa	gaa	atg	gca	aaa	act	tca	tct	aat	gta	aca	att	1188
Ser	His	Ser	Pro	Glu	Glu	Met	Ala	Lys	Thr	Ser	Ser	Asn	Val	Thr	Ile	
321				326					331					336		
ata	taa	tgtttccctt	tttgattatt	gcattgtatt	ttaatttgtg	cagaatgata										1244
Ile	*															
337																
aagaatgttc	cttttagaag	tgtgttatgt	ctgtacctgt	ctgaagagtgt	acattaaact											1304
ttgaaaggac	ttcactgctc	ctttacgata	ttccaaatag	ttttttacat	tggaaaaact											1364
aattcttggg	attcttcat	acattttcat	caaaaacttgc	agtgtgattta	tgtattcata											1424
tcttcagttt	aatatgtcag	tataatagat	attgtcaaa	agtttcttgt	tgctaaagtgt											1484
gtgtaatctg	ttcacacagat	gaatagctag	atgtggaaag	agatatgtaa	acaagaaacc											1544
tttgggtatt	gtttcttaag	taaatattgg	gacaatcatg	gtaagcaaac	ttagttctgt											1604
aactgcattt	ttcaccttaa	aagttaaatg	aaatgcattg	tggattttta	ttcccttgaat											1664

tatgcaatgc aacattttac atgtaaatag cactggtcat atactgatgt atatggttat	1724
ctgggttata tctatTTTA tgtaaactct atTTTgtttt tggcaagaag tgaaattgag	1784
acttatgtgc aggttgccat tgaatttgc tctggtaat gctgagatcc agcttttct	1844
tacaAataaaa tgggaccctg ttttccaaaa aaaaaaaaa	1882

```
<210> 173
<211> 1713
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (170)..(1153)
```

<400> 173
 aggggcttac aatcgacgc tcgataccgc tatgaccact acgctttgc aaaaagctat 60
 ttaggtgaca ctatagaagg tacgcctgca ggtaccggtc cggaattccc gggtcgaccc 120
 acgcgtccgc ggacgcgtgg gaggggtttt aagtgttagtt gccgacgca atg gca 175
 Met Ala
 1
 gcc ttt gca gtg gaa cct cag ggg ccc gcg tta gga tct gaa cca atg 223
 Ala Phe Ala Val Glu Pro Gln Gly Pro Ala Leu Gly Ser Glu Pro Met
 3 8 13 18
 atg ctg ggt tca ccc aca tct cca aag cca gga gtt aat gcc cag ttc 271
 Met Leu Gly Ser Pro Thr Ser Pro Lys Pro Gly Val Asn Ala Gln Phe
 19 24 29 34
 tta cct gga ttt tta atg ggg gat ttg cca gct ccg gtg act cca caa 319
 Leu Pro Gly Phe Leu Met Gly Asp Leu Pro Ala Pro Val Thr Pro Gln
 35 40 45 50
 cct cga tca att agt ggc cct tca gta gga gta atg gaa atg aga tca 367
 Pro Arg Ser Ile Ser Gly Pro Ser Val Gly Val Met Glu Met Arg Ser
 51 56 61 66
 cct tta ctt gca ggt ggg tca cca cca caa cca gtt gta cca gct cat 415
 Pro Leu Leu Ala Gly Gly Ser Pro Pro Gln Pro Val Val Pro Ala His
 67 72 77 82
 aaa . gat aaa agt ggc gct cca cca gtt aga agt ata tat gat gac att 463
 Lys Asp Lys Ser Gly Ala Pro Pro Val Arg Ser Ile Tyr Asp Asp Ile
 83 88 93 98
 tct agc cca gga ctt gga tca aca cct tta act tca aga aga cag cca 511
 Ser Ser Pro Gly Leu Gly Ser Thr Pro Leu Thr Ser Arg Arg Gln Pro
 99 104 109 114

aac att tca gta atg cag agt cct ctt gtt gga gtt aca tct act cct		559
Asn Ile Ser Val Met Gln Ser Pro Leu Val Gly Val Thr Ser Thr Pro		
115 120 125 130		
gga aca ggg caa agt atg ttt agt cca gca agt atc ggt cag cca cga		607
Gly Thr Gly Gln Ser Met Phe Ser Pro Ala Ser Ile Gly Gln Pro Arg		
131 136 141 146		
aag acg aca tta tct cct gcc cag ttg gat cct ttt tat actcaa gga		655
Lys Thr Thr Leu Ser Pro Ala Gln Leu Asp Pro Phe Tyr Thr Gln Gly		
147 152 157 162		
gat tct ttg act tca gaa gat cac ctc gat gac tct tgg gtg act gta		703
Asp Ser Leu Thr Ser Glu Asp His Leu Asp Asp Ser Trp Val Thr Val		
163 168 173 178		
ttt ggg ttt cct caa gca tct gct tcc tac ata tta cta caa ttt gca		751
Phe Gly Phe Pro Gln Ala Ser Ala Ser Tyr Ile Leu Leu Gln Phe Ala		
179 184 189 194		
cag tat ggg gga ata tct tat aac atg tgg atg tct aat aca gga aat		799
Gln Tyr Gly Gly Ile Ser Tyr Asn Met Trp Met Ser Asn Thr Gly Asn		
195 200 205 210		
tgg atg cat att cgt tat caa tct aaa ctg cag gct cgaa gaa gcc tta		847
Trp Met His Ile Arg Tyr Gln Ser Lys Leu Gln Ala Arg Lys Ala Leu		
211 216 221 226		
agc aaa gat ggg agg att ttt gga gaa tcc atc atg att ggt gta aaa		895
Ser Lys Asp Gly Arg Ile Phe Gly Glu Ser Ile Met Ile Gly Val Lys		
227 232 237 242		
cca tgt att gac aaa agt gtt atg gaa agc agt gac aga tgt gct tta		943
Pro Cys Ile Asp Lys Ser Val Met Glu Ser Ser Asp Arg Cys Ala Leu		
243 248 253 258		
tca tct cca tct tta gcc ttt aca cca atc aaa act cta ggt aca		991
Ser Ser Pro Ser Leu Ala Phe Thr Pro Pro Ile Lys Thr Leu Gly Thr		
259 264 269 274		
cca aca caa cct gga agt act cct agg att tct acc atg aga cct ctt		1039
Pro Thr Gln Pro Gly Ser Thr Pro Arg Ile Ser Thr Met Arg Pro Leu		
275 280 285 290		
gct aca gca tac aaa gcc tct act agt gat tat cag gtt att tct gac		1087
Ala Thr Ala Tyr Lys Ala Ser Thr Ser Asp Tyr Gln Val Ile Ser Asp		
291 296 301 306		
aga caa acg cca aaa aaa gat gaa agt ctt gta tcc aaa gca atg gag		1135
Arg Gln Thr Pro Lys Lys Asp Glu Ser Leu Val Ser Lys Ala Met Glu		
307 312 317 322		
tac atg ttt ggc tgg tag tagaac accaagaagg aggttgctac actaaaacag		1189
Tyr Met Phe Gly Trp *		
323 328		
agtagcaga gtgctgctgg ttccctcggt tagttatata actgttcctg cagtattgga		1249

tagctatctc atacttcttt tagaaagaag ccttttcat taaggataca acctatttg	1309
agctcgcact ttaaaaagatg cttgagatac attttaaaga aaactaaaaa tccctgtaaa	1369
taggattttg tgcttctgt aacagtgcac gtttcagcac agaaaactca gcattgatta	1429
ttgtaaaatta aataactgaa attgtggtga gacgtcatag ttttcatgag aacgtggggg	1489
tgaatttcat gaagggaac tatagttatt tctaccgaca caaatattat aattagcaat	1549
ttgaattatg gtctttaat ttagatagta tttaatattt taattatcct ttttgtata	1609
tgcctgtca cagagtgtcc tcttggtga ttctaaaacg agcattctt taaaaaacct	1669
aaagtttctt gataataaac attgtcaatg ataaaaaaaaa aaaa	1713

<210> 174
 <211> 4069
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (771) .. (2894)

 <220>
 <221> misc_feature
 <222> (1) .. (4069)
 <223> n = a,t,c or g

<400> 174	
tttttggaa tttttggacg cggttaacca aatttctcca aacgggaaca cggtttgtc	60
cctgtttttc gcggttttta atcaggcacc cactatgagg ggaaattttg ccctcggagg	120
cccaagaatt gggcaggag gttttttttt aaaatagtgc ccagtccaag tggaaatgg	180
agaatgaaac aaataaatct gtaaactggt tgtgatcaat tagttgtaaa caccgccca	240
ctcagaccag ccatgggttt gccctttgat aaggcaaag acacatttt cgtggtatca	300
gggaaaaaga tttaaaaaga caaggcaaat ttaagtaggc tcattggctt tccagttgg	360
ttggaaagtt cctctccgat gactgttata ttctcaaaga aatatgagga gaggggcagg	420
gcatggtggc tcacatccgt aatcctagca aatcatatgt gcctacagcc aacgccttct	480
tcgctcaactg gccaactgga aacttcagtc cccccatgcc tcccgctct cacccagggg	540
ccaataggaa tgatcagagg ttgcgaacctt agtgcatac agcatagtaa ttgcaattgg	600
ctattggagc tgtcgatcgt gaagtatgcg gggccgtcca gcttgcctat ataagacgag	660

gacannacgc cgccgcctgt gtcatccgcc attttgtag aagcaagggtg gcctccacgt	720
ttcctgagcg ttttcttcgc ttttgcctcg accggccctt gaccacagac atg tct Met Ser 1	776
cg gat cg ttc cg agt cgt ggc ggt ggc ggt ggc ttc cac agg . Arg Asp Arg Phe Arg Ser Arg Gly Gly Gly Gly Gly Phe His Arg 3 8 13 18	824
cgt gga gga ggc ggc cgc ggc ctc cac gac ttc cgt tct ccg Arg Gly Gly Gly Gly Arg Gly Gly Leu His Asp Phe Arg Ser Pro 19 24 29 ; 34	872
ccg ccc ggc atg ggc ctc aat cag aat cgc ggc ccc atg ggt cct ggc Pro Pro Gly Met Gly Leu Asn Gln Asn Arg Gly Pro Met Gly Pro Gly 35 40 45 50	920
ccg ggc cag agc ggc cct aag cct ccg atc ccg cca ccg cct cca cac Pro Gly Gln Ser Gly Pro Lys Pro Pro Ile Pro Pro Pro Pro Pro His 51 56 61 66	968
caa cag cag caa cag cca cca ccg cag cag cca ccg ccg cag cag ccg Gln Gln Gln Gln Pro Pro Pro Gln Gln Pro Pro Pro Gln Gln Pro 67 72 ,77 82	1016
cca ccg cat cag ccg ccg cat cca cag ccg cat cag cag cag cag Pro Pro His Gln Pro Pro His Pro Gln Pro His Gln Gln Gln Gln 83 88 93 98	1064
ccg ccg cca ccg ccg cag gac tct tcc aag ccc gtc gtt gct cag gga Pro Pro Pro Pro Gln Asp Ser Ser Lys Pro Val Val Ala Gln Gly 99 104 109 114	1112
ccc ggc ccc gct ccc gga gta ggc agc gca cca cca gcc tcc agc tcg Pro Gly Pro Ala Pro Gly Val Gly Ser Ala Pro Pro Ala Ser Ser Ser 115 120 125 130	1160
gcc ccg ccc gcc act cca cca acc tcg ggg gcc ccg cca ggg tcc ggg Ala Pro Pro Ala Thr Pro Pro Thr Ser Gly Ala Pro Pro Gly Ser Gly 131 136 141 146	1208
cca ggc ccg act ccg acc ccg ccg cct gca gtc acc tcg gcc cct ccc Pro Gly Pro Thr Pro Thr Pro Pro Ala Val Thr Ser Ala Pro Pro 147 152 157 162	1256
ggg gcg ccg cca ccc acc ccg cca agc agc ggg gtc cct acc aca cct Gly Ala Pro Pro Pro Thr Pro Pro Ser Ser Gly Val Pro Thr Thr Pro 163 168 173 178	1304
cct cag gcc gga ggc ccg ccg cct ccg ccc gcg gca gtc ccg ggc ccg Pro Gln Ala Gly Gly Pro Pro Pro Pro Ala Ala Val Pro Gly Pro 179 184 189 194	1352
ggt cca ggg cct aag cag ggc cca ggt ccg ggt ggt ccc aaa ggc ggc Gly Pro Gly Pro Lys Gln Gly Pro Gly Pro Gly Gly Pro Lys Gly Gly 195 200 205 210	1400

aaa atg cct ggc ggg ccg aag cca ggt ggc ggc ccg ggc cta agt acg		1448	
Lys Met Pro Gly Gly Pro Lys Pro Gly Gly Pro Gly Leu Ser Thr			
211	216	221	226
cct ggc ggc cac ccc aag ccg ccg cat cga ggc ggc ggg gag ccc cgc		1496	
Pro Gly Gly His Pro Lys Pro Pro His Arg Gly Gly Glu Pro Arg			
227	232	237	242
ggg ggc cgc cag cac cac ccg ccc tac cac cag cag cat cac cag ggg		1544	
Gly Gly Arg Gln His His Pro Pro Tyr His Gln Gln His His Gln Gly			
243	248	253	258
ccc ccg ccc ggc ggg ccc ggc ggc cgc agc gag gag aag atc tcg gac		1592	
Pro Pro Pro Gly Gly Pro Gly Gly Arg Ser Glu Glu Lys Ile Ser Asp			
259	264	269	274
tcg gag ggg ttt aaa gcc aat ttg tct ctc ttg agg agg cct gga gag		1640	
Ser Glu Gly Phe Lys Ala Asn Leu Ser Leu Leu Arg Arg Pro Gly Glu			
275	280	285	290
aaa act tac aca cag cga tgt cgg ttg ttt gtt ggg aat cta cct gct		1688	
Lys Thr Tyr Thr Gln Arg Cys Arg Leu Phe Val Gly Asn Leu Pro Ala			
291	296	301	306
gat atc acg gag gat gaa ttc aaa aga cta ttt gct aaa tat gga gaa		1736	
Asp Ile Thr Glu Asp Glu Phe Lys Arg Leu Phe Ala Lys Tyr Gly Glu			
307	312	317	322
cca gga gaa gtt ttt atc aac aaa ggc aaa gga ttc gga ttt att aag		1784	
Pro Gly Glu Val Phe Ile Asn Lys Gly Lys Gly Phe Gly Phe Ile Lys			
323	328	333	338
ctt gaa tct aga gct ttg gct gaa att gcc aaa gcc gaa ctg gat gat		1832	
Leu Glu Ser Arg Ala Leu Ala Glu Ile Ala Lys Ala Glu Leu Asp Asp			
339	344	349	354
aca ccc atg aga ggt aga cag ctt cga gtt cgc ttt gcc aca cat gct		1880	
Thr Pro Met Arg Gly Arg Gln Leu Arg Val Arg Phe Ala Thr His Ala			
355	360	365	370
gct gcc ctt tct gtt cgt aat ctt tca cct tat gtt tcc aat gaa ctg		1928	
Ala Ala Leu Ser Val Arg Asn Leu Ser Pro Tyr Val Ser Asn Glu Leu			
371	376	381	386
ttg gaa gaa gcc ttt agc caa ttt ggt cct att gaa agg gct gtt gta		1976	
Leu Glu Glu Ala Phe Ser Gln Phe Gly Pro Ile Glu Arg Ala Val Val			
387	392	397	402
ata gtg gat gat cgt gga aga tct aca ggg aaa ggc att gtt gaa ttt		2024	
Ile Val Asp Asp Arg Gly Arg Ser Thr Gly Lys Gly Ile Val Glu Phe			
403	408	413	418
gct tct aag cca gca gca aga aag gca ttt gaa cga tgc agt gaa ggt		2072	
Ala Ser Lys Pro Ala Ala Arg Lys Ala Phe Glu Arg Cys Ser Glu Gly			
419	424	429	434

gtt ttc tta ctg acg aca act cct cgt cca gtc att gtg gaa cca ctt		2120
Val Phe Leu Leu Thr Thr Pro Arg Pro Val Ile Val Glu Pro Leu		
435 440 445 450		
gaa caa cta gat gat gaa gat ggt ctt cct gaa aaa ctt gcc cag aag		2168
Glu Gln Leu Asp Asp Glu Asp Gly Leu Pro Glu Lys Leu Ala Gln Lys		
451 456 461 466		
aat cca atg tat caa aag gag aga gaa acc cct cgt ttt gcc cag		2216
Asn Pro Met Tyr Gln Lys Glu Arg Glu Thr Pro Pro Arg Phe Ala Gln		
467 472 477 482		
cat ggc acg ttt gag tac gaa tat tct cag cga tgg aag tct ttg gat		2264
His Gly Thr Phe Glu Tyr Ser Gln Arg Trp Lys Ser Leu Asp		
483 488 493 498		
gaa atg gaa aaa cag caa agg gaa caa gtt gaa aaa aac atg aaa gat		2312
Glu Met Glu Lys Gln Gln Arg Glu Gln Val Glu Lys Asn Met Lys Asp		
499 504 509 514		
gca aaa gac aaa ttg gaa agt gaa atg gaa gat gcc tat cat gaa cat		2360
Ala Lys Asp Lys Leu Glu Ser Glu Met Glu Asp Ala Tyr His Glu His		
515 520 525 530		
cag gca aat ctt ttg cgc caa gat ctg atg aga cga cag gaa gaa tta		2408
Gln Ala Asn Leu Leu Arg Gln Asp Leu Met Arg Arg Gln Glu Glu Leu		
531 536 541 546		
aga cgc atg gaa gaa ctt cac aat caa gaa atg cag aaa cgt aaa gaa		2456
Arg Arg Met Glu Glu Leu His Asn Gln Glu Met Gln Lys Arg Lys Glu		
547 552 557 562		
atg caa ttg agg caa gag gag gaa cga cgt aga aga gag gaa gag atg		2504
Met Gln Leu Arg Gln Glu Glu Arg Arg Arg Arg Glu Glu Glu Met		
563 568 573 578		
atg att cgt caa cgt gag atg gaa gaa caa atg agg cgc caa aga gag		2552
Met Ile Arg Gln Arg Glu Met Glu Glu Gln Met Arg Arg Gln Arg Glu		
579 584 589 594		
gaa agt tac agc cga atg ggc tac atg gat cca cgg gaa aga gac atg		2600
Glu Ser Tyr Ser Arg Met Gly Tyr Met Asp Pro Arg Glu Arg Asp Met		
595 600 605 610		
cga atg ggt ggc gga gga gca atg aac atg gga gat ccc tat ggt tca		2648
Arg Met Gly Gly Gly Ala Met Asn Met Gly Asp Pro Tyr Gly Ser		
611 616 621 626		
gga ggc cag aaa ttt cca cct cta gga ggt ggt ggc ata ggt tat		2696
Gly Gly Gln Lys Phe Pro Pro Leu Gly Gly Gly Gly Ile Gly Tyr		
627 632 637 642		
gaa gct aat cct ggc gtt cca cca gca acc atg agt ggt tcc atg atg		2744
Glu Ala Asn Pro Gly Val Pro Pro Ala Thr Met Ser Gly Ser Met Met		
643 648 653 658		
gga agt gac atg cgt act gag cgc ttt ggg cag gga ggt gcg ggg cct		2792

Gly	Ser	Asp	Met	Arg	Thr	Glu	Arg	Phe	Gly	Gln	Gly	Gly	Ala	Gly	Pro	
659						664				669				674		
gtg	ggt	gga	cag	ggt	cct	aga	gga	atg	ggg	cct	gga	act	cca	gca	gga	2840
Val	Gly	Gly	Gln	Gly	Pro	Arg	Gly	Met	Gly	Pro	Gly	Thr	Pro	Ala	Gly	
675						680				685				690		
tat	ggt	aga	ggg	aga	gaa	gag	tac	gaa	ggc	cca	aac	aaa	aaa	ccc	cga	2888
Tyr	Gly	Arg	Gly	Arg	Glu	Glu	Tyr	Glu	Gly	Pro	Asn	Lys	Lys	Pro	Arg	
691					696				701				706			
ttt	tag	atgtgatatt	taggcttc	ttccagttt	ttttgtttt	ttgttttagat										2944
Phe	*															
707																
accaatctt	taaattctt	gat	ttttagta	agaaagctat	cttttatgg	atgttagcag										3004
tttattgacc	taatattt	gt	aaatggtctg	tttgggcagg	taaaattatg	taatgcagt										3064
tttggAACAG	gagaattttt	ttt	cctttt	tat	ttttcttt	tttactgtat										3124
aatgtccctc	aagtttatgg	cagtgtac	ct	tgccactg	aatttccaaa	gtgtaccaat										3184
ttttttttt	ttactgtgct	tcaaataaaat	agaaaaatag	ttataatatt	gatcttcaac											3244
tttgcattc	atgcttctat	gcatattagg	ctacgtattc	cacattgaaa	gcatgagagt											3304
gtctaggcct	ttgaatggca	tatgccattt	ctggaaatg	catctggagg	ctaagtattg											3364
ctttctacaa	ataattgccc	ccttgtttt	aaaaagaaga	aatgcattt	gaagtagttt											3424
gatgatttgt	ttggcatata	ggaagcacgc	tggtgctaag	tat	ttttttaa	atggttatgt										3484
aagcaaagct	gaactgtaaa	tcttcaggaa	tatgtattaa	gattgtggaa	tgggtgttaag											3544
acaattggta	gggggtgaaa	gtgggtttga	ttaaatggat	cttttatggc	cctatgatct											3604
atcctttaact	tgaaagcttt	tgaaaagtgg	aaaggtcatt	ttgttgattt	tccccatttc											3664
ttgtttttaa	aagaccaaca	aatctcaagc	cctataaaatg	gcttgtattt	aacttttaca											3724
tttgaattaa	agatgttaaa	catgaagtct	tttcatgtat	tcaagtgatt	tataaagatg											3784
gggtgtagtc	taaaaaacaa	tacttgaaag	taagaaggtt	tagtaactga	gccactgcgc											3844
caggccgatt	aataagattt	cttggattt	agttcacttg	acagttataat	aatgttatgt											3904
ttgagaattt	ggtaactctg	attcttgtat	ccttgaggat	aatcatacc	tttaatttgc											3964
aggatcaggt	gagctgtgtc	cagaaaacca	acgagaagga	gtggaggag	aatgaacgc											4024
ttcattctcg	ttaataaaagg	cattatccaa	attaaaaaaaaa	aaaaaa												4069

<211> 1830
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (104)..(1000)

<400> 175

attgataacg gagatcgagc tcgctagcgt ttcaaactaa gcttggtacc gagctcgat	60
ccactagtcc agtgtggtgg aattcagaac acctcatgaa ata atg aga aga gaa Met Arg Arg Glu	115
1	
agc aac aga tta tct gca cct tct tat ctt gcc aga agt cta gca gat Ser Asn Arg Leu Ser Ala Pro Ser Tyr Leu Ala Arg Ser Leu Ala Asp	163
5 10 15 20	
gtc cct aga gag tat ggt tct tct cag tca ttt gta acg gaa gtt agt Val Pro Arg Glu Tyr Gly Ser Ser Gln Ser Phe Val Thr Glu Val Ser	211
21 26 31 36	
ttt gct gtt gaa aat gga gac tct ggt tcc cga tat tat tat tca gac Phe Ala Val Glu Asn Gly Asp Ser Gly Ser Arg Tyr Tyr Tyr Ser Asp	259
37 42 47 52	
aat ttt ttt gat ggt cag aga aag cgg cca ctt gga gat cgt gca cat Asn Phe Phe Asp Gly Gln Arg Lys Arg Pro Leu Gly Asp Arg Ala His	307
53 58 63 68	
gaa gac tac aga tat tat gaa tac aac cat gat ctc ttc caa aga atg Glu Asp Tyr Arg Tyr Tyr Glu Tyr Asn His Asp Leu Phe Gln Arg Met	355
69 74 79 84	
cca cag aat cag ggg agg cat gct tca ggt att ggg aga gtt gct gct Pro Gln Asn Gln Gly Arg His Ala Ser Gly Ile Gly Arg Val Ala Ala	403
85 90 95 100	
aca tct tta gga aat ttg act aac cat ggt tct gaa gat tta ccc ctt Thr Ser Leu Gly Asn Leu Thr Asn His Gly Ser Glu Asp Leu Pro Leu	451
101 106 111 116	
cct cct ggc tgg tct gtg gac tgg aca atg aga ggg aga aaa tat tat Pro Pro Gly Trp Ser Val Asp Trp Thr Met Arg Gly Arg Lys Tyr Tyr	499
117 122 127 132	
ata gat cat aac aca aat aca act cac tgg agc cat cct ctt gag cga Ile Asp His Asn Thr Asn Thr His Trp Ser His Pro Leu Glu Arg	547
133 138 143 148	
gaa gga ctt cct cct gga tgg gaa cga gtt gag tca tcc gaa ttt gga Glu Gly Leu Pro Pro Gly Trp Glu Arg Val Glu Ser Ser Glu Phe Gly	595
149 154 159 164	
acc tat tat gta gat cac aca aat aag aag gcc caa tac agg cat ccc Thr Tyr Val Asp His Thr Asn Lys Lys Ala Gln Tyr Arg His Pro	643

165	170	175	180	
tgt gct cct agt gta cct cg ^g tat gat caa cca cct cct gtc aca tac Cys Ala Pro Ser Val Pro Arg Tyr Asp Gln Pro Pro Pro Val Thr Tyr 181 186 191 196				691
cag cca cag caa act gaa aga aat cag tcc ctt ctg gta cct gca aat Gln Pro Gln Gln Thr Glu Arg Asn Gln Ser Leu Leu Val Pro Ala Asn 197 202 207 212				739
cca tat cat act gca gaa att cct gac tgg ctt cag gtt tac gca cga Pro Tyr His Thr Ala Glu Ile Pro Asp Trp Leu Gln Val Tyr Ala Arg 213 218 223 228				787
gcc cct gtg aaa tat gac cac att ctg aag tgg gaa ctc ttc cag ctg Ala Pro Val Lys Tyr Asp His Ile Leu Lys Trp Glu Leu Phe Gln Leu 229 234 239 244				835
gct gac ctg gat aca tac cag gga atg cta aag ttg ctc ttc atg aaa Ala Asp Leu Asp Thr Tyr Gln Gly Met Leu Lys Leu Leu Phe Met Lys 245 250 255 260				883
gaa ttg gag cag att gtt aaa atg tat gaa gca tac aga caa gcc ctt Glu Leu Glu Gln Ile Val Lys Met Tyr Glu Ala Tyr Arg Gln Ala Leu 261 266 271 276				931
ctt aca gag ttg gaa aac c ^g a aag cag aga cag cag tgg tat gcc caa Leu Thr Glu Leu Glu Asn Arg Lys Gln Arg Gln Gln Trp Tyr Ala Gln 277 282 287 292				979
caa cat gga aaa aat ttt tga gc tgat ^{tttttta} aaaat ^{ttta} ag ttttgtaaga Gln His Gly Lys Asn Phe *293 298				1032
gctt ^{aaaaat} atttcacag ataaaaatt gcaaacaagt actctgg ^{tta} ataaat ^{gctg} cttc ^{tttgcgt} ggaaattata aaattctaac ttacatgta ttttgttatt agaaattttc				1092 1152
ttttat ^{tgga} tgagaaaaat tagtctatca tttaagagc caatatggca aacacttca aatactgtat attagaaaac tgg ^{tttgcgt} ttcttgatgg aaaaaatgc agcgaaatg				1212 1272
tcattatgaa cagatgttaa ataggaaatt attactgtt aacttcttac agcagtagta ccttc ^{tttgcgt} aaaaaaaaaa gaatctgcgg tattttta aaaaaaaaaagt ttactgctgt				1332 1392
agtgt ^{aaaaat} attgtctgga aaggatgg ^{ttaatatcc} ccatgatgta gttgaaat aaaataggat ttggAACCTT attgtataa atatttat atgatgtatg tttgtctccc				1452 1512
ctctccaaag taaggaaccc agctgggcgt ggtggctcac tcctgtaatc ccagcattt gggaggccga ggtgggtgga ccgc ^{tgt} gagt ccacgagttt aagaccagcc tggcaacat				1572 1632
gg ^{tgaagccc} tacaaaaat aaaaaaaaaat tagccggta tgatgg ^{tgt} tgcctctag ^t cccagctact tgggaggctg aggtcagagg atggcttgag cccaa ^{gagg} gc agagg ^{tt} gca				1692 1752

gggtcaagat cgcaccaactt gcactgcagc ctgagagaga gagagccaga ctttgtctca	1812
aaaaataaaa aaaaaaaaa	1830

<210> 176
 <211> 2430
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ..(1668)

<400> 176			
atg ggc ccc ccc atc gag acc cta gtc cgt gtg gaa ttc ccg ctg	Met Gly Pro Pro Ile Glu Thr Leu Val Arg Val Val Glu Phe Pro Leu	48	
1	5	10	
tgt cct gga ggc ggc aaa gca caa ctt tcc tcc gct tct ctc ctc gga	Cys Pro Gly Gly Gly Lys Ala Gln Leu Ser Ser Ala Ser Leu Leu Gly	96	
17	22	27	32
gcc ggg ctc ctg ctg cag ccc ccg acg cca cct ccg ctg ctg ctg	Ala Gly Leu Leu Leu Gln Pro Pro Thr Pro Pro Leu Leu Leu	144	
33	38	43	48
ctc ttc ccg ctg ctg ctc ttc tcc agg ctc tgt ggt gcc tta gct gga	Leu Phe Pro Leu Leu Phe Ser Arg Leu Cys Gly Ala Leu Ala Gly	192	
49	54	59	64
cca att att gtg gag cca cat gtc aca gca gta tgg gga aag aat gtt	Pro Ile Ile Val Glu Pro His Val Thr Ala Val Trp Gly Lys Asn Val	240	
65	70	75	80
tca tta aag tgt tta att gaa gta aat gaa acc ata aca cag att tca	Ser Leu Lys Cys Leu Ile Glu Val Asn Glu Thr Ile Thr Gln Ile Ser	288	
81	86	91	96
tgg gag aag ata cat ggc aaa agt tca cag act gtt gca gtt cac cat	Trp Glu Lys Ile His Gly Lys Ser Ser Gln Thr Val Ala Val His His	336	
97	102	107	112
ccc caa tat gga ttc tct gtt caa gga gaa tat cag gga aga gtc ttg	Pro Gln Tyr Gly Phe Ser Val Gln Gly Glu Tyr Gln Gly Arg Val Leu	384	
113	118	123	128
ttt aaa aat tac tca ctt aat gat gca aca att act ctg cat aac ata	Phe Lys Asn Tyr Ser Leu Asn Asp Ala Thr Ile Thr Leu His Asn Ile	432	
129	134	139	144
gga ttc tct gat tct gga aaa tac atc tgc aaa gct gtt aca ttc ccg	Gly Phe Ser Asp Ser Gly Lys Tyr Ile Cys Lys Ala Val Thr Phe Pro	480	
145	150	155	160

ctt gga aat gcc cag tcc tct aca act gta act gtg tta gtt gaa ccc Leu Gly Asn Ala Gln Ser Ser Thr Thr Val Thr Val Leu Val Glu Pro	528
161 166 171 176	
act gtg agc ctg ata aaa ggg cca gat tct tta att gat gga gga aat Thr Val Ser Leu Ile Lys Gly Pro Asp Ser Leu Ile Asp Gly Gly Asn	576
177 182 187 192	
gaa aca gta gca gcc att tgc atc gca gcc act gga aaa ccc gtt gca Glu Thr Val Ala Ala Ile Cys Ile Ala Ala Thr Gly Lys Pro Val Ala	624
193 198 203 208	
cat att gac tgg gaa ggt gat ctt ggt gaa atg gaa tcc act aca act His Ile Asp Trp Glu Gly Asp Leu Gly Glu Met Glu Ser Thr Thr Thr	672
209 214 219 224	
tct ttt cca aat gaa acg gca acg att atc agc cag tac aag cta ttt Ser Phe Pro Asn Glu Thr Ala Thr Ile Ile Ser Gln Tyr Lys Leu Phe	720
225 230 235 240	
cca acc aga ttt gct aga gga agg cga att act tgt gtt gta aaa cat Pro Thr Arg Phe Ala Arg Gly Arg Arg Ile Thr Cys Val Val Lys His	768
241 246 251 256	
cca gcc ttg gaa aag gac atc cga tac tct ttc ata tta gac ata cag Pro Ala Leu Glu Lys Asp Ile Arg Tyr Ser Phe Ile Leu Asp Ile Gln	816
257 262 267 272	
tat gct cct gaa gtt tcg gta aca gga tat gat gga aat tgg ttt gta Tyr Ala Pro Glu Val Ser Val Thr Gly Tyr Asp Gly Asn Trp Phe Val	864
273 278 283 288	
gga aga aaa ggt gtt aat ctc aaa tgt aat gct gat gca aat cca cca Gly Arg Lys Gly Val Asn Leu Lys Cys Asn Ala Asp Ala Asn Pro Pro	912
289 294 299 304	
ccc ttc aaa tct gtg tgg agc agg ttg gat gga caa tgg cct gat ggt Pro Phe Lys Ser Val Trp Ser Arg Leu Asp Gly Gln Trp Pro Asp Gly	960
305 310 315 320	
tta ttg gct tca gac aat act ctt cat ttt gtc cat cca ttg act ttc Leu Leu Ala Ser Asp Asn Thr Leu His Phe Val His Pro Leu Thr Phe	1008
321 326 331 336	
aat tat tct ggt gtt tat atc tgt aaa gtg acc aat tcc ctt ggt caa Asn Tyr Ser Gly Val Tyr Ile Cys Lys Val Thr Asn Ser Leu Gly Gln	1056
337 342 347 352	
aga agt gac caa aaa gtc atc tac att tca gat cct cct act act acc Arg Ser Asp Gln Lys Val Ile Tyr Ile Ser Asp Pro Pro Thr Thr Thr	1104
353 358 363 368	
acc ctt cag cct aca att cag tgg cat ccc tca act gct gac atc gag Thr Leu Gln Pro Thr Ile Gln Trp His Pro Ser Thr Ala Asp Ile Glu	1152
369 374 379 384	

gat cta gca aca gaa cct aaa aaa ttg ccc ttc cca ttg tca act ttg Asp Leu Ala Thr Glu Pro Lys Lys Leu Pro Phe Pro Leu Ser Thr Leu	385	390	395	400	1200
gca aca att aag gat gac aca att gcc acg atc att gct agt gta gtg Ala Thr Ile Lys Asp Asp Thr Ile Ala Thr Ile Ile Ala Ser Val Val	401	406	411	416	1248
ggg ggt gct ctc ttc ata gta ctt gta agt gtt ttg gct gga ata ttc Gly Gly Ala Leu Phe Ile Val Leu Val Ser Val Leu Ala Gly Ile Phe	417	422	427	432	1296
tgc tat agg aga aga cgg acg ttt cgt gga gac tac ttt gcc aag aac Cys Tyr Arg Arg Arg Arg Thr Phe Arg Gly Asp Tyr Phe Ala Lys Asn	433	438	443	448	1344
tac att cca cca tca gat atg caa aaa gaa tca caa ata gat gtt ctt Tyr Ile Pro Pro Ser Asp Met Gln Lys Glu Ser Gln Ile Asp Val Leu	449	454	459	464	1392
caa caa gat gag ctt gat tct tac cca gac agt gta aaa aaa gaa aaa Gln Gln Asp Glu Leu Asp Ser Tyr Pro Asp Ser Val Lys Lys Glu Lys	465	470	475	480	1440
aaa aat cca gtg aac aat cta ata cgt aaa gac tat tta gaa gag cct Lys Asn Pro Val Asn Asn Leu Ile Arg Lys Asp Tyr Leu Glu Glu Pro	481	486	491	496	1488
gaa aaa act cag tgg aac aat gta gaa aat ctc aat agg ttt gaa aga Glu Lys Thr Gln Trp Asn Asn Val Glu Asn Leu Asn Arg Phe Glu Arg	497	502	507	512	1536
cca atg gat tat tat gaa gat cta aaa atg gga atg aag ttt gtc agt Pro Met Asp Tyr Tyr Glu Asp Leu Lys Met Gly Met Lys Phe Val Ser	513	518	523	528	1584
gat gaa cat tat gat gaa aac gaa gat gac tta gtt tca cat gta gat Asp Glu His Tyr Asp Glu Asn Glu Asp Asp Leu Val Ser His Val Asp	529	534	539	544	1632
ggg tcc gta att tcc agg agg gag tgg tat gtt tag caac cactgaatgt Gly Ser Val Ile Ser Arg Arg Glu Trp Tyr Val *	545	550	555		1682
gacttaacta tgtacaatgt tcattcacac tagttgatca ttttcagatt gttcatactt					1742
tttcttgagg aagaataagc ttttcaagt tgatttcaa gcttactttt tatattctaa					1802
tctgacaaat gaaaatgtaa aatctgagtt cagtgtatct aagctgcttt acaatttttt					1862
ttcaatgctg tactactgtc tcaagattta aattttaatg cagagtactt tattgggtgtg					1922
aggcacacag gtaagaagaa atgtcaacat taaaatgtatg acttacttgg tacaaaaatt					1982
ttttaaaaag ggaactacct tgacattgtg tattaaatgt ttacctaaga ctataatctc					2042
aagtatgatg tttgttaac atataccctct caaaatttat caccactcaa tgacactgca					2102

tcaaaattga ctataaaaact aattcaagaa atatttatat atattttta atatacaaaa	2162
aatattttagc ctgatggaat ggcttcctt ttcaaacatt attttctaag tttctataca	2222
aatgaaatct ttacctctgc atattaatga gccttgccat aattactgt a gatggcttt	2282
tcaaagatat tttgttgcac taaaactgtg gtagtaaact cagtgaacat gatgtgtgga	2342
agagcataat tagctggtca atattttgt caaaaatacc tgcaagagta ataaaataca	2402
tacctttcaa acatgaaaaa aaaaaaaaaa	2430

v

<210> 177
<211> 1670
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (278) .. (658)

<400> 177	
ctgcgatgag gatgatgtat afaactatct attcgatgtat gaagatacc caccaaacc	60
aaaaaaaaagag atctctcgag gatccgaatt cgccggccgcg tcgacctagg gtgttgtgag	120
tgtaaattag tgcgatgagt aggggaaggg agcctactag ggtgtagaat aggaagtatg	180
tgcctgcgtt caggcggttct ggctgggttgc ctcatgggt gatgatagcc aaggtgggaa	240
taagtgtggt tgcgaaagtgg gctcgtgggt tggcagt atg aga gtt gta atg gcc	295
Met Arg Val Val Met Ala	
1	
cga ctg ttg agt gag ggg gag cag ggg atc cca acg gct tgc gct gcc	343
Arg Leu Leu Ser Glu Gly Glu Gln Gly Ile Pro Thr Ala Cys Ala Ala	
7 12 17 22	
ttt gcg cag cag ccg gcg ggc gag cca cgt cgc ggc ctg gct ggg gta	391
Phe Ala Gln Gln Pro Ala Gly Glu Pro Arg Arg Gly Leu Ala Gly Val	
23 28 33 38	
gga gag ggc ggt ccc cag tgc agt tgg gtg aac tac cgt tgc aca ctg	439
Gly Glu Gly Pro Gln Cys Ser Trp Val Asn Tyr Arg Cys Thr Leu	
39 44 49 54	
gag ttt ctg gtg tct ttg ctt gga act gac cta gct cgt ggc agg ggg	487
Glu Phe Leu Val Ser Leu Leu Gly Thr Asp Leu Ala Arg Gly Arg Gly	
55 60 65 70	
aac tcg gct agc ggc ccc aca gcc cct gct gac tca aaa caa cta atg	535
Asn Ser Ala Ser Gly Pro Thr Ala Pro Ala Asp Ser Lys Gln Leu Met	
71 76 81 86	

aac tct gga agc cca gcc agg gac aat gca cct tca cag aga ttc tgc	583
Asn Ser Gly Ser Pro Ala Arg Asp Asn Ala Pro Ser Gln Arg Phe Cys	
87 92 97 102	
act aat ctg agt gaa ggt cta agg ttt gga atc tcc ccc tca tgg aga	631
Thr Asn Leu Ser Glu Gly Leu Arg Phe Gly Ile Ser Pro Ser Trp Arg	
103 108 113 118	
gaa gct ttg tat ggc tgt cat gct tag acagt gattcctgca acttgacctt	683
Glu Ala Leu Tyr Gly Cys His Ala *	
119 124	
caggctggga gaggtggaga gccatgcctg ttctccttcc ttgctatgga atttgctgac	743
acaatatctt ccgcctggtg ctggcataat cctaagaact tacaactttc ctgtattatc	803
ctgtgtgagc agctgtcacc ttattggggg aaaaatgcct gaaaatttagg gggcacttca	863
agtagatagc ttcttatttcc tatatttttc ttactttaa aatgctttat tggaattatt	923
ttgataaaag caaatacttg tatataagac aaatataggaa aatagaagct atctacttga	983
agtccccct aattttcagg cattttccc ccaataaggt gacagctgct cacacaggat	1043
aatacaggaa agttgttaagt tcttaggata tgcccagcac caggcgaaag atattgtgtc	1103
agcaaattcc atagcaagga aggagaacag gcatggctct ccacctctcc cagcctgaag	1163
gtcaagttgc aggaatcaact gtctaagcat gacagccata caaagcttct ctccatgagg	1223
gggagattcc aaaccttaga ctttactca gattagtgc gaatctctgt gaaggtgcat	1283
tgtccctggc tgggcttcca gagttcattt tttactcaag gataacacgg cgatgaacgt	1343
cttacaactc agttgtttt agtcagcagg ggctgtgggg ccgctagccg agttccccct	1403
gccacgagct aggtcagttc caagcaaaga caccagaaac tccagtgtgc aacggtagtt	1463
cacccaaactg cactggggac cgcctctcc tacccagcc aggccgcgac gtggccgccc	1523
gccggctgct gcgcaaaggc agcgcaagcc gttggatcc cctgctcccc ctcactcaac	1583
agtcgggcca ttacaactct catactgcc acccacgagc ccactctcggt gccgctcggt	1643
ccgaattctt ggcctcgagg gccaaat	1670

<210> 178
 <211> 1702
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (167)..(1093)

<400> 178
tatgtatgacc gttgtacccgg tccggaaattc ccgggtcgac ccacgcgtcc gcggggcccag 60
|
ccgcctccac ggcccgcgct cgtactggag cgaagagcgg ctcctgaag gaggggaagg 120
gacgtggggg cggccacggc aggattaacc tccatttcag ctaatc atg gga gag 175
Met Gly Glu
1

att aaa gtc tct cct gat tat aac tgg ttt aga ggt aca gtt ccc ctt 223
Ile Lys Val Ser Pro Asp Tyr Asn Trp Phe Arg Gly Thr Val Pro Leu
4 9 14 19

aaa aag att att gtg gat gat gac agt aag ata tgg tcg ctc tat 271
Lys Lys Ile Ile Val Asp Asp Asp Ser Lys Ile Trp Ser Leu Tyr
20 25 30 35

gac gcg ggc ccc cga agt atc agg tgt cct ctc ata ttc ctg ccc cct 319
Asp Ala Gly Pro Arg Ser Ile Arg Cys Pro Leu Ile Phe Leu Pro Pro
36 41 46 51

gtc agt gga act gca gat gtc ttt ttc cgg cag att ttg gct ctg act 367
Val Ser Gly Thr Ala Asp Val Phe Phe Arg Gln Ile Leu Ala Leu Thr
52 57 62 67

gga tgg ggt tac cgg gtt atc gct ttg cag tat cca gtt tat tgg gac 415
Gly Trp Gly Tyr Arg Val Ile Ala Leu Gln Tyr Pro Val Tyr Trp Asp
68 73 78 83

cat ctc gag ttc tgt gat gga ttc aga aaa ctt tta gac cat tta caa 463
His Leu Glu Phe Cys Asp Gly Phe Arg Lys Leu Leu Asp His Leu Gln
84 89 94 99

ttg gat aaa gtt cat ctt ttt ggc gct tct ttg gga ggc ttt ttg gcc 511
Leu Asp Lys Val His Leu Phe Gly Ala Ser Leu Gly Gly Phe Leu Ala
100 105 110 115

cag aaa ttt gct gaa tac act cac aaa tct cct aga gtc cat tcc cta 559
Gln Lys Phe Ala Glu Tyr Thr His Lys Ser Pro Arg Val His Ser Leu
116 121 126 131

atc ctc tgc aat tcc ttc agt gac acc tct atc ttc aac caa act tgg 607
Ile Leu Cys Asn Ser Phe Ser Asp Thr Ser Ile Phe Asn Gln Thr Trp
132 137 142 147

act gca aac agc ttt tgg ctg atg cct gca ttt atg ctc aaa aaa ata 655
Thr Ala Asn Ser Phe Trp Leu Met Pro Ala Phe Met Leu Lys Lys Ile
148 153 158 163

gtt ctt gga aat ttt tca tct ggc ccg gtg gac cct atg atg gct gat 703
Val Leu Gly Asn Phe Ser Ser Gly Pro Val Asp Pro Met Met Ala Asp
164 169 174 179

gcc att gat ttc atg gta gac agg cta gaa agt ttg ggt cag agt gaa 751
Ala Ile Asp Phe Met Val Asp Arg Leu Glu Ser Leu Gly Gln Ser Glu

180	185	190	195	
ctg gct tca aga ctt acc ttg aat tgt caa aat tct tat gtg gaa cct Leu Ala Ser Arg Leu Thr Leu Asn Cys Gln Asn Ser Tyr Val Glu Pro				799
196	201	206	211	
cat aaa att cg ^g gac ata cct gta act att atg gat gtg ttt gat cag His Lys Ile Arg Asp Ile Pro Val Thr Ile Met Asp Val Phe Asp Gln				847
212	217	222	227	
agt gcg ctt tca act gaa gct aaa gaa gaa atg tac aag ctg tat cct Ser Ala Leu Ser Thr Glu Ala Lys Glu Glu Met Tyr Lys Leu Tyr Pro				895
228	233	238	243	
aat gcc cga aga gct cat ctg aaa aca gga ggc aat ttc cca tac ctg Asn Ala Arg Arg Ala His Leu Lys Thr Gly Gly Asn Phe Pro Tyr Leu				943
244	249	254	259	
tgc aga agt gca gag gtc aat ctt tat gta cag ata cat ttg ctg caa Cys Arg Ser Ala Glu Val Asn Leu Tyr Val Gln Ile His Leu Leu Gln				991
260	265	270	275	
ttc cat gga acc aaa tac gcg gcc att gac cca tca atg gtc agt gcc Phe His Gly Thr Lys Tyr Ala Ala Ile Asp Pro Ser Met Val Ser Ala				1039
276	281	286	291	
gag gag ctt gag gtg cag aaa ggc agc ctt ggc atc agc cag gag gag Glu Glu Leu Glu Val Gln Lys Gly Ser Leu Gly Ile Ser Gln Glu Glu				1087
292	297	302	307	
cag tag tgggtctctc gctgtcaatg atgagttgac ccgggtgttt cttgtatagt Gln *				1143
308				
cagtggcatc agcacccg ^t c agccggc ^t tt ttccttcagg tt ^c gtcaggc tcaccgg ^t tc				1203
tcactgtgtc tgggaagtag gactgatggt catcttcatg acaggcggca tctccactaa				1263
gcctgtgtaa ctgttccctc ttgggttttc tt ^a gcttttg aatttgaaga agtacttttg				1323
aagactcccc tttaagaac cgtgcaaatt ttgctaccaa aagtcttcac cactgtgttc				1383
ttaagtgaat gttaatttct gaggtttggg actttgtggt ggtttttttc ttcttttctt				1443
ttccattctt ctttctttct ttatgttg tt ^t gctgtaa atgctgcaca tccagattgc				1503
atatcaggac attggttatt ttatgctt ^c ttggatataa ccatgatcag agtgc ^c atgg				1563
ccactacccc actgtttgct ctcctgcaaa tcaactgctt ttaatttaca cttaaacaaa				1623
ttgtttt ^t gag tgtagctac tgcctttcta gatattagtc atttggataaaaattcaat				1683
ttcaaaaaaaaaaaaaaaa				1702

<210> 179
<211> 2821
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (234) .. (2492)

<400> 179

atttggccct cgaggccaag aattcggcac gaggcaaagg tttcacccctt cagttcagtc 60
cccaatccct gcttattatt tccctaacag aagaccatcc cccttgccac tccctggttt 120
ttcttctctg gcagcaatga agcagctgct gaccagctc tagtttcgg gaagtcagat 180
gacctttcc ctcccgccgc tctctacctc tcgcccggcc tagggaggac acc atg 236
Met
1

ggc cca ctg atg gtt ctt ttt tgc ctg ttc ctg tac cca ggt ctg 284
Gly Pro Leu Met Val Leu Phe Cys Leu Leu Phe Leu Tyr Pro Gly Leu
2 7 12 17

gca gac tcg gct ccc tcc tgc cct cag aac gtg aat atc tcg ggt ggc 332
Ala Asp Ser Ala Pro Ser Cys Pro Gln Asn Val Asn Ile Ser Gly Gly
18 23 28 33

acc ttc acc ctc agc cat ggc tgg gct cct ggg agc ctt ctc acc tac 380
Thr Phe Thr Leu Ser His Gly Trp Ala Pro Gly Ser Leu Leu Thr Tyr
34 39 44 49

tcc tgc ccc cag ggc ctg tac cca tcc cca gca tca cgg ctg tgc aag 428
Ser Cys Pro Gln Gly Leu Tyr Pro Ser Pro Ala Ser Arg Leu Cys Lys
50 55 60 65

agc agc gga cag tgg cag acc cca gga gcc acc cgg tct ctg tct aag 476
Ser Ser Gly Gln Trp Gln Thr Pro Gly Ala Thr Arg Ser Leu Ser Lys
66 71 76 81

gcg gtc tgc aaa cct gtg cgc tgt cca gcc cct gtc tcc ttt gag aat 524
Ala Val Cys Lys Pro Val Arg Cys Pro Ala Pro Val Ser Phe Glu Asn
82 87 92 97

ggc att tat acc cca cgg ctg ggg tcc tat ccc gtg ggt ggc aat gtg 572
Gly Ile Tyr Thr Pro Arg Leu Gly Ser Tyr Pro Val Gly Gly Asn Val
98 103 108 113

agc ttc gag tgt gag gat ggc ttc ata ttg cgg ggc tcg cct gtg cgt 620
Ser Phe Glu Cys Glu Asp Gly Phe Ile Leu Arg Gly Ser Pro Val Arg
114 119 124 129

cag tgt cgc ccc aac ggc atg tgg gat gga gaa aca gct gtg tgt gat 668
Gln Cys Arg Pro Asn Gly Met Trp Asp Gly Glu Thr Ala Val Cys Asp
130 135 140 145

aat ggg gct ggc cac tgc ccc aac cca ggc att tca ctg ggc gca gtg 716

Asn	Gly	Ala	Gly	His	Cys	Pro	Asn	Pro	Gly	Ile	Ser	Leu	Gly	Ala	Val	
146				151					156				161			
cgg	aca	ggc	tcc	cgc	ttt	ggt	cat	ggg	gac	aag	gtc	cgc	tat	cgc	tgc	764
Arg	Thr	Gly	Phe	Arg	Phe	Gly	His	Gly	Asp	Lys	Val	Arg	Tyr	Arg	Cys	
162				167					172				177			
tcc	tcg	aat	ctt	gtg	ctc	acg	ggg	tct	tcg	gag	cg	gag	tgc	cag	ggc	812
Ser	Ser	Asn	Leu	Val	Leu	Thr	Gly	Ser	Ser	Glu	Arg	Glu	Cys	Gln	Gly	
178				183					188				193			
aac	ggg	gtc	tgg	agt	gga	acg	gag	ccc	atc	tgc	cgc	caa	ccc	tac	tct	860
Asn	Gly	Val	Trp	Ser	Gly	Thr	Glu	Pro	Ile	Cys	Arg	Gln	Pro	Tyr	Ser	
194				199					204				209			
tat	gac	ttc	cct	gag	gac	gtg	gcc	cct	gcc	ctg	ggc	act	tcc	ttc	tcc	908
Tyr	Asp	Phe	Pro	Glu	Asp	Val	Ala	Pro	Ala	Leu	Gly	Thr	Ser	Phe	Ser	
210				215					220				225			
cac	atg	ctt	ggg	gcc	acc	aat	ccc	acc	cag	aag	aca	aag	gaa	agc	ctg	956
His	Met	Leu	Gly	Ala	Thr	Asn	Pro	Thr	Gln	Lys	Thr	Lys	Glu	Ser	Leu	
226				231					236				241			
ggc	cgt	aaa	atc	caa	atc	cag	cgc	tct	ggt	cat	ctg	aac	ctc	tac	ctg	1004
Gly	Arg	Lys	Ile	Gln	Ile	Gln	Arg	Ser	Gly	His	Leu	Asn	Leu	Tyr	Leu	
242				247					252				257			
ctc	ctg	gac	tgt	tcg	cag	agt	gtg	tcg	gaa	aat	gac	ttt	ctc	atc	ttc	1052
Leu	Leu	Asp	Cys	Ser	Gln	Ser	Val	Ser	Glu	Asn	Asp	Phe	Leu	Ile	Phe	
258				263					268				273			
aag	gag	agc	gcc	tcc	ctc	atg	gtg	gac	agg	atc	ttc	agc	ttt	gag	atc	1100
Lys	Glu	Ser	Ala	Ser	Leu	Met	Val	Asp	Arg	Ile	Phe	Ser	Phe	Glu	Ile	
274				279					284				289			
aat	gtg	agc	gtt	gcc	att	atc	acc	ttt	gcc	tca	gag	ccc	aaa	gtc	ctc	1148
Asn	Val	Ser	Val	Ala	Ile	Ile	Thr	Phe	Ala	Ser	Glu	Pro	Lys	Val	Leu	
290				295					300				305			
atg	tct	gtc	ctg	aac	gac	aac	tcc	cg	gat	atg	act	gag	gtg	atc	agc	1196
Met	Ser	Val	Leu	Asn	Asp	Asn	Ser	Arg	Asp	Met	Thr	Glu	Val	Ile	Ser	
306				311					316				321			
agc	ctg	gaa	aat	gcc	aac	tat	aaa	gat	cat	gaa	aat	gga	act	ggg	act	1244
Ser	Leu	Glu	Asn	Ala	Asn	Tyr	Lys	Asp	His	Glu	Asn	Gly	Thr	Gly	Thr	
322				327					332				337			
aac	acc	tat	gct	gcc	tta	aac	agt	gtc	tat	ctc	atg	atg	aac	aac	caa	1292
Asn	Thr	Tyr	Ala	Ala	Leu	Asn	Ser	Val	Tyr	Leu	Met	Met	Asn	Asn	Gln	
338				343					348				353			
atg	cga	ctc	ctc	ggc	atg	gaa	acg	atg	gcc	tgg	cag	gaa	atc	cga	cat	1340
Met	Arg	Leu	Leu	Gly	Met	Glu	Thr	Met	Ala	Trp	Gln	Glu	Ile	Arg	His	
354				359					364				369			
gcc	atc	atc	ctt	ctg	aca	gat	gga	aag	tcc	aat	atg	ggt	ggc	tct	ccc	1388
Ala	Ile	Ile	Leu	Leu	Thr	Asp	Gly	Lys	Ser	Asn	Met	Gly	Gly	Ser	Pro	

370	375	380	385	
aag aca gct gtt gac cat atc aga gag atc ctg aac atc aac cag aag Lys Thr Ala Val Asp His Ile Arg Glu Ile Leu Asn Ile Asn Gln Lys 386 391 396 401				1436
agg aat gac tat ctg gac atc tat gcc atc ggg gtg ggc aag ctg gat Arg Asn Asp Tyr Leu Asp Ile Tyr Ala Ile Gly Val Gly Lys Leu Asp 402 407 412 417				1484
gtg gac tgg aga gaa ctg aat gag cta ggg tcc aag aag gat ggt gag Val Asp Trp Arg Glu Leu Asn Glu Leu Gly Ser Lys Lys Asp Gly Glu 418 423 428 433				1532
agg cat gcc ttc att ctg cag gac aca aag gct ctg cac cag gtc ttt Arg His Ala Phe Ile Leu Gln Asp Thr Lys Ala Leu His Gln Val Phe 434 439 444 449				1580
gaa cat atg ctg gat gtc tcc aag ctc aca gac acc atc tgc ggg gtg Glu His Met Leu Asp Val Ser Lys Leu Thr Asp Thr Ile Cys Gly Val 450 455 460 465				1628
ggg aac atg tca gca aac gcc tct gac cag gag agg aca ccc tgg cat Gly Asn Met Ser Ala Asn Ala Ser Asp Gln Glu Arg Thr Pro Trp His 466 471 476 481				1676
gtc act att aag ccc aag agc caa gag acc tgc cgg ggg gcc ctc atc Val Thr Ile Lys Pro Lys Ser Gln Glu Thr Cys Arg Gly Ala Leu Ile 482 487 492 497				1724
tcc gac caa tgg gtc ctg aca gca gct cat tgc ttc cgc gat ggc aac Ser Asp Gln Trp Val Leu Thr Ala Ala His Cys Phe Arg Asp Gly Asn 498 503 508 513				1772
gac cac tcc ctg tgg agg gtc aat gtg gga gac ccc aaa tcc cag tgg Asp His Ser Leu Trp Arg Val Asn Val Gly Asp Pro Lys Ser Gln Trp 514 519 524 529				1820
ggc aaa gaa ttc ctt att gag aag gcg gtg atc tcc cca ggg ttt gat Gly Lys Glu Phe Leu Ile Glu Lys Ala Val Ile Ser Pro Gly Phe Asp 530 535 540 545				1868
gtc ttt gcc aaa aag aac cag gga atc ctg gag ttc tat ggt gat gac Val Phe Ala Lys Lys Asn Gln Gly Ile Leu Glu Phe Tyr Gly Asp Asp 546 551 556 561				1916
ata gct ctg ctg aag ctg gcc cag aaa gta aag atg tcc acc cat gcc Ile Ala Leu Leu Lys Leu Ala Gln Lys Val Lys Met Ser Thr His Ala 562 567 572 577				1964
agg ccc atc tgc ctt ccc tgc acg atg gag gcc aat ctg gct ctg cgg Arg Pro Ile Cys Leu Pro Cys Thr Met Glu Ala Asn Leu Ala Leu Arg 578 583 588 593				2012
aga cct caa ggc agc acc tgt agg gac cat gag aat gaa ctg ctg aac Arg Pro Gln Gly Ser Thr Cys Arg Asp His Glu Asn Glu Leu Leu Asn 594 599 604 609				2060

aaa cag agt gtt cct gct cat ttt gtc gcc ttg aat ggg agc aaa ctg		2108
Lys Gln Ser Val Pro Ala His Phe Val Ala Leu Asn Gly Ser Lys Leu		
610	615	620
		625
aac att aac ctt aag atg gga gtg gag tgg aca agc tgt gcc gag gtt		2156
Asn Ile Asn Leu Lys Met Gly Val Glu Trp Thr Ser Cys Ala Glu Val		
626	631	636
		641
gtc tcc caa gaa aaa acc atg ttc ccc aac ttg aca gat gtc agg gag		2204
Val Ser Gln Glu Lys Thr Met Phe Pro Asn Leu Thr Asp Val Arg Glu		
642	647	652
		657
gtg gtg aca gac cag ttc cta tgc agt ggg acc cag gag gat gag agt		2252
Val Val Thr Asp Gln Phe Leu Cys Ser Gly Thr Gln Glu Asp Glu Ser		
658	663	668
		673
ccc tgc aag gga gaa tct ggg gga gca gtt ttc ctt gag cgg aga ttc		2300
Pro Cys Lys Gly Glu Ser Gly Gly Ala Val Phe Leu Glu Arg Arg Phe		
674	679	684
		689
agg ttt ttt cag gtg ggt ctg gtg agc tgg ggt ctt tac aac ccc tgc		2348
Arg Phe Phe Gln Val Gly Leu Val Ser Trp Gly Leu Tyr Asn Pro Cys		
690	695	700
		705
ctt ggc tct gct gac aaa aac tcc cgc aaa agg gcc cct cgt agc aag		2396
Leu Gly Ser Ala Asp Lys Asn Ser Arg Lys Arg Ala Pro Arg Ser Lys		
706	711	716
		721
gtc ccg ccg cca cga gac ttt cac atc aat ctc ttc cgc atg cag ccc		2444
Val Pro Pro Pro Arg Asp Phe His Ile Asn Leu Phe Arg Met Gln Pro		
722	727	732
		737
tgg ctg agg cag cac ctg ggg gat gtc ctg aat ttt tta ccc ctc tag		2492
Trp Leu Arg Gln His Leu Gly Asp Val Leu Asn Phe Leu Pro Leu *		
738	743	748
		753
ccatggccac tgagccctct gctgccctgc cagaatctgc cgcccccca tcttctacct		2552
ctgaatggcc acccttagac cctgtgatcc atcctctctc ctagctgagt aaatccgggt		2612
ctctaggatg ccagaggcag cgcacacaag ctggaaaatc ctcagggctc ctaccagcag		2672
gactgcctcg ctgccccacc tcccgtcct tggcctgtcc ccagattcct tccctggttg		2732
acttgactca tgcttggttc actttcacat ggaatttccc agttatgaaa ttaataaaaa		2792
tcaatggttt ccacaaaaaaaaaaaaaaaaaaaa		2821

<210> 180
 <211> 1494
 <212> DNA
 <213> Homo sapiens

<220>
<221> CDS
<222> (184)..(498)

<400> 180
ctcccaagtc cagttatTTT tcctctctaa tagagacaaa cgagacacat tttatccatg 60
gaccggaaaac tctggcgcca gtcaccaact taggaagaca gcctaccctt ggtgtttaat 120
cattgcaggg tgtgcctgct tgattattca cccacacccc attgggtct gatcaccacg 180
ggg atg cct gcc ttg gtc att cac cca cat tcc ctt ggt ggc aag tca 228
Met Pro Ala Leu Val Ile His Pro His Ser Leu Gly Gly Lys Ser
1 5 10
att gtg ggg aca cgt gct ttg gct gct cac cca cat tgc agc cca gga 276
Ile Val Gly Thr Arg Ala Leu Ala His Pro His Cys Ser Pro Gly
16 21 26 31
ctg ctc ccc acc ccg ctt ctc cgt gtc tct acc ctt ctc ttt aaa ctt 324
Leu Leu Pro Thr Pro Leu Leu Arg Val Ser Thr Leu Leu Phe Lys Leu
32 37 42 47
gcc tcc ttt act atg ggc aac ctt cca ccc tcc att cct cct tct tct 372
Ala Ser Phe Thr Met Gly Asn Leu Pro Pro Ser Ile Pro Pro Ser Ser
48 53 58 63
ccc tta gcc tgt gtt ctc aaa aac tta aaa cct ctt caa ctc aca cct 420
Pro Leu Ala Cys Val Leu Lys Asn Leu Lys Pro Leu Gln Leu Thr Pro
64 69 74 79
gac cta aaa cct aag tgt ctt att ttc ttc tgc aac acc gct ggg ccc 468
Asp Leu Lys Pro Lys Cys Leu Ile Phe Phe Cys Asn Thr Ala Gly Pro
80 85 90 95
caa tac aaa ctc gac aat gat tcc aaa tag c cagaaaaacgg cactttcgag 519
Gln Tyr Lys Leu Asp Asn Asp Ser Lys *
96 101
ttctccatcc tacaaggTCT agataattct tgcataaaa tgggcaaATG gtctgaggtg 579
cctgacgtcc aggcatTTT ttacacattg gtcCCTCCCT agtctctgct cccaatgtga 639
ctcatcccaa atctttcttc ttctctcctt ttctgttccct tcggtctcca ccccaagtTC 699
cgagtccTCT gaatccttct ttcttatgga ctcatctgac ctccccCTT ctccccaggc 759
tgctcctcgc caggctgagc caggtcccaa ttctcaCTTA gcctctgctc cccCACCCta 819
taatcctttt atcacCTCCC ctccTcacac ctggTCCGGC ttacagTTTC attccgtgac 879
tagccctccc ccacctgccc agcaatttac tcttaaaaag gtggctggag ctaaaggcat 939
agtcaaggTTT aatgctcTTT ttctttatc ccaaATcaga agtgtttagg ctcttttca 999
tcaaataaa aaatccagcc cagttcatgg ctcgttggc agcaaccctg agacacttta 1059

cagccctaga ccctaaaagg tcaaaaggcc gtcttattct caaaaatacat tttattaccc	1119
aatctgctcc cgacattaaa taaaactcca aaaattaaat tccggccctc aaaccccaca	1179
acaggattta attaacctcg cttcaagggt gtacaataat agaaaaaaagt tgcaattcct	1239
tgcctccact gtgagacaaa cccagccac atctccagca cacaagaact tccaaacgcc	1299
tgaaccgcag cagccaggcg ttccctcaga acctcctccc acaggagctt gctacacgtg	1359
ccggaaatct ggccactggg caagggaatg cccgcagccc gggattcctc ctaagccgcf	1419
tcccatctct ctgggacccc actgaaaatc ggactgttca actcacctgg cagccactcc	1479
cagagccccct ggaag	1494

<210> 181
 <211> 1682
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (889)..(1056)

<400> 181	
tccttcggcc atgcttggca cgaggcgcag aaggctgcag gccctatagg ggacgacggg	60
ctggggacgc cctgagcttc ctggctgtgt ggcaggtgct ggggaagctc tctgggccat	120
agggacctgg ctcccccttg agaggcccgc ctgcctggg acacccaggg ctgtgctggt	180
ggcctgaggg tgggaacttg gttcctggg ctctgctggc gcctgggctt tgtggggcc	240
gaaggtggtt gccccggcg gcagggggct gtgtgggccc tcgtggggcc accttcctgt	300
cagtccccga gggacggtgg gacagttgcc cctgcgc当地 gggagccac tgccatcccc	360
cgtgggctgg cgctgcagtc gcgcaccctg tggcctgc tgacttgctt atgtctgtt	420
ggaagctgct tctgtttggc cacaggcctg tggcctggg ctgatggcoa cagagctgac	480
acttggggtt ttagttccag acttgcagac cctggatcc gtttactcct ccgcgccacg	540
gctgctgtgc ttccagaggt ggcgtgatgc ctccggggc cacgggtggg tgaaggatgg	600
cgagccggac ataccattgt tggatgtatt tttttaaaa cagcaataat tagccatttt	660
aaaggagggta tggatgttgc tggatgttgc tggatgttgc tggatgttgc tggatgttgc	720
caagtgggtt cttggatatg tggatgttgc gcatgtgtgc atgtgtgagc ctgtgcacgt	780
gcatgttgcataag catgtacacg cgtgagcatg catgtgcgtg tacacgtgtt	840

taggtgtaca tgtgcatgag ttgtgtacat gcgtgagcac gtgtatacg atg tac gtg Met Tyr Val 1	897
tgt gtg cgc atg tgt gcg tgt aca tgt gtt tgt gtc ttg ggt atg cat Cys Val Arg Met Cys Ala Cys Thr Cys Val Cys Val Leu Gly Met His 4 9 14 19	945
aag cat gca cgt gtg tat gaa tgt gcg tgt gta tgc atg agc acg tat Lys His Ala Arg Val Tyr Glu Cys Ala Cys Val Cys Met Ser Thr Tyr 20 25 30 35	993
gca tgt gtg atg cgc atg ttc ttg tgt act tct ctq agg ggg cac ata Ala Cys Val Met Arg Met Phe Leu Cys Thr Ser Leu Arg Gly His Ile 36 41 46 51	1041
tgt atg agt gta tga gtgcatacat atgcataatgg tgtacgtgtg tgtactttgt Cys Met Ser Val * 52	1096
gtgtggcat gtatgcgtat gagtacttgt gtgtggctgg tgtatgggtg agcatgcaca	1156
tgtgtatgga tgcataatgtg agctgtacat gtagagtgtatgtt gcatgagcat	1216
gcatgcgtgc gagtgccgtgt gtgtgtactt gcatataatgt ggctgtgcag gtaccggcg	1276
gtgggtggct ggcagtgcgc ggggaagcag gtcctgctca cggcttcctc gctgggcccc	1336
aggccccggg ctgagcctcc ctggcccttc ttgcccctca gtggagcagg gcctgggtgg	1396
aggccctggg cagctccagg gcaggtccgg ggaggccagg cttggggagc acagggggtg	1456
gggttcacct gctgctgttt gttcccgaaa ctgtactgtg agcccacggc gggggcagat	1516
tgttctgagg ccccagatgt gccaaaacag ccccccagggt gggggcgagc gagttctgag	1576
gagaggggct gcggggccg ggggtgggtg tgtgcccctc ccctgaatgg ccccaatgc	1636
tgctgttttt caataaaaacc agagttgaag gaaaaaaaaaaaaaa	1682

<210> 182
<211> 3526
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (118)..(3159)

<400> 182

agacccacccg ggccggaaatt cccgggtcga cgatttcgtc cagcccaagc ctgagcctga	60
gccccccccg aggtccccgc cccgccccgc tggctctctc gccgcggagc cgccaag atg ggg gac aag aaa gat gac aag gac tca ccc aag aac aag ggc	117
	165

Met	Gly	Asp	Lys	Lys	Asp	Asp	Lys	Asp	Ser	Pro	Lys	Lys	Asn	Lys	Gly		
1					5				10					15			
aag	gag	cgc	cgc	gac	ctg	gat	gac	ctc	aag	aag	gag	gtg	gct	atg	aca	213	
Lys	Glu	Arg	Arg	Asp	Leu	Asp	Asp	Leu	Lys	Lys	Glu	Val	Ala	Met	Thr		
17					22				27					32			
gag	cac	aag	atg	tca	gtg	gaa	gag	gtc	tgc	cg	aaa	tac	aac	aca	gac	261	
Glu	His	Lys	Met	Ser	Val	Glu	Glu	Val	Cys	Arg	Lys	Tyr	Asn	Thr	Asp		
33					38				43					48			
tgt	gtg	cag	ggt	ttg	acc	cac	agc	aaa	gcc	cag	gag	atc	ctg	gcc	cg	309	
Cys	Val	Gln	Gly	Leu	Thr	His	Ser	Lys	Ala	Gln	Glu	Ile	Leu	Ala	Arg		
49					54				59					64			
gat	ggg	cct	aac	gca	ctc	acg	cca	ccg	cct	acc	acc	cca	gag	tgg	gtc	357	
Asp	Gly	Pro	Asn	Ala	Leu	Thr	Pro	Pro	Pro	Thr	Thr	Pro	Glu	Trp	Val		
65					70				75					80			
aag	ttt	tgc	cg	cgt	ctc	ttc	ggg	ggc	ttc	tcc	atc	ctg	ctg	tgg	atc	405	
Lys	Phe	Cys	Arg	Gln	Leu	Phe	Gly	Gly	Phe	Ser	Ile	Leu	Leu	Trp	Ile		
81					86				91					96			
ggg	gct	atc	ctc	tgc	ttc	ctg	gcc	tac	gg	atc	cag	g	gc	gg	acc	453	
Gly	Ala	Ile	Leu	Cys	Phe	Leu	Ala	Tyr	Gly	Ile	Gln	Ala	Gly	Thr	Glu		
97					102				107					112			
gac	gac	ccc	tct	gg	gac	aa	ctg	tac	ctg	gg	atc	gt	ctg	gc	gc	501	
Asp	Asp	Pro	Ser	Gly	Asp	Asn	Leu	Tyr	Leu	Gly	Ile	Val	Leu	Ala	Ala		
113					118				123					128			
gtg	gtg	atc	atc	act	gg	tc	tg	tt	c	tcc	tac	tac	cag	gag	gg	aa	459
Val	Val	Ile	Ile	Thr	Gly	Cys	Phe	Ser	Tyr	Tyr	Gln	Glu	Ala	Lys	Ser		
129					134				139					144			
tcc	aag	atc	atg	gag	tcc	ttc	aag	aa	atg	gt	ccc	cag	caa	gg	ct	597	
Ser	Lys	Ile	Met	Glu	Ser	Phe	Lys	Asn	Met	Val	Pro	Gln	Gln	Ala	Leu		
145					150				155					160			
gtg	atc	cg	gaa	gg	gag	aa	atg	cag	gt	aa	gct	gag	gag	gt	gt	645	
Val	Ile	Arg	Glu	Gly	Glu	Lys	Met	Gln	Val	Asn	Ala	Glu	Glu	Val	Val		
161					166				171					176			
gtc	ggg	gac	ctg	gt	gag	atc	aag	gg	ga	gac	cg	gt	cc	gct	ga	693	
Val	Gly	Asp	Leu	Val	Glu	Ile	Lys	Gly	Gly	Asp	Arg	Val	Pro	Ala	Asp		
177					182				187					192			
ctg	cg	atc	atc	tca	gg	cac	gg	tgc	aag	gt	gac	aa	tcc	tcc	ct	741	
Leu	Arg	Ile	Ile	Ser	Ala	His	Gly	Cys	Lys	Val	Asp	Asn	Ser	Ser	Leu		
193					198				203					208			
act	gg	gaa	tcc	gag	cc	cag	act	cg	tct	cc	gac	tgc	ac	ca	gac	789	
Thr	Gly	Glu	Ser	Glu	Pro	Gln	Thr	Arg	Ser	Pro	Asp	Cys	Thr	His	Asp		
209					214				219					224			
aac	cc	ttg	gag	act	cg	aa	atc	acc	ttt	tcc	acc	aa	t	gt	gt	837	
Asn	Pro	Leu	Glu	Thr	Arg	Asn	Ile	Thr	Phe	Phe	Ser	Thr	Asn	Cys	Val		

225	230	235	240	
gaa ggc acg gct cgg ggc gtg gtg gcc acg ggc gac cgc act gtc Glu Gly Thr Ala Arg Gly Val Val Val Ala Thr Gly Asp Arg Thr Val				885
241	246	251	256	
atg ggc cgt atc gcc acc ctg gca tca ggg ctg gag gtg ggc aag acg Met Gly Arg Ile Ala Thr Leu Ala Ser Gly Leu Glu Val Gly Lys Thr				933
257	262	267	272	
ccc atc gcc atc gag att gag cac ttc atc cag ctc atc acc ggc gtg Pro Ile Ala Ile Glu Ile Glu His Phe Ile Gln Leu Ile Thr Gly Val				981
273	278	283	288	
gct gtc ttc ctg ggt gtc tcc ttc atc ctc tcc ctc att ctc gga Ala Val Phe Leu Gly Val Ser Phe Ile Leu Ser Leu Ile Leu Gly				1029
289	294	299	304	
tac acc tgg ctt gag gct gtc atc ttc ctc atc ggc atc atc gtg gcc Tyr Thr Trp Leu Glu Ala Val Ile Phe Leu Ile Gly Ile Ile Val Ala				1077
305	310	315	320	
aat gtc cca gag ggt ctg ctg gcc act gtc act gtg tgt ctg acg ctg Asn Val Pro Glu Gly Leu Leu Ala Thr Val Thr Val Cys Leu Thr Leu				1125
321	326	331	336	
acc gcc aag cgc atg gcc cgg aag aac tgc ctg gtg aag aac ctg gag Thr Ala Lys Arg Met Ala Arg Lys Asn Cys Leu Val Lys Asn Leu Glu				1173
337	342	347	352	
gct gta gaa acc ctg ggc tcc acg tcc acc atc tgc tca gat aag aca Ala Val Glu Thr Leu Gly Ser Thr Ser Thr Ile Cys Ser Asp Lys Thr				1221
353	358	363	368	
ggg acc ctc act cag aac cgc atg aca gtc gcc cac atg tgg ttt gac Gly Thr Leu Thr Gln Asn Arg Met Thr Val Ala His Met Trp Phe Asp				1269
369	374	379	384	
aac cag atc cac gag gct gac acc act gag gac cag tca ggg acc tca Asn Gln Ile His Glu Ala Asp Thr Thr Glu Asp Gln Ser Gly Thr Ser				1317
385	390	395	400	
ttt gac aag agt tcg cac acc tgg gtg gcc ctg tct cac atc gct ggg Phe Asp Lys Ser Ser His Thr Trp Val Ala Leu Ser His Ile Ala Gly				1365
401	406	411	416	
ctc tgc aat cgc gct gtc ttc aag ggt cag gac aac atc cct gtg Leu Cys Asn Arg Ala Val Phe Lys Gly Gly Gln Asp Asn Ile Pro Val				1413
417	422	427	432	
ctc aag agg gat gtg gct ggg gat gcg tct gag tct gcc ctg ctc aag Leu Lys Arg Asp Val Ala Gly Asp Ala Ser Glu Ser Ala Leu Leu Lys				1461
433	438	443	448	
tgc atc gag ctg tcc tct ggc tcc gtg aag ctg atg cgt gaa cgc aac Cys Ile Glu Leu Ser Ser Gly Ser Val Lys Leu Met Arg Glu Arg Asn				1509
449	454	459	464	

aag aaa gtg gct gag att ccc ttc aat tcc acc aac aaa tac cag ctc		1557
Lys Lys Val Ala Glu Ile Pro Phe Asn Ser Thr Asn Lys Tyr Gln Leu		
465 470 475 480		
tcc atc cat gag acc gag gac ccc aac gac aac cga tac ctg ctg gtg		1605
Ser Ile His Glu Thr Glu Asp Pro Asn Asp Asn Arg Tyr Leu Leu Val		
481 486 491 496		
atg aag ggt gcc ccc gag cgc atc ctg gac cgc tgc tcc acc atc ctg		1653
Met Lys Gly Ala Pro Glu Arg Ile Leu Asp Arg Cys Ser Thr Ile Leu		
497 502 507 512		
cta cag ggc aag gag cag cct ctg gac gag gaa atg aag gag gcc ttc		1701
Leu Gln Gly Lys Glu Gln Pro Leu Asp Glu Glu Met Lys Glu Ala Phe		
513 518 523 528		
cag aat gcc tac ctt gag ctc ggt ggc ctg ggc gag cgc gtg ctt ggt		1749
Gln Asn Ala Tyr Leu Glu Leu Gly Leu Gly Glu Arg Val Leu Gly		
529 534 539 544		
ttc tgc cat tat tac ctg ccc gag gag cag ttc ccc aag ggc ttt gcc		1797
Phe Cys His Tyr Tyr Leu Pro Glu Glu Gln Phe Pro Lys Gly Phe Ala		
545 550 555 560		
ttc gac tgt gat gac gtg aac ttc acc acg gac aac ctc tgc ttt gtg		1845
Phe Asp Cys Asp Asp Val Asn Phe Thr Thr Asp Asn Leu Cys Phe Val		
561 566 571 576		
ggc ctc atg tcc atg atc gac cca ccc cg ^g gca gcc gtc cct gac gcg		1893
Gly Leu Met Ser Met Ile Asp Pro Pro Arg Ala Ala Val Pro Asp Ala		
577 582 587 592		
gtg ggc aag tgt cgc agc gca ggc atc aag gtc atc atg gtc acc ggc		1941
Val Gly Lys Cys Arg Ser Ala Gly Ile Lys Val Ile Met Val Thr Gly		
593 598 603 608		
gat cac ccc atc acg gcc aag gcc att gcc aag ggt gtg ggc atc atc		1989
Asp His Pro Ile Thr Ala Lys Ala Ile Ala Lys Gly Val Gly Ile Ile		
609 614 619 624		
ttt gag ggc aac gag act gtg gag gac atc gcc gcc cg ^g ctc aac att		2037
Phe Glu Gly Asn Glu Thr Val Glu Asp Ile Ala Ala Arg Leu Asn Ile		
625 630 635 640		
ccc gtc agc cag gtt aac ccc cg ^g gat gcc aag gcc tgc gtg atc cac		2085
Pro Val Ser Gln Val Asn Pro Arg Asp Ala Lys Ala Cys Val Ile His		
641 646 651 656		
ggc acc gac ctc aag gac ttc acc tcc gag caa atc gac gag atc ctg		2133
Gly Thr Asp Leu Lys Asp Phe Thr Ser Glu Gln Ile Asp Glu Ile Leu		
657 662 667 672		
cag aat cac acc gag atc gtc ttc gcc cgc aca tcc ccc cag cag aag		2181
Gln Asn His Thr Glu Ile Val Phe Ala Arg Thr Ser Pro Gln Gln Lys		
673 678 683 688		

ctc atc att gtg gag ggc tgt cag aga cag ggt gca att gtg gct gtg Leu Ile Ile Val Glu Gly Cys Gln Arg Gln Gly Ala Ile Val Ala Val	2229
689 694 699 704	
acc ggg gat ggt gtg aac gac tcc ccc gct ctg aag aag gcc gac att Thr Gly Asp Gly Val Asn Asp Ser Pro Ala Leu Lys Lys Ala Asp Ile	2277
705 710 715 720	
ggg gtg gcc atg ggc atc gct ggc tct gac gtc tcc aag cag gca gct Gly Val Ala Met Gly Ile Ala Gly Ser Asp Val Ser Lys Gln Ala Ala	2325
721 726 731 736	
gac atg atc ctg ctg gac gac aac ttt gcc tcc atc gtc aca ggg gtg Asp Met Ile Leu Leu Asp Asp Asn Phe Ala Ser Ile Val Thr Gly Val	2373
737 742 747 752	
gag gag ggc cgc ctg atc ttc gac aac cta aag aag tcc att gcc tac Glu Glu Gly Arg Leu Ile Phe Asp Asn Leu Lys Lys Ser Ile Ala Tyr	2421
753 758 763 768	
acc ctg acc agc aat atc ccg gag atc acg ccc ttc ctg ctg ttc atc Thr Leu Thr Ser Asn Ile Pro Glu Ile Thr Pro Phe Leu Leu Phe Ile	2469
769 774 779 784	
atg gcc aac atc ccg ctg ccc ctg ggc acc atc acc atc ctc tgc atc Met Ala Asn Ile Pro Leu Pro Leu Gly Thr Ile Thr Ile Leu Cys Ile	2517
785 790 795 800	
gat ctg ggc act gac atg gtc cct gcc atc tca ctg gcg tac gag gct Asp Leu Gly Thr Asp Met Val Pro Ala Ile Ser Leu Ala Tyr Glu Ala	2565
801 806 811 816	
gcc gaa agc gac atc atg aag aga cag ccc agg aac ccg cgg acg gac Ala Glu Ser Asp Ile Met Lys Arg Gln Pro Arg Asn Pro Arg Thr Asp	2613
817 822 827 832	
aaa ttg gtc aat gag aga ctc atc agc atg gcc tac ggg cag att gga Lys Leu Val Asn Glu Arg Leu Ile Ser Met Ala Tyr Gly Gln Ile Gly	2661
833 838 843 848	
atg atc cag gct ctc ggt ggc ttc ttc tct tac ttt gtg atc ctg gca Met Ile Gln Ala Leu Gly Gly Phe Phe Ser Tyr Phe Val Ile Leu Ala	2709
849 854 859 864	
gaa aat ggc ttc ttg ccc ggc aac ctg gtg ggc atc cgg ctg aac tgg Glu Asn Gly Phe Leu Pro Gly Asn Leu Val Gly Ile Arg Leu Asn Trp	2757
865 870 875 880	
gat gac cgc acc gtc aat gac ctg gaa gac agt tac ggg cag cag tgg Asp Asp Arg Thr Val Asn Asp Leu Glu Asp Ser Tyr Gly Gln Gln Trp	2805
881 886 891 896	
aca tac gag cag agg aag gtg gtg gag ttc acc tgc cac acg gcc ttc Thr Tyr Glu Gln Arg Lys Val Val Glu Phe Thr Cys His Thr Ala Phe	2853
897 902 907 912	
ttt gtg agc atc gtt gtc gtc cag tgg gcc gat ctg atc atc tgc aag	2901

Phe Val Ser Ile Val Val Gln Trp Ala Asp Leu Ile Ile Cys Lys			
913	918	923	928
acc cgg agg aac tcg gtc ttc cag cag ggc atg aag aac aag atc ctg	2949		
Thr Arg Arg Asn Ser Val Phe Gln Gln Gly Met Lys Asn Lys Ile Leu			
929	934	939	944
atc ttc ggg ctg ttt gag gag acg gcc ctg gct gcc ttc ctg tcc tac	2997		
Ile Phe Gly Leu Phe Glu Glu Thr Ala Leu Ala Ala Phe Leu Ser Tyr			
945	950	955	960
tgc ccc ggc atg gac gtg gcc ctg cgc atg tac cct ctc aag ccc agc	3045		
Cys Pro Gly Met Asp Val Ala Leu Arg Met Tyr Pro Leu Lys Pro Ser			
961	966	971	976
tgg tgg ttc tgt gcc ttc ccc tac agt ttc ctc atc ttc gtc tac gac	3093		
Trp Trp Phe Cys Ala Phe Pro Tyr Ser Phe Leu Ile Phe Val Tyr Asp			
977	982	987	992
gaa atc cgc aaa ctc atc ctg cgc agg aac cca ggg ggt tgg gtg gag	3141		
Glu Ile Arg Lys Leu Ile Leu Arg Arg Asn Pro Gly Gly Trp Val Glu			
993	998	1003	1008
aag gaa acc tac tac tga cctcag cccccaccaca tcgccccatct cttccccgtc	3195		
Lys Glu Thr Tyr Tyr *			
1009	1014		
ccgcaggccc aggaccgccc ctgtcagtcc ccccaatttt gtattctggg gggaggagcc	3255		
ctctttccct gtggcccccac ctggcccccc accccctcca ctatctcctg ccgcccccac	3315		
tctggctggc ttctctcccc tgcccaaacc ctctctcctc tctctttct gtgtcagttt	3375		
ctctccctct cctcacccct ctatccattc ctcccgcccc agccacctcc ctgggctctt	3435		
tttactccc cttcagcccc ccggctgatg ccatctctgg ttctggacaa ttatcaaata	3495		
tatcagtggg gagagagaaa aaaaaaaaaa a	3526		

<210> 183
<211> 1428
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (38)..(1306)

<220>
<221> misc_feature
<222> (1)...(1428)
<223> n = a,t,c or g

<400> 183

gcacgaggcg ccggcccagg cgctggacgg cagcagg atg ggg aag gcg aag gtc Met Gly Lys Ala Lys Val	55
1	
ccc gcc tcc aag cgc gcc ccg agc agc ccc gtg gct aag ccg ggt cct Pro Ala Ser Lys Arg Ala Pro Ser Ser Pro Val Ala Lys Pro Gly Pro	103
7 12 17 22	
gtc aag acg ctc act cgg aag aaa aac aag aag aaa agg ttt tgg Val Lys Thr Leu Thr Arg Lys Lys Asn Lys Lys Lys Arg Phe Trp	151
23 28 33 38	
aaa agc aag gcg cgg gaa gta agc aag aag cca gca agc ggc ccc ggt Lys Ser Lys Ala Arg Glu Val Ser Lys Lys Pro Ala Ser Gly Pro Gly	199
39 44 49 54	
gct gtg gtg cga cct cca aag gca cca gaa gac ttt tct caa aac tgg Ala Val Val Arg Pro Pro Lys Ala Pro Glu Asp Phe Ser Gln Asn Trp	247
55 60 65 70	
aag gcg ctg caa gag tgg ctg ctg aaa caa aaa tct cag gcc cca gaa Lys Ala Leu Gln Glu Trp Leu Leu Lys Gln Lys Ser Gln Ala Pro Glu	295
71 76 81 86	
aag cct ctt gtc atc tct cag atg ggt tcc aaa aag aag ccc aaa att Lys Pro Leu Val Ile Ser Gln Met Gly Ser Lys Lys Pro Lys Ile	343
87 92 97 102	
atc cag caa aac aaa aaa gag acc tcg cct caa gtg aag gga gag gag Ile Gln Gln Asn Lys Lys Glu Thr Ser Pro Gln Val Lys Gly Glu Glu	391
103 108 113 118	
atg ccg gca gga aaa gac cag gag gcc agc agg ggc tct gtt cct tca Met Pro Ala Gly Lys Asp Gln Glu Ala Ser Arg Gly Ser Val Pro Ser	439
119 124 129 134	
ggg tcc aag atg gac agg agg gcg cca gta cct cgc acc aag gcc agt Gly Ser Lys Met Asp Arg Arg Ala Pro Val Pro Arg Thr Lys Ala Ser	487
135 140 145 150	
gga aca gag cac aat aag aaa gga acc aag gaa agg aca aat ggt gat Gly Thr Glu His Asn Lys Lys Gly Thr Lys Glu Arg Thr Asn Gly Asp	535
151 156 161 166	
att gtt cca gaa cga ggg gac atc gag cat aag aag cgg aaa gct aag Ile Val Pro Glu Arg Gly Asp Ile Glu His Lys Lys Arg Lys Ala Lys	583
167 172 177 182	
gag gca gcc cca gcc cca ccc acc gag gaa gac atc tgg ttt gac gac Glu Ala Ala Pro Ala Pro Pro Thr Glu Glu Asp Ile Trp Phe Asp Asp	631
183 188 193 198	
gtg gac cca gcg gat atc gaa gct gcc ata ggt cca gag gcg gcc aag Val Asp Pro Ala Asp Ile Glu Ala Ala Ile Gly Pro Glu Ala Ala Lys	679
199 204 209 214	
ata gcg agg aaa cag ttg ggt cag agc gag ggc agc gtc agc ctc agc	727

Ile Ala Arg Lys Gln Leu Gly Gln Ser Glu Gly Ser Val Ser Leu Ser			
215	220	225	230
ctc gtg aaa gag cag gcc ttc ggc ggc ctg aca aga gac tta gcc ttg			775
Leu Val Lys Glu Gln Ala Phe Gly Gly Leu Thr Arg Ala Leu Ala Leu			
231	236	241	246
gac tgt gag atg gtg ggc gtg ggc cct aag ggg gag gag agc atg gcc			823
Asp Cys Glu Met Val Gly Val Gly Pro Lys Gly Glu Glu Ser Met Ala			
247	252	257	262
gcc cgt gtg tcc atc gtg aac cag tat ggg aag tgc gtt tat gac aag			871
Ala Arg Val Ser Ile Val Asn Gln Tyr Gly Lys Cys Val Tyr Asp Lys			
263	268	273	278
tac gtc aaa cca acc gag ccc gtg acg gac tat agg aca gcg gtc agt			919
Tyr Val Lys Pro Thr Glu Pro Val Thr Asp Tyr Arg Thr Ala Val Ser			
279	284	289	294
ggg att cgg cct gag aac ctc aag cag gga gaa gag ctt gaa gtt gtt			967
Gly Ile Arg Pro Glu Asn Leu Lys Gln Gly Glu Glu Leu Glu Val Val			
295	300	305	310
cag aag gaa gtg gca gag atg ctg aag ggc aga att cta gtg ggg cac			1015
Gln Lys Glu Val Ala Glu Met Leu Lys Gly Arg Ile Leu Val Gly His			
311	316	321	326
gct ctg cat aat gac cta aag gta cta ttt ctt gat cat cca aaa aag			1063
Ala Leu His Asn Asp Leu Lys Val Leu Phe Leu Asp His Pro Lys Lys			
327	332	337	342
aag att cgg gac aca cag aaa tat aaa cct ttc aag agt caa gta aag			1111
Lys Ile Arg Asp Thr Gln Lys Tyr Lys Pro Phe Lys Ser Gln Val Lys			
343	348	353	358
agt gga agg ccg tct ctg aga cta ctt tca gag aag atc ctt ggg ctc			1159
Ser Gly Arg Pro Ser Leu Arg Leu Leu Ser Glu Lys Ile Leu Gly Leu			
359	364	369	374
cag gtc cag cag gcg gag cac tgt tca att cag gat gcc cag gca gca			1207
Gln Val Gln Gln Ala Glu His Cys Ser Ile Gln Asp Ala Gln Ala Ala			
375	380	385	390
atg agg .ctg tac gtc atg gtg aag aag gag tgg gag agc atg gcc cga			1255
Met Arg Leu Tyr Val Met Val Lys Lys Glu Trp Glu Ser Met Ala Arg			
391	396	401	406
gac agg cgc ccc ctg ctg act gct cca gac cac tgc agt gac gac gcc			1303
Asp Arg Arg Pro Leu Leu Thr Ala Pro Asp His Cys Ser Asp Asp Ala			
407	412	417	422
tag cagt cctgccctgc ttgctgcttg cccgccccgc ttacagaggc aatgttgacc			1360
*			
423			
agtcacaggg gacagttcac atnttcccca gagttggcaa tttttgggtt naaacctttt			1420

ttaagatt

1428

<210> 184
<211> 2086
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (212)..(1561)

<p><400> 184 aattgatacg cctgtcaggt actaggccgg gaattccccgg gtcgaccac gcgtccgccc acgcgtccgg gcggccatcat gcttggccct gctggcgctg tgtctgctgc tgccgctgct gctgctggga ggatgaaagc gctggcgccg gggggggggcgc gcccggcatg tagtagcggt ggtgctgggc gacgtgggcc gcagcccccg t - atg cag tac cac gcg ctg tcg Met Gln Tyr His Ala Leu Ser 1 5</p> <p>ttg gcc atg cac ggc ttc tcg gtg acc ctc ctg ggg ttc tgc aac tcc Leu Ala Met His Gly Phe Ser Val Thr Leu Leu Gly Phe Cys Asn Ser 8 13 18 23</p> <p>aaa ccc cat gat gag ctc ttg cag aac aac aga att cag att gtg ggg Lys Pro His Asp Glu Leu Leu Gln Asn Asn Arg Ile Gln Ile Val Gly 24 29 34 39</p> <p>ttg aca gaa ctt cag agt ctt gca gtt ggg ccc cga gtt ttc cag tac Leu Thr Glu Leu Gln Ser Leu Ala Val Gly Pro Arg Val Phe Gln Tyr 40 45 50 55</p> <p>gga gtc aaa gtt gta ctt cag gct atg tac ttg ctg tgg aag ttg atg Gly Val Lys Val Val Leu Gln Ala Met Tyr Leu Leu Trp Lys Leu Met 56 61 66 71</p> <p>tgg agg gag cca ggt gcc tat atc ttt ctc cag aac ccc cca ggt ctg Trp Arg Glu Pro Gly Ala Tyr Ile Phe Leu Gln Asn Pro Pro Gly Leu 72 77 82 87</p> <p>cct agc att gct gtc tgc tgg ttc gtg ggc tgc ctt tgt gga agc aag Pro Ser Ile Ala Val Cys Trp Phe Val Gly Cys Leu Cys Gly Ser Lys 88 93 98 103</p> <p>ctc gtc att gac tgg cac aac tat ggc tac tcc atc atg ggt ctg gtg Leu Val Ile Asp Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val 104 109 114 119</p> <p>cat ggc ccc aac cat ccc ctc gtt ctg ctg gcc aag tgg tgc aca tcc His Gly Pro Asn His Pro Leu Val Leu Leu Ala Lys Trp Cys Thr Ser 120 125 130 135</p>	60 120 180 232 280 328 376 424 472 520 568 616
--	---

agc ctc cgt gtg cat gtc cag ctg ctg cgt gta ctt ccg gcc ttg ggc		664
Ser Leu Arg Val His Val Gln Leu Leu Arg Val Leu Pro Ala Leu Gly		
136	141	146
		151
cat tgg ctg gct gtg gcc ttc gcc ctg ata gtt tgt tca ctg gca gtg		712
His Trp Leu Ala Val Ala Phe Ala Leu Ile Val Cys Ser Leu Ala Val		
152	157	162
		167
gtg aca gca gca gca aac agc tta gtt gag caa atg gag cag aat ggt		760
Val Thr Ala Ala Ala Asn Ser Leu Val Glu Gln Met Glu Gln Asn Gly		
168	173	178
		183
caa tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac ctg tgt		808
Gln Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn Leu Cys		
184	189	194
		199
gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac atc agg		856
Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His Ile Arg		
200	205	210
		215
gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag aca cct		904
Ala Val-Thr-Val-Tyr-Asp-Lys-Pro-Ala-Ser-Phe-Lys-Glu-Thr-Pro-		
216	221	226
		231
ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg cac tct		952
Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met His Ser		
232	237	242
		247
ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag cgg tcg		1000
Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu Arg Ser		
248	253	258
		263
gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt ctc cgt		1048
Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg		
264	269	274
		279
gag cgg cca gcc ctg gtc agc agc acg agc tgg aca gag gac gaa		1096
Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu		
280	285	290
		295
gac ttc tcc atc ctg ctg gca gct tta gaa agc aaa ggg cct ctg agg		1144
Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Ser Lys Gly Pro Leu Arg		
296	301	306
		311
gag tat tat agc cgc ctc atc cac cag aag cac tac cag cac atc cag		1192
Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys His Phe Gln His Ile Gln		
312	317	322
		327
gtc tgc acc ccc tgg ctg gag gcc gag gac tac ccc ctg ctt cta ggg		1240
Val Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr Pro Leu Leu Leu Gly		
328	333	338
		343
tcg gcg gac ctg ggt gtc tgt ctg cac acg tcc tcc agt ggc ctg gac		1288
Ser Ala Asp Leu Gly Val Cys Leu His Thr Ser Ser Gly Leu Asp		
344	349	354
		359
ctg ccc atg aag gtg .gtg gac atg ttc ggg tgc tgt ttg cct gtg tgt		1336

Leu	Pro	Met	Lys	Val	Val	Asp	Met	Phe	Gly	Cys	Cys	Leu	Pro	Val	Cys		
360				365					370				375				
gct gtg aac ttc aag tgt tta cat gag ctg gtg aaa cat gaa gaa aat															1384		
Ala	Val	Asn	Phe	Lys	Cys	Leu	His	Glu	Leu	Val	Lys	His	Glu	Glu	Asn		
376				381					386				391				
ggc ctg gtc ttt gag gac tca gag gaa ctg gca gct cag ctg cag atg															1432		
Gly	Leu	Val	Phe	Glu	Asp	Ser	Glu	Glu	Leu	Ala	Ala	Gln	Leu	Gln	Met		
392				397					402				407				
ctt ttc tca aac ttt cct gat cct gcg ggc aag cta aac cag ttc cg															1480		
Leu	Phe	Ser	Asn	Phe	Pro	Asp	Pro	Ala	Gly	Lys	Leu	Asn	Gln	Phe	Arg		
408				413					418				423				
aag aac ctg cgg gag tcg cag cag ctc cga tgg gat gag agc tgg gt															1528		
Lys	Asn	Leu	Arg	Glu	Ser	Gln	Gln	Leu	Arg	Trp	Asp	Glu	Ser	Trp	Val		
424				429					434				439				
cag act gtg ctc cct ttg gtt atg gac aca taa ctcctggg ccagaggcta															1579		
Gln	Thr	Val	Leu	Pro	Leu	Val	Met	Asp	Thr	*							
440				445					450								
aaacccagg acccctgctg tccttcccgc agcttcttct tggagtctca gggcaaacc															1639		
tttcgagcag	cacctcccag	tggccagaag	ctgaaatgac	agcagtggta	ctgcctggta											1699	
aaagaattgg	ttctgtgacc	cggaaagctt	tggttggcct	tgatttctc	tctggaggct											1759	
tggaaaacgct	tcctcttttc	ttctgttctt	cacgccccat	gcccctgcta	gcgttattact											1819	
gttctgtgac	ttccctgtga	cctctgcaga	actcctcatc	ctgcgtttgg	tctccagggt											1879	
tcccctttct	gccgtgttcc	taacattttgc	attcctgtct	tgaaaaaaagc	acctgctgca											1939	
ccgtaagccc	agggatgtgg	cagctgcagt	gggcttggct	ttgtgaggaa	ctgagtggt											1999	
ccacgttggg	ggaacatcat	acttgataca	cacgtttta	tttgcacaaa	gaaaatgcta											2059	
tttttggagc	cagaaaaaaaaaaaaaa															2086	

<210> 185
 <211> 1927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (212)..(1402)

<400> 185							
aattgatacg	cctgtcaggt	actaggtccg	gaattcccg	gtcgacccac	gcgtccgccc		60
acgcgtccgg	gcggcctcat	gcttggtcct	gctggcgctg	tgtctgctgc	tgccgctgct		120

gctgctggga	ggatggaagc	gctggcgccg	ggggcgggcg	ccccggcatg	tagtagcggt	180
/ggtgctgggc	gacgtgggcc	gcagcccccgt	t	atg cag tac cac gcg ctg tcg	Met Gln Tyr His Ala Leu Ser	232
				1	5	
ttg gcc atg cac ggc ttc tcg	gtg acc ctc ctg	ggg ttc tgc	aac tcc			280
Leu Ala Met His Gly Phe	Ser Val Thr Leu	Leu Gly Phe Cys Asn Ser				
8	13	18	23			
aaa ccc cat gat gag ctc ttg cag	aac aac aga att cag att	gtg ggg				328
Lys Pro His Asp Glu Leu	Leu Gln Asn Asn Arg Ile	Gln Ile Val Gly				
24	29	34	39			
ttg aca gaa ctt cag agt ctt gca	gtt ggg ccc cga	gtt ttc cag tac				376
Leu Thr Glu Leu Gln Ser	Leu Ala Val Gly Pro	Arg Val Phe Gln Tyr				
40	45	50	55			
gga gtc aaa gtt gta ctt cag	gct atg tac ttg ctg	tgg aag ttg atg				424
Gly Val Lys Val Val Leu	Gln Ala Met Tyr Leu	Leu Trp Lys Leu Met				
56	61	66	71			
tgg agg gag cca ggt gcc tat atc	ttt ctc cag aac ccc cca	ggt ctg				472
Trp Arg Glu Pro Gly Ala Tyr Ile	Phe Leu Gln Asn Pro	Pro Gly Leu				
72	77	82	87			
cct agc att gct gtc tgc tgg	ttc gtg ggc tgc	ctt tgt gga	agc aag			520
Pro Ser Ile Ala Val Cys Trp	Phe Val Gly Cys Leu	Cys Gly Ser Lys				
88	93	98	103			
ctc gtc att gac tgg cac aac	tat ggc tac tcc atc	atg ggt ctg	gtg			568
Leu Val Ile Asp Trp His	Asn Tyr Gly Tyr Ser	Ile Met Gly Leu Val				
104	109	114	119			
cat ggc ccc aac cat ccc ctc	gtt ctg gcc aag tgg	tac gag aag				616
His Gly Pro Asn His Pro	Leu Val Leu Ala Lys	Trp Tyr Glu Lys				
120	125	130	135			
ttc ttt ggg cgc ctg tcc	cac ctg aac ctg	tgt gtt acc aat	gct atg			664
Phe Phe Gly Arg Leu Ser	His Leu Asn Leu	Cys Val Thr Asn Ala	Met			
136	141	146	151			
cga gaa gac ctg gcg	aat tgg cac atc	agg gct gtg	acc gtc tac			712
Arg Glu Asp Leu Ala Asp	Asn Trp His Ile	Arg Ala Val Thr Val	Tyr			
152	157	162	167			
gac aag ccc gca tct ttc	ttt aaa gag aca	cct ctg gac	ctg cag cac			760
Asp Lys Pro Ala Ser Phe	Phe Lys Glu Thr	Pro Leu Asp Leu	Gln His			
168	173	178	183			
cggtcc ttc atg aag	ctg ggc agc atg	cac tct ccg	ttc agg gcc	cgc		808
Arg Leu Phe Met Lys	Leu Gly Ser Met	His Ser Pro	Phe Arg Ala	Arg		
184	189	194	199			
tca gaa cct gag gac	cca gtc acg gag	cggtcc acg gag	cggtcc acg gag	cggtcc		856
Ser Glu Pro Glu Asp	Pro Val Thr Glu	Arg Ser Ala	Phe Thr Glu	Arg		

200	205	210	215	
gat gct ggg agc ggg ctg gtg acg cgt ctc cgt gag cg ^g cca gcc ctg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg Glu Arg Pro Ala Leu 216 221 226 231				904
ctg gtc agc agc acg agc tgg aca gag gac gaa gac ttc tcc atc ctg Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu Asp Phe Ser Ile Leu 232 237 242 247				952
ctg gca gct tta gaa agc aaa ggg cct ctg agg gag tat tat agc cgc Leu Ala Ala Leu Glu Ser Lys Gly Pro Leu Arg Glu Tyr Tyr Ser Arg 248 253 258 263				1000
ctc atc cac cag aag cac ttc cag cac atc cag gtc tgc acc ccc tgg Leu Ile His Gln Lys His Phe Gln His Ile Gln Val Cys Thr Pro Trp 264 269 274 279				1048
ctg gag gcc gag gac tac ccc ctg ctt cta ggg tcg gcg gac ctg ggt Leu Glu Ala Glu Asp Tyr Pro Leu Leu Leu Ser Ala Asp Leu Gly 280 285 290 295				1096
gtc tgt ctg cac acg tcc tcc agt ggc ctg gac ctg ccc atg aag gtg Val Cys Leu His Thr Ser Ser Gly Leu Asp Leu Pro Met Lys Val 296 301 306 311				1144
gtg gac atg ttc ggg tgc tgt ttg cct gtg tgt gct gtg aac ttc aag Val Asp Met Phe Gly Cys Cys Leu Pro Val Cys Ala Val Asn Phe Lys 312 317 322 327				1192
tgt tta cat gag ctg gtg aaa cat gaa gaa aat ggc ctg gtc ttt gag Cys Leu His Glu Leu Val Lys His Glu Glu Asn Gly Leu Val Phe Glu 328 333 338 343				1240
gac tca gag gaa ctg gca gct cag ctg cag atg ctt ttc tca aac ttt Asp Ser Glu Glu Leu Ala Ala Gln Leu Gln Met Leu Phe Ser Asn Phe 344 349 354 359				1288
cct gat cct gcg ggc aag cta aac cag ttc cgg aag aac ctg cgg gag Pro Asp Pro Ala Gly Lys Leu Asn Gln Phe Arg Lys Asn Leu Arg Glu 360 365 370 375				1336
tcg cag cag ctc cga tgg gat gag agc tgg gtg cag act gtg ctc cct Ser Gln Gln Leu Arg Trp Asp Glu Ser Trp Val Gln Thr Val Leu Pro 376 381 386 391				1384
ttg gtt atg gac aca taa ctccctg ggccagaggg taaaacccca ggaccctgc Leu Val Met Asp Thr *	392	397		1438
tgcccttccc gcagcttctt ctggagtct caggcaaac ccttcgagc agcacctccc				1498
agtggccaga agctgaaatg acagcagtgg tactgcctgg taaaagaatt ggttctgtga				1558
ccccggaaac tttgggttggc ctgttattct tctctggagg cttggaaacg cttccctct				1618
tcttctgttc ttcacgcccc atgccccctgc tagcgtatta ctgttctgtg acttccctgt				1678

gacctctgca gaactcctca tcctgcgttt ggtctccagg tgc	ccccttt ctgc	ccgttt	1738
cctaacat	tt tgattcctgt cttgaaaaaa gcac	ctgctg caccgt aagc ccaggatgt	1798
ggcagctgca gtgggcttgg ctttgcgagg aactgagtgt gtcc	acgtttt gggaaacatc	1858	
atacttgata cacacgtttt tatttgac aagaaaatgc tattttgga	gccagaaaaaa	1918	
aaaaaaaaaa		1927	

<210> 186
 <211> 2146
 <212> DNA
 <213> Homo sapiens

<220>

<221> CDS

<222> (212) .. (1621)

<400> 186

aattgatacg cctgtcaggt actaggtccg gaattccqgg gtc	gacccac gcgtccgccc	60
acgcgtccgg cgccgcctcat gcttggtcct gctggcgctg tgt	ctgctgc tgccgctgct	120
gtcgctggga ggatggaagc gctggcgccg ggggcgggcg gccc	ggcgtatg tagtagcggt	180
ggtgctgggc gacgtgggcc gcagcccccg t atg cag tac	cac gcg ctg tcg	232
Met Gln Tyr His Ala Leu Ser		
1	5	

ttg gcc atg cac ggc ttc tcg gtg acc ctc ctg ggg ttc	tgc aac tcc	280
Leu Ala Met His Gly Phe Ser Val Thr Leu Leu Gly Phe	Cys Asn Ser	
8	13	23

aaa ccc cat gat gag ctc ttg cag aac aac aga att cag	att gtg ggg	328
Lys Pro His Asp Glu Leu Leu Gln Asn Asn Arg Ile Gln	Ile Val Gly	
24	29	39

ttg aca gaa ctt cag agt ctt gca gtt ggg ccc cga	gtt ttc cag tac	376
Leu Thr Glu Leu Gln Ser Leu Ala Val Gly Pro Arg	Val Phe Gln Tyr	
40	45	55

gga gtc aaa gtt gta ctt cag gct atg tac ttg ctg tgg	aag ttg atg	424
Gly Val Lys Val Val Leu Gln Ala Met Tyr Leu Leu Trp	Lys Leu Met	
56	61	71

tgg agg gag cca ggt gcc tat atc ttt ctc cag aac	ccc cca ggt ctg	472
Trp Arg Glu Pro Gly Ala Tyr Ile Phe Leu Gln Asn	Pro Pro Gly Leu	
72	77	87

cct agc att gct gtc tgc tgg ttc gtg ggc tgc ctt	tgt gga agc aag	520
Pro Ser Ile Ala Val Cys Trp Phe Val Gly Cys Leu	Cys Gly Ser Lys	
88	93	103

ctc gtc att gac tgg cac aac tat ggc tac tcc atc atg ggt ctg gtg		568	
Leu Val Ile Asp Trp His Asn Tyr Gly Tyr Ser Ile Met Gly Leu Val			
104	109	114	119
cat ggc ccc aac cat ccc ctc gtt ctg ctg gcc aag tgg tgc aca tcc		616	
His Gly Pro Asn His Pro Leu Val Leu Ala Lys Trp Cys Thr Ser			
120	125	130	135
agc ctc cgt gtg cat gtc cag ctg cgt gta ctt ccg gcc ttg ggc		664	
Ser Leu Arg Val His Val Gln Leu Leu Arg Val Leu Pro Ala Leu Gly			
136	141	146	151
cat tgg ctg gct gtg gcc ttc gcc ctg ata gtt tgt tca ctg gca gtg		712	
His Trp Leu Ala Val Ala Phe Ala Leu Ile Val Cys Ser Leu Ala Val			
152	157	162	167
gtg aca gca gca gca aac agc tta gtt gag caa atg gag cag aat ggt		760	
Val Thr Ala Ala Ala Asn Ser Leu Val Glu Gln Met Glu Gln Asn Gly			
168	173	178	183
caa tgg tac gag aag ttc ttt ggg cgc ctg tcc cac ctg aac ctg tgt		808	
Gln Trp Tyr Glu Lys Phe Phe Gly Arg Leu Ser His Leu Asn Leu Cys			
184	189	194	199
gtt acc aat gct atg cga gaa gac ctg gcg gat aac tgg cac atc agg		856	
Val Thr Asn Ala Met Arg Glu Asp Leu Ala Asp Asn Trp His Ile Arg			
200	205	210	215
gct gtg acc gtc tac gac aag ccc gca tct ttc ttt aaa gag aca cct		904	
Ala Val Thr Val Tyr Asp Lys Pro Ala Ser Phe Phe Lys Glu Thr Pro			
216	221	226	231
ctg gac ctg cag cac cgg ctc ttc atg aag ctg ggc agc atg cac tct		952	
Leu Asp Leu Gln His Arg Leu Phe Met Lys Leu Gly Ser Met His Ser			
232	237	242	247
ccg ttc agg gcc cgc tca gaa cct gag gac cca gtc acg gag cgg tcg		1000	
Pro Phe Arg Ala Arg Ser Glu Pro Glu Asp Pro Val Thr Glu Arg Ser			
248	253	258	263
gcc ttc acg gag cgg gat gct ggg agc ggg ctg gtg acg cgt ctc cgt		1048	
Ala Phe Thr Glu Arg Asp Ala Gly Ser Gly Leu Val Thr Arg Leu Arg			
264	269	274	279
gag cgg cca gcc ctg ctg gtc agc agc acg agc tgg aca gag gac gaa		1096	
Glu Arg Pro Ala Leu Leu Val Ser Ser Thr Ser Trp Thr Glu Asp Glu			
280	285	290	295
gac ttc tcc atc ctg ctg gca gct tta gaa aag ttt gaa caa ctg act		1144	
Asp Phe Ser Ile Leu Leu Ala Ala Leu Glu Lys Phe Glu Gln Leu Thr			
296	301	306	311
ctt gat gga cac aac ctt cct tct ctc gtc tgt gtg ata aca ggc aaa		1192	
Leu Asp Gly His Asn Leu Pro Ser Leu Val Cys Val Ile Thr Gly Lys			
312	317	322	327

ggg cct ctg agg gag tat tat agc cgc ctc atc cac cag aag cac ttc Gly Pro Leu Arg Glu Tyr Tyr Ser Arg Leu Ile His Gln Lys His Phe 328 333 338 343	1240
cag cac atc cag gtc tgc acc ccc tgg ctg gag gcc gag gac tac ccc Gln His Ile Gln Val Cys Thr Pro Trp Leu Glu Ala Glu Asp Tyr Pro 344 349 354 359	1288
ctg ctt cta ggg tcg gcg gac ctg ggt gtc tgt ctg cac acg tcc tcc Leu Leu Leu Gly Ser Ala Asp Leu Gly Val Cys Leu His Thr Ser Ser 360 365 370 375	1336
agt ggc ctg gac ctg ccc atg aag gtg gtg gac atg ttc ggg tgc tgt Ser Gly Leu Asp Leu Pro Met Lys Val Val Asp Met Phe Gly Cys Cys 376 381 386 391	1384
ttg cct gtg tgt gct gtg aac ttc aag tgt tta cat gag ctg gtg aaa Leu Pro Val Cys Ala Val Asn Phe Lys Cys Leu His Glu Leu Val Lys 392 397 402 407	1432
cat gaa gaa aat ggc ctg gtc ttt gag gac tca gag gaa ctg gca gct His Glu Glu Asn Gly Leu Val Phe Glu Asp Ser Glu Glu Leu Ala Ala 408 413 418 423	1480
cag ctg cag atg ctt ttc tca aac ttt cct gat cct gcg ggc aag cta Gln Leu Gln Met Leu Phe Ser Asn Phe Pro Asp Pro Ala Gly Lys Leu 424 429 434 439	1528
aac cag ttc cgg aag aac ctg cgg gag tcg cag cag ctc cga tgg gat Asn Gln Phe Arg Lys Asn Leu Arg Glu Ser Gln Gln Leu Arg Trp Asp 440 445 450 455	1576
gag agc tgg gtg cag act gtg ctc cct ttg gtt atg gac aca taa ctc Glu Ser Trp Val Gln Thr Val Leu Pro Leu Val Met Asp Thr *456 461 466	1624
ctggggccaga ggctaaaacc ccaggacccc tgctgtcctt cccgcagctt cttcttgag	1684
tctcagggca aaccctttcg agcagcacct cccagtggcc agaagctgaa atgacagcag	1744
tggtaactgcc tggtaaaaaga attggttctg tgacccggga agctttggtt ggccttgatt	1804
tcttctctgg aggcttggaa acgcttcctc tcttcttctg ttcttcacgc cccatgcccc	1864
tgctagcgta ttactgttct gtgacttccc tgtgacctct gcagaactcc tcatacgtcg	1924
tttggctcc aggtgtcccc tttctgccgt gttcctaaca ttttGattcc tgtcttgaaa	1984
aaagcacctg ctgcaccgta agcccaggaa tgtggcagct gcagtggcgt tggctttgtg	2044
aggaaactgag tgtgtccacg ttggggaaac atcatacttg atacacacgt ttttatttgc	2104
acaaagaaaa tgctatttt ggagccagaa aaaaaaaaaa aa	2146

<210> 187
<211> 4419
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (144) .. (3425)

<400> 187

tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt	60
tttttttttt tttttttttt tttttttttt ttttttgcgg cccactcaga cttaattcaa	120
agaccacggg cgaccggaggc gcg atg gct ggg gcg gcg gga ctc acg gca	170
Met Ala Gly Ala Ala Gly Leu Thr Ala	
1 5	
gaa gtg agc tgg aag gtc ttg gag cga aga gct cgg acc aag cgc tca	218
Glu Val Ser Trp Lys Val Leu Glu Arg Arg Ala Arg Thr Lys Arg Ser	
10 15 20 25	
ggc tca gtt tat gaa cct ctt aaa agc att aat ctt cca aga cct gat	266
Gly Ser Val Tyr Glu Pro Leu Lys Ser Ile Asn Leu Pro Arg Pro Asp	
26 31 36 41	
aat gaa act ctc tgg gat aag ttg gac cat tat tac aga att gtc aag	314
Asn Glu Thr Leu Trp Asp Lys Leu Asp His Tyr Tyr Arg Ile Val Lys	
42 47 52 57	
tca aca ttg ctg ctg tat caa agt cca act acc ggt ctc ttt ccc act	362
Ser Thr Leu Leu Tyr Gln Ser Pro Thr Thr Gly Leu Phe Pro Thr	
58 63 68 73	
aaa aca tgc ggt ggt gac cag aag gcc aag atc cag gac agc cta tac	410
Lys Thr Cys Gly Gly Asp Gln Lys Ala Lys Ile Gln Asp Ser Leu Tyr	
74 79 84 89	
tgc gct gct ggg gcc tgg gct ttg gct ctt gca tac agg cga att gat	458
Cys Ala Ala Gly Ala Trp Ala Leu Ala Leu Ala Tyr Arg Arg Ile Asp	
90 95 100 105	
gat gac aag gga agg acc cat gag ctg gag cac tca gct ata aaa tgc	506
Asp Asp Lys Gly Arg Thr His Glu Leu Glu His Ser Ala Ile Lys Cys	
106 111 116 121	
atg aga gga att ctc tac tgc tat atg cgt cag gcc gat aag gtc cag	554
Met Arg Gly Ile Leu Tyr Cys Tyr Met Arg Gln Ala Asp Lys Val Gln	
122 127 132 137	
cag ttt aag cag gat cca cgc cca aca aca tgt ctt cac tct gtt ttc	602
Gln Phe Lys Gln Asp Pro Arg Pro Thr Thr Cys Leu His Ser Val Phe	
138 143 148 153	
aat gtg cat aca gga gat gag ttg ctt tcc tat gag gaa tat ggt cat	650
Asn Val His Thr Gly Asp Glu Leu Leu Ser Tyr Glu Glu Tyr Gly His	
154 159 164 169	

ctt cag ata aat gca gtg tca ctt tat ctc ctt tac ctt gtg gaa atg Leu Gln Ile Asn Ala Val Ser Leu Tyr Leu Tyr Leu Val Glu Met 170 175 180 185	698
att tcc tca gga ctc cag att atc tac aac act gat gag gtc tct ttt Ile Ser Ser Gly Leu Gln Ile Ile Tyr Asn Thr Asp Glu Val Ser Phe 186 191 196 201	746
att caa aac ctt gta ttt tgt gtg gaa aga gtt tac cgt gtg cct gac Ile Gln Asn Leu Val Phe Cys Val Glu Arg Val Tyr Arg Val Pro Asp 202 207 212 217	794
ttt ggt gtc tgg gaa aga gga agc aaa tat aat aat ggc agc aca gag Phe Gly Val Trp Glu Arg Gly Ser Lys Tyr Asn Asn Gly Ser Thr Glu 218 223 228 233	842
cta cat tcg agc tcg gtt ggt tta gca aaa gca gct cta gaa gca att Leu His Ser Ser Val Gly Leu Ala Lys Ala Ala Leu Glu Ala Ile 234 239 244 249	890
aat gga ttc aac ctt ttt ggc aac cag ggc tgt tcg tgg tca gtt ata Asn Gly Phe Asn Leu Phe Gly Asn Gln Gly Cys Ser Trp Ser Val Ile 250 255 260 265	938
ttt gtg gat ctc gat gct cac aat cgc aac aggcaa act ttg tgc tcg Phe Val Asp Leu Asp Ala His Asn Arg Asn Arg Gln Thr Leu Cys Ser 266 271 276 281	986
ctg tta ccc aga gaa tca aga tca cat aat aca gat gct gcc ctg ctc Leu Leu Pro Arg Glu Ser Arg Ser His Asn Thr Asp Ala Ala Leu Leu 282 287 292 297	1034
ccc tgc atc agt tat cct gca ttt gcc ctg gat gat gaa gtt ctt ttt Pro Cys Ile Ser Tyr Pro Ala Phe Ala Leu Asp Asp Glu Val Leu Phe 298 303 308 313	1082
agc cag aca ctt gat aaa gtg gtt aga aaa tta aaa gga aaa tat gga Ser Gln Thr Leu Asp Lys Val Val Arg Lys Leu Lys Gly Lys Tyr Gly 314 319 324 329	1130
ttt aaa cgt ttc ttg aga gat ggg tat aga aca tca ttg gaa gat ccc Phe Lys Arg Phe Leu Arg Asp Gly Tyr Arg Thr Ser Leu Glu Asp Pro 330 335 340 345	1178
aac aga tgc tac tac aag cca gct gaa att aag cta ttt gat ggc att Asn Arg Cys Tyr Tyr Lys Pro Ala Glu Ile Lys Leu Phe Asp Gly Ile 346 351 356 361	1226
gaa tgt gaa ttt ccc ata ttt ttc ctt tat atg atg att gat gga gtt Glu Cys Glu Phe Pro Ile Phe Phe Leu Tyr Met Met Ile Asp Gly Val 362 367 372 377	1274
ttt aga ggc aat cct aag caa gta cag gaa tat cag gat ctt ttg act Phe Arg Gly Asn Pro Lys Gln Val Gln Glu Tyr Gln Asp Leu Leu Thr 378 383 388 393	1322

cca gta ctt cat cat acc aca gaa gga tat cct gtt gta cca aag tac Pro Val Leu His His Thr Thr Glu Gly Tyr Pro Val Val Pro Lys Tyr 394 399 404 409	1370
	/
tat tat gtg cca gct gac ttt gta gaa tat gaa aaa aat aac cct ggt Tyr Tyr Val Pro Ala Asp Phe Val Glu Tyr Glu Lys Asn Asn Pro Gly 410 415 420 425	1418
agt caa aaa cga ttt cct agc aac tgt ggc cgt gat gga aaa ctg ttt Ser Gln Lys Arg Phe Pro Ser Asn Cys Gly Arg Asp Gly Lys Leu Phe 426 431 436 441	1466
ctt tgg gga caa gca ctt tat atc atc gca aaa ctc ctg gct gat gaa Leu Trp Gly Gln Ala Leu Tyr Ile Ile Ala Lys Leu Leu Ala Asp Glu 442 447 452 457	1514
ctt att agt cct aaa gac att gat cct gtc cag cgc tat gtc cca cta Leu Ile Ser Pro Lys Asp Ile Asp Pro Val Gln Arg Tyr Val Pro Leu 458 463 468 473	1562
aag gat caa cgt aac gtg agc atg agg ttt tcc aat cag ggc cca ctg Lys Asp Gln Arg Asn Val Ser Met Arg Phe Ser Asn Gln Gly Pro Leu 474 479 484 489	1610
	B
gaa aat gac ttg gta gtt cat gtg gca ctt ata gca gaa agc caa aga Glu Asn Asp Leu Val Val His Val Ala Leu Ile Ala Glu Ser Gln Arg 490 495 500 505	1658
ctt caa gtt ttt ctg aac aca tat ggt att caa act caa act cct caa Leu Gln Val Phe Leu Asn Thr Tyr Gly Ile Gln Thr Gln Thr Pro Gln 506 511 516 521	1706
	C
caa gta gaa ccc att cag ata tgg cct cag gag ctt gtg aaa gct Gln Val Glu Pro Ile Gln Ile Trp Pro Gln Gln Glu Leu Val Lys Ala 522 527 532 537	1754
	D
tat ttg cag ctg ggt atc aat gaa aag tta gga ctc tct gga agg cca Tyr Leu Gln Leu Gly Ile Asn Glu Lys Leu Gly Leu Ser Gly Arg Pro 538 543 548 553	1802
	E
gac agg ccc att ggc tgc ctc ggg aca tca aag att tat cgc att cta Asp Arg Pro Ile Gly Cys Leu Gly Thr Ser Lys Ile Tyr Arg Ile Leu 554 559 564 569	1850
	F
gga aag act gtg gtt tgt tac ccg att att ttc gac cta agt gat ttc Gly Lys Thr Val Val Cys Tyr Pro Ile Ile Phe Asp Leu Ser Asp Phe 570 575 580 585	1898
	G
tac atg tct cag gat gtt ttc ctg ctg ata gat gac ata aag aat gcg Tyr Met Ser Gln Asp Val Phe Leu Leu Ile Asp Asp Ile Lys Asn Ala 586 591 596 601	1946
	H
ctg cag ttc att aaa caa tat tgg aaa atg cat gga cgt cca ctt ttc Leu Gln Phe Ile Lys Gln Tyr Trp Lys Met His Gly Arg Pro Leu Phe 602 607 612 617	1994
	I
ctt gtt ctc atc cgg gaa gac aat ata aga ggt agc cgg ttc aac ccc	2042

Leu Val Leu Ile Arg Glu Asp Asn Ile Arg Gly Ser Arg Phe Asn Pro			
618	623	628	633
ata tta gat atg ctg gca gcc ctt aaa aaa gga ata att gga gga gtc			2090
Ile Leu Asp Met Leu Ala Ala Leu Lys Lys Gly Ile Ile Gly Gly Val			
634	639	644	649
aaa gtt cat gtg gat cgt cta cag aca cta ata tct gga gct gtg gta			2138
Lys Val His Val Asp Arg Leu Gln Thr Leu Ile Ser Gly Ala Val Val			
650	655	660	665
gaa caa ctt gat ttc cta cga atc agt gac aca gaa gag ctt cca gaa			2186
Glu Gln Leu Asp Phe Leu Arg Ile Ser Asp Thr Glu Glu Leu Pro Glu			
666	671	676	681
ttt aag agt ttt gag gaa cta gaa cct ccc aaa cat tca aaa gtc aaa			2234
Phe Lys Ser Phe Glu Leu Glu Pro Pro Lys His Ser Lys Val Lys			
682	687	692	697
cg g caa agc agc acc cct agt gct cct gaa ctg gga cag cag ccg gat			2282
Arg Gln Ser Ser Thr Pro Ser Ala Pro Glu Leu Gly Gln Gln Pro Asp			
698	703	708	713
gtc aac att agt gaa tgg aag gac aaa ccc acc cac gaa att ctt caa			2330
Val Asn Ile Ser Glu Trp Lys Asp Lys Pro Thr His Glu Ile Leu Gln			
714	719	724	729
aaa ctg aat gat tgc agt tgt ctg gct agc caa gcc atc ctg ctg ggt			2378
Lys Leu Asn Asp Cys Ser Cys Leu Ala Ser Gln Ala Ile Leu Leu Gly			
730	735	740	745
ata ctg ctc aaa aga gaa ggc ccc aac ttc atc aca aag gaa ggt acc			2426
Ile Leu Leu Lys Arg Glu Gly Pro Asn Phe Ile Thr Lys Glu Gly Thr			
746	751	756	761
gtt tct gat cac att gag aga gtc tat aga aga gct ggc agc caa aaa			2474
Val Ser Asp His Ile Glu Arg Val Tyr Arg Arg Ala Gly Ser Gln Lys			
762	767	772	777
ctt tgg ttg gcg gtg cgc tac ggg gct gca ttt acc cag aaa ttt tct			2522
Leu Trp Leu Ala Val Arg Tyr Gly Ala Ala Phe Thr Gln Lys Phe Ser			
778	783	788	793
tcc tct ata gcc cca cac att act act ttt ctg gta cat ggg aaa cag			2570
Ser Ser Ile Ala Pro His Ile Thr Thr Phe Leu Val His Gly Lys Gln			
794	799	804	809
gta act ctg ggt gcc ttt ggg cat gaa gaa gaa gtt atc tct aat cct			2618
Val Thr Leu Gly Ala Phe Gly His Glu Glu Glu Val Ile Ser Asn Pro			
810	815	820	825
ttg tct cca aga gtg att caa aac atc atc tat tat aag tgt aac acc			2666
Leu Ser Pro Arg Val Ile Gln Asn Ile Ile Tyr Tyr Lys Cys Asn Thr			
826	831	836	841
cat gat gag agg gaa gcg gtc att cag caa gaa ctg gtc atc cat att			2714
His Asp Glu Arg Glu Ala Val Ile Gln Gln Glu Leu Val Ile His Ile			

842	847	852	857	
ggc tgg atc atc tcc aat aac cct gag tta ttc agt ggc acg ctg aaa Gly Trp Ile Ile Ser Asn Asn Pro Glu Leu Phe Ser Gly Thr Leu Lys 858 863 868 873				2762
ata cga atc ggg tgg atc atc cat gcc atg gag tat gaa ctt cag atc Ile Arg Ile Gly Trp Ile Ile His Ala Met Glu Tyr Glu Leu Gln Ile 874 879 884 889				2810
cgt ggc gga gac aag cca gcc ttg gac ttg tat cag ctg tca cct agt Arg Gly Gly Asp Lys Pro Ala Leu Asp Leu Tyr Gln Leu Ser Pro Ser 890 895 900 905				2858
gaa gtt aaa cag ctt ctg ctg ggt ata ctg cag cct caa cag aat gga Glu Val Lys Gln Leu Leu Gly Ile Leu Gln Pro Gln Gln Asn Gly 906 911 916 921				2906
aga tgt tgg ctg aac agg cgt cag atc gat ggg tct ttg aat aga act Arg Cys Trp Leu Asn Arg Arg Gln Ile Asp Gly Ser Leu Asn Arg Thr 922 927 932 937				2954
ccc acc ggg ttc tat gac cga gtg tgg cag att ctg gag cgc acg ccc Pro Thr Gly Phe Tyr Asp Arg Val Trp Gln Ile Leu Glu Arg Thr Pro 938 943 948 953				3002
aat ggg atc att gtt gct ggg aag cat ttg cct cag caa cca acc ctg Asn Gly Ile Ile Val Ala Gly Lys His Leu Pro Gln Gln Pro Thr Leu 954 959 964 969				3050
tca gat atg acc atg tat gag atg aat ttc tct ctc ctt gtt gaa gac Ser Asp Met Thr Met Tyr Glu Met Asn Phe Ser Leu Leu Val Glu Asp 970 975 980 985				3098
acg ttg gga aat att gac cag cca cag tac aga cag atc gtt gta gag Thr Leu Gly Asn Ile Asp Gln Pro Gln Tyr Arg Gln Ile Val Val Glu 986 991 996 1001				3146
tta ctt atg gtt gta tcc att gta ctg gaa aga aac ccc gag cta gaa Leu Leu Met Val Val Ser Ile Val Leu Glu Arg Asn Pro Glu Leu Glu 1002 1007 1012 1017				3194
ttt caa gac aaa gta gat cta gac aga ctg gtc aaa gaa gca ttt aat Phe Gln Asp Lys Val Asp Leu Asp Arg Leu Val Lys Glu Ala Phe Asn 1018 1023 1028 1033				3242
gaa ttt caa aaa gat cag agt cgg cta aag gaa att gaa aaa caa gat Glu Phe Gln Lys Asp Gln Ser Arg Leu Lys Glu Ile Glu Lys Gln Asp 1034 1039 1044 1049				3290
gac atg act tcc ttt tac aac act cct ccc ctg gga aaa aga gga aca Asp Met Thr Ser Phe Tyr Asn Thr Pro Pro Leu Gly Lys Arg Gly Thr 1050 1055 1060 1065				3338
tgc agc tat ttg aca aag gcg gtg atg aat ctg ctg ctg gaa gga gaa Cys Ser Tyr Leu Thr Lys Ala Val Met Asn Leu Leu Glu Gly Glu 1066 1071 1076 1081				3386

gtc aag cca aac aat gat gac ccg tgt ctg att agc tag tggggaaagg	3435
Val Lys Pro Asn Asn Asp Asp Pro Cys Leu Ile Ser *	
1082 / 1087 1092	
 gtaggaagct ctgtttagac acatgttctg aagtgtgttg tgtttcatgt tcaagcttaa	3495
tcaaggcagc catataatata cgaactgagc atgctgggg a ggtgaatgcc acatccttgg	3555
cggggttatg gacctcttgc atgtcatagc caatctaacc gtaatggtaa atgctttaa	3615
tcaagcagga aaaagttctc atgattatgc caactataat agtaatccctc actgagtgat	3675
aaaaatagtt tatgaattga aaatttgcgg ctgcattgttg tatgtatcaaa tagttcatca	3735
aatgaatct ttgctcttgc gactgaattc ttaccataact gccattaaaa taaatttgcgg	3795
aactagtaat gcataactgga aatcaaaaaga tactgaaaga atggtaact tctcttagtg	3855
gtattgtcat gctaaaagat gttaatatac atcataaaaag caaagtcagc cagctgat	3915
 tttggttctc aaaaactgca ttattaataa tatttttagta tacagagcta ttctacagtt	3975
tttacattgt aaacatgact gtggttttgt atttgctaaa tataggggtt ggactaaaat	4035
ataataaaatc tgtacccat caaacatttt cttttagctc ctgctaaaaa taggacatgt	4095
ctatgattgt tcaaaaatat gttaaattta ggctcagcac agtagctcac acctgaaatc	4155
ttagcacttc gggaggctga ggcagggtgga tcacttgagg ttaggagttc aagaccagcc	4215
cagccaacat ggtgaaaacc ctgtctctac taaaataaca aaaatttagcc aggcatgtg	4275
gtgcatgcct ttaaaccctg ctactgagga ggctgaggca tgagaattgc ttgaaccagg	4335
agacggaggt tgcagtgagc tggaaatccctg ccactgcaca ccagcctggg tgacagagcg	4395
agactccatc tcaaaaaaaaaaaa aaaa	4419

<210> 188
<211> 1521
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (595)..(1083)

<220>
<221> misc_feature
<222> (1)...(1521)
<223> n = a,t,c or g

<400> 188

ttttttaaat	aaaatagaat	gtatttctct	ccatacgaca	atcttaggat	agtccagggc	60
aggtaggcaa	ttccgttcca	caaggtcata	aggagaacag	gctagaggag	cagccctctc	120
ttccttaaca	tgtaatttct	gaattttgggt	cccagtgagt	cctgtacttt	tcatcatttc	180
cgagccagag	agaagagggaa	aaaagaatag	aagacaggca	aatttctcat	aaaaataaaaa	240
tccagaaggc	acacatttca	cttctgctaa	catctcattt	gccaaaactt	agaacctggc	300
tatagttacc	tgcaaaggag	gctggaaatg	cagtctctag	ctaagcaatc	atatgtcaga	360
aattggcatt	tccaaatacc	cagtggatat	tcatcaggat	atacaaatga	gaagttggaa	420
ncctggaaat	tcttagaaat	ttctgaaata	ataagttatc	ctttttaaaaa	aaaaaaacttt	480
tatTTAGGT	tcagggatac	atgtataggt	ttgttataaa	gataaaactcg	tgtttattctg	540
aaaagacttc	catttgcaga	catcgctgct	gcccagaact	ccctgccacc	agcc atg	597
					Met	
					1	
gcc aac ccc act	gtg ttc aac	att gca att	gat agt gag	tcc ttg		645
Ala Asn Pro Thr	Val Phe Phe Asn	Ile Ala Ile	Asp Ser Glu Ser	Leu		
2	7	12	17			
ggc tgc atc tcc ttc aag	cta ttt gca gac	aaa gtt cta aag	atg gaa			693
Gly Cys Ile Ser Phe	Lys Leu Phe Ala	Asp Lys Val	Leu Lys Met	Glu		
18	23	28	33			
gaa aat ttt tgt gct	ctg aac act gga	gag aaa gta ttt	ggt gat aaa			741
Glu Asn Phe Cys Ala	Leu Asn Thr Gly	Glu Lys Val	Phe Gly Asp	Lys		
34	39	44	49			
ggt ccc tgc ttt tac	aga att att ccg	ggg tgt ttt	cag ggt ggt	gac		789
Gly Pro Cys Phe Tyr	Arg Ile Ile Pro	Gly Cys Cys	Gln Gly Gly	Asp		
50	55	60	65			
ttc aca cac cat aat	ggc act ggt	ggc aag tcc	ctc tac agc	aag gaa		837
Phe Thr His His Asn	Gly Thr Gly Lys	Ser Leu Tyr	Ser Lys Glu			
66	71	76	81			
ttt gat gat gag aac	ttc atc cta aag	cat aca gct	cct ggc gtc	ttt		885
Phe Asp Asp Glu Asn	Phe Ile Leu Lys	His Thr Ala	Pro Gly Val	Leu		
82	87	92	97			
tcc acg gca aat gct	gga ccc acc aca	aat ggt tcc	cag ttt ttc	atc		933
Ser Thr Ala Asn Ala	Gly Pro Thr Thr	Asn Gly Ser	Gln Phe Phe	Ile		
98	103	108	113			
tgt act gcc aag aca	gag gat gga	tgc cag cat	gtg gtc ttt	ggc aag		981
Cys Thr Ala Lys Thr	Glu Asp Gly Cys	Gln His Val	Val Phe Gly	Lys		
114	119	124	129			
gtg aaa gat ggc atg	agt att gtg	gaa gcc ctg	gaa cgc tct	ggg tcc		1029
Val Lys Asp Gly Met	Ser Ile Val	Glu Ala	Leu Glu Arg	Ser Gly		
130	135	140	145			

agg aat ggt aag acc agc aag aag atc aca gct gct aac tgt gga caa	1077
Arg Asn Gly Lys Thr Ser Lys Lys Ile Thr Ala Ala Asn Cys Gly Gln	
146 151 156 161	
ctc taa taaatttgat tgtttatct gaaccaccag atcgttcctt ctatacgctca	1133
Leu *	
162	
ggaaagcatg cttccacccc atttgctcac agcatcctat aatcttgca cagtccttg	1193
ggttccatat ttcccttatac ctcttccatg tctagctgga tcgcagagtt aagttataa	1253
ttacaaaatg aaaactaagt aacaagaaga aaataaaaga cttccagcaa ttttatact	1313
cttttagtcat tactgtggat atctaaaaga aattggtttataaaataaga aatattacat	1373
ttagcaaatt tataaacaac tatagcctga gatnnngn gntcaaactt tagaaaatac	1433
cagtgaacat ttttggtaa tattcaaaga atgtgacatt cagatctcnt ggntccncg	1493
acgggttcctc aggtctctaa ngggacct	1521

<210> 189
 <211> 2413
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (258)..(1922)

<400> 189

aagctggtagt gcctgcaggt accggtccgg aattcccgaa tcgacgattt cgtcccagcc	60
cctccccagg ccgcgcagcgc ccctgccggc gtgcctggcc tccccctccca gactgcaggg	120
acagcacccg gtaactgcga gtggagcggg ggaccggagc ggctgaggag agaggaggcg	180
gcggcttagc tgctacgggg tccggccggc gccctcccgaa ggggggctca ggaggaggaa	240
ggaggacccg tgcgaga atg cct ctg ccc tgg agc ctt gcg ctc ccg ctg	290
Met Pro Leu Pro Trp Ser Leu Ala Leu Pro Leu	
1 5	
ctg ctc tcc tgg gtg gca ggt ggt ttc ggg aac gcg gcc agt gca agg	338
Leu Leu Ser Trp Val Ala Gly Gly Phe Gly Asn Ala Ala Ser Ala Arg	
12 17 22 27	
cat cac ggg ttg tta gca tcg gca cgt cag cct ggg gtc tgt cac tat	386
His His Gly Leu Leu Ala Ser Ala Arg Gln Pro Gly Val Cys His Tyr	
28 33 38 43	
gga act aaa ctg gcc tgc tac ggc tgg aga aga aac agc aag gga	434

Gly	Thr	Lys	Leu	Ala	Cys	Cys	Tyr	Gly	Trp	Arg	Arg	Asn	Ser	Lys	Gly	
44				49					54			59				
gtc	tgt	gaa	gct	aca	tgc	gaa	cct	gga	tgt	aag	ttt	ggg	gag	tgc	gtg	482
Val	Cys	Glu	Ala	Thr	Cys	Glu	Pro	Gly	Cys	Lys	Phe	Gly	Glu	Cys	Val	
60				65					70			75				
gga	cca	aac	aaa	tgc	aga	tgc	ttt	cca	gga	tac	acc	ggg	aaa	acc	tgc	530
Gly	Pro	Asn	Lys	Cys	Arg	Cys	Phe	Pro	Gly	Tyr	Thr	Gly	Lys	Thr	Cys	
76				81					86			91				
agt	caa	gat	gtg	aat	gag	tgt	gga	atg	aaa	ccc	cg	cca	tgc	caa	cac	578
Ser	Gln	Asp	Val	Asn	Glu	Cys	Gly	Met	Lys	Pro	Arg	Pro	Cys	Gln	His	
92				97					102			107				
aga	tgt	gtg	aat	aca	cac	gga	agc	tac	aag	tgc	ttt	tgc	ctc	agt	ggc	626
Arg	Cys	Val	Asn	Thr	His	Gly	Ser	Tyr	Lys	Cys	Phe	Cys	Leu	Ser	Gly	
108				113					118			123				
cac	atg	ctc	atg	cca	gat	gct	acg	tgt	gtg	aac	tct	agg	aca	tgt	gcc	674
His	Met	Leu	Met	Pro	Asp	Ala	Thr	Cys	Val	Asn	Ser	Arg	Thr	Cys	Ala	
124				129					134			139				
atg	ata	aac	tgt	cag	tac	agc	tgt	gaa	gac	aca	gaa	ggg	cca	cag	722	
Met	Ile	Asn	Cys	Gln	Tyr	Ser	Cys	Glu	Asp	Thr	Glu	Glu	Gly	Pro	Gln	
140				145					150			155				
tgc	ctg	tgt	cca	tcc	tca	gga	ctc	cgc	ctg	gcc	cca	aat	gga	aga	gac	770
Cys	Leu	Cys	Pro	Ser	Ser	Gly	Leu	Arg	Leu	Ala	Pro	Asn	Gly	Arg	Asp	
156				161					166			171				
tgt	cta	gat	att	gat	gaa	tgt	gcc	tct	gg	aaa	gtc	atc	tgt	ccc	tac	818
Cys	Leu	Asp	Ile	Asp	Glu	Cys	Ala	Ser	Gly	Lys	Val	Ile	Cys	Pro	Tyr	
172				177					182			187				
aat	cga	aga	tgt	gtg	aac	aca	ttt	gga	agc	tac	tac	tgc	aaa	tgt	cac	866
Asn	Arg	Arg	Cys	Val	Asn	Thr	Phe	Gly	Ser	Tyr	Tyr	Cys	Lys	Cys	His	
188				193					198			203				
att	gg	ttc	gaa	ctg	caa	tat	atc	agt	gga	cga	tat	gac	tgt	ata	gat	914
Ile	Gly	Phe	Glu	Leu	Gln	Tyr	Ile	Ser	Gly	Arg	Tyr	Asp	Cys	Ile	Asp	
204				209					214			219				
ata	aat	gaa	tgt	act	atg	gat	agc	cat	acg	tgc	agc	cac	cat	gcc	aat	962
Ile	Asn	Glu	Cys	Thr	Met	Asp	Ser	His	Thr	Cys	Ser	His	His	Ala	Asn	
220				225					230			235				
tgc	tcc	aat	acc	caa	ggg	tcc	tcc	aag	tgt	aaa	tgc	aag	cag	gga	tat	1010
Cys	Phe	Asn	Thr	Gln	Gly	Ser	Phe	Lys	Cys	Lys	Cys	Lys	Gln	Gly	Tyr	
236				241					246			251				
aaa	ggc	aat	gga	ctt	cg	tgt	tct	gct	atc	cct	gaa	aat	tct	gtg	aag	1058
Lys	Gly	Asn	Gly	Leu	Arg	Cys	Ser	Ala	Ile	Pro	Glu	Asn	Ser	Val	Lys	
252				257					262			267				
gaa	gtc	ctc	aga	gca	cct	gg	tgt	acc	atc	aaa	gac	aga	atc	aag	aag	1106
Glu	Val	Leu	Arg	Ala	Pro	Gly	Thr	Ile	Lys	Asp	Arg	Ile	Lys	Lys	Leu	

268	273	278	283	
ctt gct cac aaa aac agc atg aaa aag aag gca aaa att aaa aat gtt				1154
Leu Ala His Lys Asn Ser Met Lys Lys Ala Lys Ile Lys Asn Val				
284	289	294	299	
acc cca gaa ccc acc agg act cct acc cct aag gtg aac ttg cag ccc				1202
Thr Pro Glu Pro Thr Arg Thr Pro Thr Pro Lys Val Asn Leu Gln Pro				
300	305	310	315	
ttc aac tat gaa gag ata gtt tcc aga ggc ggg aac tct cat gga ggt				1250
Phe Asn Tyr Glu Glu Ile Val Ser Arg Gly Gly Asn Ser His Gly Gly				
316	321	326	331	
aaa aaa ggg aat gaa gag aaa atg aaa gag ggg ctt gag gat gag aaa				1298
Lys Lys Gly Asn Glu Glu Lys Met Lys Glu Gly Leu Glu Asp Glu Lys				
332	337	342	347	
aga gaa gag aaa gcc ctg aag aat gac ata gag gag cga agc ctg cga				1346
Arg Glu Glu Lys Ala Leu Lys Asn Asp Ile Glu Glu Arg Ser Leu Arg				
348	353	358	363	
gga gat gtg ttt ttc cct aag gtg aat gaa gca ggt gaa ttc ggc ctg				1394
Gly Asp Val Phe Phe Pro Lys Val Asn Glu Ala Gly Glu Phe Gly Leu				
364	369	374	379	
att ctg gtc caa agg aaa gcg cta act tcc aaa ctg gaa cat aaa gca				1442
Ile Leu Val Gln Arg Lys Ala Leu Thr Ser Lys Leu Glu His Lys Ala				
380	385	390	395	
gat tta aat atc tcg gtt gac tgc agc ttc aat cat ggg atc tgt gac				1490
Asp Leu Asn Ile Ser Val Asp Cys Ser Phe Asn His Gly Ile Cys Asp				
396	401	406	411	
tgg aaa cag gat aga gaa gat gat ttt gac tgg aat cct gct gat cga				1538
Trp Lys Gln Asp Arg Glu Asp Asp Phe Asp Trp Asn Pro Ala Asp Arg				
412	417	422	427	
gat aat gct att ggc ttc tat atg gca gtt ccg gcc ttg gca ggt cac				1586
Asp Asn Ala Ile Gly Phe Tyr Met Ala Val Pro Ala Leu Ala Gly His				
428	433	438	443	
aag aaa gac att ggc cga ttg aaa ctt ctc cta cct gac ctg caa ccc				1634
Lys Lys Asp Ile Gly Arg Leu Lys Leu Leu Pro Asp Leu Gln Pro				
444	449	454	459	
caa agc aac ttc tgt ttg ctc ttt gat tac ccg ctg gcc gga gac aaa				1682
Gln Ser Asn Phe Cys Leu Leu Phe Asp Tyr Arg Leu Ala Gly Asp Lys				
460	465	470	475	
gtc ggg aaa ctt cga gtg ttt gtg aaa aac agt aac aat gcc ctg gca				1730
Val Gly Lys Leu Arg Val Phe Val Lys Asn Ser Asn Ala Leu Ala				
476	481	486	491	
tgg gag aag acc acg agt gag gat gaa aag tgg aag aca ggg aaa att				1778
Trp Glu Lys Thr Thr Ser Glu Asp Glu Lys Trp Lys Thr Gly Lys Ile				
492	497	502	507	

cag ttg tat caa gga act gat gct acc aaa agc atc att ttt gaa gca Gln Leu Tyr Gln Gly Thr Asp Ala Thr Lys Ser Ile Ile Phe Glu Ala 508 513 518 523	1826
gaa cgt ggc aag ggc aaa acc ggc gaa atc gca gtg gat ggc gtc ttg Glu Arg Gly Lys Gly Lys Thr Gly Glu Ile Ala Val Asp Gly Val Leu 524 529 534 539	1874
ctt gtt tca ggc tta tgt cca gat agc ctt tta tct gtg gat gac tga Leu Val Ser Gly Leu Cys Pro Asp Ser Leu Leu Ser Val Asp Asp * 540 545 550 555	1922
atgttactat ctttatattt gactttgtat gtcagttccc tggtttttt gatattgcat	1982
cataggacct ctggcatttt agaattacta gctaaaaat tctaattgtac caacagaaaat	2042
attattgtaa gatgccttcc ttgtataaga tatgccaata tttgctttaa atatcatatc	2102
actgttatctt ctcagtcatt tctgaatctt tccacattat attataaaaat atggaaatgt	2162
cagtttatctt cccctcctca gtatatctga ttgtataag taagttgtatc agcttctctc	2222
tacaacattt ctagaaaata gaaaaaaaaag cacagagaaa tgtttaactg tttgactctt	2282
atgataacttc ttggaaacta tgacatcaa gatagacttt tgcctaagtg gcttagctgg	2342
gtctttcata gccaaacttg tatatttaa ttctttgtaa taataatatc caaatcatca	2402
aaaaaaaaaaaa a	2413

```
<210> 190  
<211> 6088  
<212> DNA  
<213> Homo sapiens
```

<220>
<221> CDS
<222> (170) .. (3448)

```

<400> 190
ttaactgcc a gctaaagtaa ccctcactaa agggaataag cttgcggccg ctcat tttttt 60
ttttttttt tttgcattgtc cccgcctcgc gcggcgccgg cgccgggtga ggagcctgag 120
gcggcgccgg gggtgttcc gcgcgccgtg gtctcgaaaaaaaataac atg gca 175
Met Ala
1

gcc aga cga att aca cag gag act ttt gat gct gta tta caa gaa aaa 223
Ala Arg Arg Ile Thr Gln Glu Thr Phe Asp Ala Val Leu Gln Glu Lys
3 8 13 18

gcc aaa cga tat cac atg gat gcc agt ggt gag gct gta agc gaa act . 271

```

Ala Lys Arg Tyr His Met Asp Ala Ser Gly Glu Ala Val Ser Glu Thr			
19	24	29	34
ctt cag ttt aaa gct caa gat ctc tta agg gca gtc cca aga tcc aga			319
Leu Gln Phe Lys Ala Gln Asp Leu Leu Arg Ala Val Pro Arg Ser Arg			
35	40	45	50
gca gag atg tat gat gac gtc cac agc gat ggc aga tac tcc ctc agt			367
Ala Glu Met Tyr Asp Asp Val His Ser Asp Gly Arg Tyr Ser Leu Ser			
51	56	61	66
gga tct gta gct cac tct aga gat gcc gga aga gaa ggc ctg aga agt			415
Gly Ser Val Ala His Ser Arg Asp Ala Gly Arg Glu Gly Leu Arg Ser			
67	72	77	82
gac gta ttt cca ggg cct tcc ttc aga tca agc aac cct tcc atc agt			463
Asp Val Phe Pro Gly Pro Ser Phe Arg Ser Ser Asn Pro Ser Ile Ser			
83	88	93	98
gat gac agc tac ttt cgc aaa gaa tgt ggc cggt gat ctg gaa ttt tct			511
Asp Asp Ser Tyr Phe Arg Lys Glu Cys Gly Arg Asp Leu Glu Phe Ser			
99	104	109	114
cac tct gat tct cgg gac cag gtc att ggc cac cgg aaa ttg ggg cat			559
His Ser Asp Ser Arg Asp Gln Val Ile Gly His Arg Lys Leu Gly His			
115	120	125	130
ttc cgt tct cag gac tgg aaa ttt gcg ctc cgt ggt tct tgg gaa caa			607
Phe Arg Ser Gln Asp Trp Lys Phe Ala Leu Arg Gly Ser Trp Glu Gln			
131	136	141	146
gac ttt ggc cat cca gtt tct caa gag tcc tct tgg tca cag gag tat			655
Asp Phe Gly His Pro Val Ser Gln Glu Ser Ser Trp Ser Gln Glu Tyr			
147	152	157	162
agt ttt ggt ccc tct gca gtt ttg ggg gac ttt gga tct tcc agg ctg			703
Ser Phe Gly Pro Ser Ala Val Leu Gly Asp Phe Gly Ser Ser Arg Leu			
163	168	173	178
att gag aaa gag tgt ttg gag aag gag agt cgg gat tat gac gtg gac			751
Ile Glu Lys Glu Cys Leu Glu Lys Glu Ser Arg Asp Tyr Asp Val Asp			
179	184	189	194
cat cct ggg gag gct gac tct gtg ctt agg ggc agc agt caa gtc cag			799
His Pro Gly Glu Ala Asp Ser Val Leu Arg Gly Ser Ser Gln Val Gln			
195	200	205	210
gcc aga ggt cga gct cta aac atc gtt gac cag gaa ggt tcc ctc cta			847
Ala Arg Gly Arg Ala Leu Asn Ile Val Asp Gln Glu Gly Ser Leu Leu			
211	216	221	226
gga aag ggg gag act cag ggc ctg ctc aca gct aag ggg ggt gtt ggg			895
Gly Lys Gly Glu Thr Gln Gly Leu Leu Thr Ala Lys Gly Gly Val Gly			
227	232	237	242
aaa ctt gtc aca ttg aga aat gtg agc aca aaa aaa ata ccc acc gtg			943
Lys Leu Val Thr Leu Arg Asn Val Ser Thr Lys Lys Ile Pro Thr Val			

243	248	253	258	
aat cgt att act ccc aaa act cag ggc act aac caa atc cag aaa aac Asn Arg Ile Thr Pro Lys Thr Gln Gly Thr Asn Gln Ile Gln Lys Asn 259 264 269 274				991
act cca agt cct gat gtg acc ctg ggg aca aac cca ggg aca gaa gat Thr Pro Ser Pro Asp Val Thr Leu Gly Thr Asn Pro Gly Thr Glu Asp 275 280 285 290				1039
atc cag ttc ccc att cag aag atc cct ctg ggg ctg gat ctg aag aat Ile Gln Phe Pro Ile Gln Lys Ile Pro Leu Gly Leu Asp Leu Lys Asn 291 296 301 306				1087
ctt cgg ctc ccc aga aga aag atg agc ttt gac atc ata gat aag tct Leu Arg Leu Pro Arg Arg Lys Met Ser Phe Asp Ile Ile Asp Lys Ser 307 312 317 322				1135
gat gtt ttt tca aga ttt ggg ata gaa ata atc aaa tgg gca gga ttc Asp Val Phe Ser Arg Phe Gly Ile Glu Ile Ile Lys Trp Ala Gly Phe 323 328 333 338				1183
cac acc ata aaa gat gat att aaa ttt tcc caa ctt ttc cag act ctc His Thr Ile Lys Asp Asp Ile Lys Phe Ser Gln Leu Phe Gln Thr Leu 339 344 349 354				1231
ttt gaa ctt gaa aca gaa acc tgt gct aaa atg ctt gcc tca ttc aaa Phe Glu Leu Glu Thr Glu Thr Cys Ala Lys Met Leu Ala Ser Phe Lys 355 360 365 370				1279
tgt tcc tta aaa cca gag cac aga gat ttt tgc ttt ttt act atc aaa Cys Ser Leu Lys Pro Glu His Arg Asp Phe Cys Phe Phe Thr Ile Lys 371 376 381 386				1327
ttt tta aag cac tct gct ttg aaa aca ccc aga gtt gat aat gag ttt Phe Leu Lys His Ser Ala Leu Lys Thr Pro Arg Val Asp Asn Glu Phe 387 392 397 402				1375
tta aac atg ctt tta gac aaa ggt gct gtg aag acc aaa aat tgc ttt Leu Asn Met Leu Leu Asp Lys Gly Ala Val Lys Thr Lys Asn Cys Phe 403 408 413 418				1423
ttt gaa atc ata aag cct ttt gac aag tac ata atg aga ctt caa gac Phe Glu Ile Ile Lys Pro Phe Asp Lys Tyr Ile Met Arg Leu Gln Asp 419 424 429 434				1471
cgg ctt ctg aag agt gtc aca cct ttg ctt atg gcc tgc aat gcc tac Arg Leu Leu Lys Ser Val Thr Pro Leu Leu Met Ala Cys Asn Ala Tyr 435 440 445 450				1519
gag cta agt gtc aag atg aag acc ctc agt aac ccc ctg gac ttg gct Glu Leu Ser Val Lys Met Lys Thr Leu Ser Asn Pro Leu Asp Leu Ala 451 456 461 466				1567
ctt gcc cta gaa acc acc aac tct ctc tgc cgg aag tct ttg gcc ctt Leu Ala Leu Glu Thr Thr Asn Ser Leu Cys Arg Lys Ser Leu Ala Leu 467 472 477 482				1615

ttg gga cag aca ttt tcc ttg gcc tct tct ttc cg ^g cag gag aaa atc Leu Gly Gln Thr Phe Ser Leu Ala Ser Ser Phe Arg Gln Glu Lys Ile 483 488 493 498	1663
tta gaa gct gtc ggc ctg caa gat ata gct ccc tca cct gct gcg ttt Leu Glu Ala Val Gly Leu Gln Asp Ile Ala Pro Ser Pro Ala Ala Phe 499 504 509 514	1711
cca aac ttc gaa gac tcc act ttg ttt ggg cga gag tac ata gac cac Pro Asn Phe Glu Asp Ser Thr Leu Phe Gly Arg Glu Tyr Ile Asp His 515 520 525 530	1759
ctg aag gcc tgg cta gtc agc agc gga tgt ccc ctc cag gtt aag aaa Leu Lys Ala Trp Leu Val Ser Ser Gly Cys Pro Leu Gln Val Lys Lys 531 536 541 546	1807
gcc gaa cca gag ccg atg cga gag gag aaa atg att cct cct acg Ala Glu Pro Glu Pro Met Arg Glu Glu Lys Met Ile Pro Pro Thr 547 552 557 562	1855
aaa cct gaa att cag gcc aag gct cca agt agt ctg agt gat gct gtc Lys Pro Glu Ile Gln Ala Lys Ala Pro Ser Ser Leu Ser Asp Ala Val 563 568 573 578	1903
ccc cag cga gca gat cac agg gta gtg ggc acc atc gac cag ctt gtg Pro Gln Arg Ala Asp His Arg Val Val Gly Thr Ile Asp Gln Leu Val 579 584 589 594	1951
aaa cgt gtc atc gaa ggc agc ctg tct ccc aaa gag aga act ctt ctc Lys Arg Val Ile Glu Gly Ser Leu Ser Pro Lys Glu Arg Thr Leu Leu 595 600 605 610	1999
aaa gag gac cct gct tac tgg ttt ttg tct gat gaa aat agt ctg gag Lys Glu Asp Pro Ala Tyr Trp Phe Leu Ser Asp Glu Asn Ser Leu Glu 611 616 621 626	2047
tat aaa tat tac aag ctg aag ttg gca gaa atg cag cg ^g atg agc gag Tyr Lys Tyr Tyr Lys Leu Lys Leu Ala Glu Met Gln Arg Met Ser Glu 627 632 637 642	2095
aac ttg cga gga gcc gac cag aag ccg acc tca gca gac tgt gca gtg Asn Leu Arg Gly Ala Asp Gln Lys Pro Thr Ser Ala Asp Cys Ala Val 643 648 653 658	2143
agg gcc atg ctg tac tcc cgg gct gtc cgc aac ctc aag aag aaa ctc Arg Ala Met Leu Tyr Ser Arg Ala Val Arg Asn Leu Lys Lys Lys Leu 659 664 669 674	2191
ctt ccg tgg cag cgg cgg ggg ctc ctc cgt gct caa ggg ctc cgg ggc Leu Pro Trp Gln Arg Arg Gly Leu Leu Arg Ala Gln Gly Leu Arg Gly 675 680 685 690	2239
tgg aag gcg agg aga gcg acc acc ggg acc cag acc ctc cta tcc tca Trp Lys Ala Arg Arg Ala Thr Thr Gly Thr Gln Thr Leu Leu Ser Ser 691 696 701 706	2287

ggc acc agg ctg aaa cac cac ggc cg ^g cag gct cca ggc ctc tca cag Gly Thr Arg Leu Lys His His Gly Arg Gln Ala Pro Gly Leu Ser Gln 707 712 717 722	2335
gca aaa cca tcc ctg cca gac aga aat gat gct gcc aag gac tgc cc ^g Ala Lys Pro Ser Leu Pro Asp Arg Asn Asp Ala Ala Lys Asp Cys Pro 723 728 733 738	2383
cca gac cca gtt gga cct tct cct cag gac ccc agc tta gaa gcc tca Pro Asp Pro Val Gly Pro Ser Pro Gln Asp Pro Ser Leu Glu Ala Ser 739 744 749 754	2431
ggc cca tcc ccc aag cca gca gga gtg gac atc tct gaa gca cct cag Gly Pro Ser Pro Lys Pro Ala Gly Val Asp Ile Ser Glu Ala Pro Gln 755 760 765 770	2479
acc tct tct ccc tgc cca tct gct gac att gac atg aag aca atg gag Thr Ser Ser Pro Cys Pro Ser Ala Asp Ile Asp Met Lys Thr Met Glu 771 776 781 786	2527
act gca gag aaa ctg gct aga ttt gtt gct cag gtg gga cca gag atc Thr Ala Glu Lys Leu Ala Arg Phe Val Ala Gln Val Gly Pro Glu Ile 787 792 797 802	2575
gaa caa ttc agc ata gaa aac agc acc gat aac cct gac ctg tgg ttt Glu Gln Phe Ser Ile Glu Asn Ser Thr Asp Asn Pro Asp Leu Trp Phe 803 808 813 818	2623
cta cat gac caa aat a ^{gt} tct gct ttc aaa ttc tat cga aag aaa gtg Leu His Asp Gln Asn Ser Ser Ala Phe Lys Phe Tyr Arg Lys Lys Val 819 824 829 834	2671
ttt gaa cta tgt cca tca att tgt ttc acg tca tct ccg cac aac ctt Phe Glu Leu Cys Pro Ser Ile Cys Phe Thr Ser Ser Pro His Asn Leu 835 840 845 850	2719
cac act ggt ggt gac acc acg ggt tct cag gag agc ccc gtg gac His Thr Gly Gly Asp Thr Thr Gly Ser Gln Glu Ser Pro Val Asp 851 856 861 866	2767
ctc atg gaa ggg gaa gca gag ttt gaa gac gag ccc cct ccg ccg gag Leu Met Glu Gly Glu Ala Glu Phe Glu Asp Glu Pro Pro Pro Arg Glu 867 872 877 882	2815
gct gag ctg gag agc cca gag gtg atg cct gag gag gag gac gag gac Ala Glu Leu Glu Ser Pro Glu Val Met Pro Glu Glu Asp Glu Asp 883 888 893 898	2863
gat gag gat ggg gga gag gag gcc ccc gct cct gga ggg gcg ggc aag Asp Glu Asp Gly Gly Glu Ala Pro Ala Pro Gly Gly Ala Gly Lys 899 904 909 914	2911
tct gag ggc agc acc cct gcc gac ggc ctt ccc ggc gag gct gcc gag Ser Glu Gly Ser Thr Pro Ala Asp Gly Leu Pro Gly Glu Ala Ala Glu 915 920 925 930	2959
gac gac ctg gct gga gca cct gcc ttg tca cag gcc tcc tca ggt acc	3007

Asp Asp Leu Ala Gly Ala Pro Ala Leu Ser Gln Ala Ser Ser Gly Thr			
931	936	941	946
tgc ttc cct cg ^a aag agg atc agc agc aag tca ttg aag gtt ggc atg			3055
Cys Phe Pro Arg Lys Arg Ile Ser Ser Lys Ser Leu Lys Val Gly Met			
947	952	957	962
att cca gct ccc aag aga gtg tgt ctc atc cag gag cca aaa gtc cat			3103
Ile Pro Ala Pro Lys Arg Val Cys Leu Ile Gln Glu Pro Lys Val His			
963	968	973	978
gaa cca gtt cga att gcc tat gac agg cct cg ^b ggt cgt ccc atg tcc			3151
Glu Pro Val Arg Ile Ala Tyr Asp Arg Pro Arg Gly Arg Pro Met Ser			
979	984	989	994
aaa aag aag aaa ccc aag gac ttg gac ttc gcc cag cag aag ctg acc			3199
Lys Lys Lys Pro Lys Asp Leu Asp Phe Ala Gln Gln Lys Leu Thr			
995	1000	1005	1010
gat aag aac ctg ggc ttc cag atg ctg cag aag atg ggc tgg aag gag			3247
Asp Lys Asn Leu Gly Phe Gln Met Leu Gln Lys Met Gly Trp Lys Glu			
1011	1016	1021	1026
ggc cat ggc ctg ggc tcc ctc gga aag ggc atc agg gag ccg gtc agc			3295
Gly His Gly Leu Gly Ser Leu Gly Lys Gly Ile Arg Glu Pro Val Ser			
1027	1032	1037	1042
gtg tac gca gca ggc agc ctg ggg tgg gag tgg gtg ggg cct cag tcc			3343
Val Tyr Ala Ala Gly Ser Leu Gly Trp Glu Trp Val Gly Pro Gln Ser			
1043	1048	1053	1058
tcc cac ctg cag cct gcc gct tgg ctc ctt cac agc caa gat ggc tta			3391
Phe His Leu Gln Pro Ala Ala Trp Leu Leu His Ser Gln Asp Gly Leu			
1059	1064	1069	1074
cag ctg gca gtt gat ttt tgt ttt tta aac aga agg cat ctt cag atg			3439
Gln Leu Ala Val Asp Phe Cys Phe Leu Asn Arg Arg His Leu Gln Met			
1075	1080	1085	1090
aga agc tga tcattta catgtcagg tg ^c ttcacagg gtcctttct gtcctgggt			3495
Arg Ser *			
1091			
agat ^d tttta accagcttgt tggccctgggt cattttggcc acatttgtga ccatcataaa			3555
agctaagtgg tatttctgtg tagtttccgt ctggaactgc tttcccattc ccggaaaccc			3615
atagccgggc cagccagggt cccgaacaca ggcccaaagt ttat ^e aaacc ccgatcataa			3675
cctccagcag gcatttcatt taatactgag ctttagttcct gctgggtaag gcattccgag			3735
gtaaccaggg ccctctgggc acccccctcaa aagccagctc ttcgagggtg agtactcctt			3795
gtttctactg tgagtcgcgt ctgtat ^f ttc cttttctttg atgtctcagt gtgtgtcccc			3855
aacacctgca tctcatggac tg ^g tttgcc catgcccagt tcctggcatg ccaggccctg			3915

ggctcaggtg cacaactgac tctttttc actccctagg ggaaccccct cggaaggggaa	3975
agggttgggt gctgacgggc aggagcacaa agaagacaca ttcatgtgt tccgacagag	4035
gatgatgcag atgtacagac acaagcgggc caacaaatag gtatgttcac aggccagtgt	4095
gtaaggccgt ctgccctcgc tggcgtgctg gtatgcagag aaatttcccc caacaaagtt	4155
gatgttccct gctcccaa aaatgccaca cacaaaaaaa atcacaaaat tctgtgaggg	4215
aaacaaaagg gtctatggat gtggatatgc cccattctta cttccaggt ttgctgaagg	4275
agcaaacctc acactggcca agggcagatg cgcatggcct gcetggtgcc ccggctgtga	4335
gcccctcaag gcctccaggc cagcctccgt ggatgtgcgt gtggaaatag gccacgcctg	4395
tctttctct tgctcaagtt ttctctcaca gatgacagcc acctaccaca taacatgacc	4455
agcaaaacgga ctgttcctag tccagagggc cttgccatca tgcaagtggaa agggcgactg	4515
tgacagccac tgccacagag gatggcagtt ggctgtgtcc ctttgtgagg gtctcaaataat	4575
ccttttcctt ctgcagggcc ttgggcctgt aaatatcctc atctttctat tctttttttt	4635
tttttagttt ccccctcacc taatttccac ctcagttttg aacaaaatcg ttcttttcct	4695
gaatagatca aaaccactga tttgtaaagat aagccttggaa gcagcaattg ccctaaaaac	4755
atcatccctg ccctggatcg gcctggagcc agtgcctaag tacggtttgg tgtgtacatg	4815
aaaacaaaacg tctctgcagt ctctggggcg gaggtttcgc tggctttct ttctctcaaa	4875
aaaaaaaaaca tgcaccattt tcaatgtgct tttgcctctc ctctctgttc acatgctttt	4935
agcagcaagt cccctccaaa tctgtcttgg ttccccttca gaaggtggcg ctgcccccgaa	4995
aaggcacctc agcctgtgag tgctgaggaa ccagctcctc tggctgattt tccagttggaa	5055
ctggccattt ctctccagaa gtgctctgtt agcaaacgtg atgtggaaac gatcacagat	5115
ggtgtttctt cgttggcgc cagaatttat acgggggaga caaattcccg gtaattacca	5175
agtctgcact cgggtaccaa agctctgaag ctctctgaac agttgccata cttgagttga	5235
tgaatgtgtt attcatggtg tctcatctca tcaatgcata ttgagagact taatgaaatt	5295
tttagcaacag tatagaatag ctctatcggg tggggagtaa tcattaaaca gatgaaatcg	5355
gccccagatt tacatgtctc tttagaatcc acagtgtaaag caaactacag ttacaaaggg	5415
atgggggttg taaaccctct gagactctgc acttttcga cgtatggcat cgtcaagtgc	5475
tgtcttatta cagccttgc aaggagagggc aggctcctcc tgggggtgggc tctgcagctg	5535
ctctatcccttcc aggcatgtga tcgcccccgcc tctccagatt ccccagcact ctgctgcgtg	5595
taactccact caattctcca ctcatccttc cttgtgaagc aggtatcgaa aagtttaag	5655

tatggcaaa aatctggaaa acttaggatc cctctgacac cccaggatta ggggacacag	5715
cagtggctag ggcatacgcc acagaactga gcgggaaatg ccacttgtat tggctgtaaa	5775
gaaatcctgg ctggggcca ggcacagtgg ctcaagcctg taatcccagc actttaggag	5835
gttgaggcgg atggatcacc tgaggtcagg agtttgagac cagcctggcc aacatggtgt	5895
aaccccgctct tactaaaaaa tacaaaaaaa ttggccaggc gtggtagcgg gcacctgtaa	5955
tccccagctac tcaggaggct gaggcaggag aatcaattga accggggagg cagaggttgc	6015
agtgagctga gatcatgccatccacttgcgc cagagcaaga ctccatctcc	6075
aaaaaaaaaa aaa	6088

<210> 191
 <211> 1915
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (179)..(1522)

<400> 191			
acggggccca tagaacgcct gaggtaccgc tccggaaattc ccgggtcgac ccacgcgtcc	60		
ggttcaggca gtgacgtaac ttgctgcctt aggtggcctt ccgctctggc ggctgtcgcg	120		
acgggggttc agggaatatt tactgggcct ctccgcgtccc tctgcgttgc gaggtgcc	178		
atg agg tca gtt agc tac gtg cag cgc gtg gcg ctg gag ttc agc ggg	226		
Met Arg Ser Val Ser Tyr Val Gln Arg Val Ala Leu Glu Phe Ser Gly			
1	5	10	15
agc ctc ttc ccg cac gca atc tgc ctc gga gac gtt gat aac gat acg	274		
Ser Leu Phe Pro His Ala Ile Cys Leu Gly Asp Val Asp Asn Asp Thr			
17	22	27	32
tta aat gaa ctg gtg gtg gga gac acc agc ggg aag gtg tct gtg tat	322		
Leu Asn Glu Leu Val Val Gly Asp Thr Ser Gly Lys Val Ser Val Tyr			
33	38	43	48
aaa aat gat gac agt cgg cca tgg ctc acc tgt tcc tgc cag gga atg	370		
Lys Asn Asp Asp Ser Arg Pro Trp Leu Thr Cys Ser Cys Gln Gly Met			
49	54	59	64
ctg act tgc gtt ggg gtt gga gac gtg tgt aat aaa gga aag aac ctg	418		
Leu Thr Cys Val Gly Val Gly Asp Val Cys Asn Lys Gly Lys Asn Leu			
65	70	75	80
ttg gtg gca gtg agt gct gaa ggc tgg ttt cat ttg ttt gac ctg aca	466		
Leu Val Ala Val Ser Ala Glu Gly Trp Phe His Leu Phe Asp Leu Thr			

81

86

91

96

cct gcc aag gtg ttg gat gct tct ggg cac cac gag aca cta atc gga Pro Ala Lys Val Leu Asp Ala Ser Gly His His Glu Thr Leu Ile Gly	514
97 102 107 112	
gag gag cag cgt cca gtc ttc aag cag cac atc cct gcc aac acc aag Glu Glu Gln Arg Pro Val Phe Lys Gln His Ile Pro Ala Asn Thr Lys	562
113 118 123 128	
gtc atg ctg atc agc gac atc gat gga gat ggg tgt cgt gag ctg gtg Val Met Leu Ile Ser Asp Ile Asp Gly Asp Gly Cys Arg Glu Leu Val	610
129 134 139 144	
gtg ggc tac aca gac cgt gtg gtg cga gct ttc cgc tgg gag gag cta Val Gly Tyr Thr Asp Arg Val Val Arg Ala Phe Arg Trp Glu Glu Leu	658
145 150 155 160	
gtt gag ggt cct gaa cat ctg aca ggg cag ctg gtg tcc ctc aag aaa Gly Glu Gly Pro Glu His Leu Thr Gly Gln Leu Val Ser Leu Lys Lys	706
161 166 171 176	
tgg atg ctg gag ggt cag gtg gac agc ctc tca gtg act ctg ggg cca Trp Met Leu Glu Gly Gln Val Asp Ser Leu Ser Val Thr Leu Gly Pro	754
177 182 187 192	
ctg ggt ctt cct gaa ctg atg gtg tct cag cca ggt tgt gcg tat gca Leu Gly Leu Pro Glu Leu Met Val Ser Gln Pro Gly Cys Ala Tyr Ala	802
193 198 203 208	
att cta ctg tgt acc tgg aaa aag gac act ggg tcc cct gcc tct Ile Leu Leu Cys Thr Trp Lys Lys Asp Thr Gly Ser Pro Pro Ala Ser	850
209 214 219 224	
gaa ggg ccc acg gat ggt agt agg gag acc cca gct gcc cga gac gtg Glu Gly Pro Thr Asp Gly Ser Arg Glu Thr Pro Ala Ala Arg Asp Val	898
225 230 235 240	
gtg ctg cac cag aca tct ggc cgt atc cac aac aag aat gtc tcc act Val Leu His Gln Thr Ser Gly Arg Ile His Asn Lys Asn Val Ser Thr	946
241 246 251 256	
cac cta att ggc aac atc aaa caa ggc cac ggc act gag agt agt ggc His Leu Ile Gly Asn Ile Lys Gln Gly His Gly Thr Glu Ser Ser Gly	994
257 262 267 272	
tct ggc ctc ttt gcc ctg tgc acc ctg gat ggg aca ctg aag ctc atg Ser Gly Leu Phe Ala Leu Cys Thr Leu Asp Gly Thr Leu Lys Leu Met	1042
273 278 283 288	
gaa gaa atg gaa gaa gca gac aag ctg ctg tgg tca gtg cag gtg gat Glu Glu Met Glu Glu Ala Asp Lys Leu Leu Trp Ser Val Gln Val Asp	1090
289 294 299 304	
cac cag ctc ttt gcc ctg gag aaa ctg gat gtc acc ggc aac ggg cat His Gln Leu Phe Ala Leu Glu Lys Leu Asp Val Thr Gly Asn Gly His	1138
305 310 315 320	

gag gag gta gtt gca tgc gcc tgg gat gga cag aca tat atc att gat		1186
Glu Glu Val Val Ala Cys Ala Trp Asp Gly Gln Thr Tyr Ile Ile Asp		
321 326 331 336		
 cac aac cgc acc gtc gtc cgc ttc caa gtg gat gaa aat atc cgt gcc		1234
His Asn Arg Thr Val Val Arg Phe Gln Val Asp Glu Asn Ile Arg Ala		
337 342 347 352		
 ttc tgt gca ggc ctg tac gcc tgc aaa gag ggc cgc aac agc ccc tgc		1282
Phe Cys Ala Gly Leu Tyr Ala Cys Lys Glu Gly Arg Asn Ser Pro Cys		
353 358 363 368		
 ctc gta tat gtc act ttc aac cag aag atc tat gtg tac tgg gag gtg		1330
Leu Val Tyr Val Thr Phe Asn Gln Lys Ile Tyr Val Tyr Trp Glu Val		
369 374 379 384		
 cag ctg gag cg ^g atg gag tct acc aat ctg gtg aaa ctg ctg gag acc		1378
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr		
385 390 395 400		
 aag ccg gag tac cac agc ctg ctg cag gag ctg ggc gtg gat cct gac		1426
Lys Pro Glu Tyr His Ser Leu Leu Gln Glu Leu Gly Val Asp Pro Asp		
401 406 411 416		
 gac ctc cct gtg act cgt gcc ctg ctt cac caa acg ctc tac cat cca		1474
Asp Leu Pro Val Thr Arg Ala Leu Leu His Gln Thr Leu Tyr His Pro		
417 422 427 432		
 gac cag cca cca cag tgt gct ccc tca agc ctc cag gat ccc acc tag		1522
Asp Gln Pro Pro Gln Cys Ala Pro Ser Ser Leu Gln Asp Pro Thr *		
433 438 443 448		
 ctgtacttgc ctcatagctg gtgaaggatt cttctgaacc cccaccctac cccctaaagg		1582
cgtctttgga tcacactgctg cggctgctgg ctccatcaca aaacaatgaa ggagggaaagtg		1642
ggacgcagag agaaaacgcac atggggagaaa cgccacgtga aggctgaggt cgggataatg		1702
catctgcaag ccaaggaaca cctaagagga ccagcaaacc accagaagcc aggggagagg		1762
cgtggaacag accctgcctt acagctgtca gaaggaacca accctgccaa caccttcctg		1822
ttgtactttc agcttccaga actgtgcctg cagggcttga gagaaatgga gacaaagaag		1882
gccgtgggca ggaggccaag agaagcccag cag		1915

<210> 192
 <211> 1136
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

<222> (82) .. (918)

<400> 192
atttggccct cgaggcaaga aattcggcac gaggcgcatc tcccgctagg agttcctagt 60
aaagtggcgg gagccgcagc t atg gag ccg cag gag gag aga gaa acg cag 111
Met Glu Pro Gln Glu Glu Arg Glu Thr Gln
1 5
gtt gct gcg tgg tta aaa aaa ata ttt gga gat cat cct att cca cag 159
Val Ala Ala Trp Leu Lys Lys Ile Phe Gly Asp His Pro Ile Pro Gln
11 16 21 26
tat gag gtg aac cca cgg acc aca gag att tta cat cac ctt tca gaa 207
Tyr Glu Val Asn Pro Arg Thr Thr Glu Ile Leu His His Leu Ser Glu
27 32 37 42
cgc aac agg gtc cgg gac agg gat gtc tac ctg gta ata gag gac ttg 255
Arg Asn Arg Val Arg Asp Arg Val Tyr Leu Val Ile Glu Asp Leu
43 48 53 58
aag cag aaa gca agt gaa tac gag tca gaa gcc aag tat ctt caa gac 303
Lys Gln Lys Ala Ser Glu Tyr Glu Ser Glu Ala Lys Tyr Leu Gln Asp
59 64 69 74
ctt ctc atg gag agt gtg aat ttt tcc ccc gcc aat ctc tct agc act 351
Leu Leu Met Glu Ser Val Asn Phe Ser Pro Ala Asn Leu Ser Ser Thr
75 80 85 90
ggc tcc agg tat ctg aat gct ttg gtt gac agt gcg gtg gcc ctt gaa 399
Gly Ser Arg Tyr Leu Asn Ala Leu Val Asp Ser Ala Val Ala Leu Glu
91 96 101 106
aca aag gat acc tcg cta gct agt ttt atc cct gca gtg aat gat ttg 447
Thr Lys Asp Thr Ser Leu Ala Ser Phe Ile Pro Ala Val Asn Asp Leu
107 112 117 122
acc tct gat ctc ttt cgt acc aaa tcc aaa agt gaa gaa atc aag att 495
Thr Ser Asp Leu Phe Arg Thr Lys Ser Lys Ser Glu Glu Ile Lys Ile
123 128 133 138
gaa ctg gaa aaa ctt gaa aaa aat tta act gca act tta gta tta gaa 543
Glu Leu Glu Lys Leu Glu Lys Asn Leu Thr Ala Thr Leu Val Leu Glu
139 144 149 154
aaa tgt cta caa gag gat gtc aag aaa gca gag ttg cat ctg tct aca 591
Lys Cys Leu Gln Glu Asp Val Lys Lys Ala Glu Leu His Leu Ser Thr
155 160 165 170
gaa agg gcc aaa gtt gat aat cgt cgt cag aac atg gac ttt cta aaa 639
Glu Arg Ala Lys Val Asp Asn Arg Arg Gln Asn Met Asp Phe Leu Lys
171 176 181 186
gca aag tca gag gaa ttc aga ttt gga atc aag gct gca gag gag caa 687
Ala Lys Ser Glu Glu Phe Arg Phe Gly Ile Lys Ala Ala Glu Glu Gln
187 192 197 202

ctt tca gcc aga ggc atg gat gct tct ctg tct cat cag tcc tta gta
 Leu Ser Ala Arg Gly Met Asp Ala Ser Leu Ser His Gln Ser Leu Val
 203 208 213 218

gca cta tca gag aaa ctg gca aga tta aag caa cag act ata cct ttg 783
 Ala Leu Ser Glu Lys Leu Ala Arg Leu Lys Gln Gln Thr Ile Pro Leu
 219 224 229 234

```

aag aaa aaa ttg gag tcc tat tta gac tta atg ccg aat ccg tct ctt      831
Lys Lys Lys Leu Glu Ser Tyr Leu Asp Leu Met Pro Asn Pro Ser Leu
235          240          245          250

```

gct caa gtg aaa att gaa gaa gca aag cga gaa cta gat agc att gaa 879
 Ala Gln Val Lys Ile Glu Glu Ala Lys Arg Glu Leu Asp Ser Ile Glu
 251 256 261 266

gct gaa ctt aca aga aga gta gac atg atg gaa ctg tga caaaagccaa 928
 Ala Glu Leu Thr Arg Arg Val Asp Met Met Glu Leu *

267	272	277
-----	-----	-----

ataaacatcc tttccctaa caaagtaat tgaataggac ttacagagt tctttttcct 988

cttggcattt cctaataaca aaactttctg tgttcttaga ttacagaata tcataattga 1048

taqaatatqq tttcttactq tgatgtgcat ttttgtgccc aaatacatacg ttttcattttt 1108

aaaaagcctt ttctcttaaa aaaaaaaaaa 1136

```
<210> 193  
<211> 1486  
<212> DNA  
<213> Homo sapiens
```

<220>
<221> CDS
<222> (103) .. (915)

<400> 193

atcgataagg cagtacccag ctggctagcg tttaaactta agcttggtag cgagctcggga 60

tccactagtc cagtgtggtg gaattccggg actctgggaa aa atg gct gcg tct 114
Met Ala Ala Ser
1

gcg ggt ggt aac agc aca cga gag cgg ctg ctg tct gcg ctt gag gac 210
 Ala Gly Gly Asn Ser Thr Arg Glu Arg Leu Leu Ser Ala Leu Glu Asp
 21 26 31 36

ttg gag gtc ctg tct agg gaa ctt ata gaa atg ctg gca att tca aga 258
Leu Glu Val Leu Ser Arg Glu Leu Ile Glu Met Leu Ala Ile Ser Arg

37	42	47	52	
aac caa aag ttg tta cag gct gga gag gaa aac cag gtc ctg gag ttg Asn Gln Lys Leu Leu Gln Ala Gly Glu Asn Gln Val Leu Glu Leu 53 58 63 68				306
tta att cac cga gat ggg gaa ttt caa gaa cta atg aaa ttg gca ctt Leu Ile His Arg Asp Gly Glu Phe Gln Glu Leu Met Lys Leu Ala Leu 69 74 79 84				354
aat cag gga aaa att cat cat gaa atg caa gtt tta gaa aaa gaa gta Asn Gln Gly Lys Ile His His Glu Met Gln Val Leu Glu Lys Glu Val 85 90 95 100				402
gag aag aga gac agt gat att cag cag cta caa aaa cag cta aag gaa Glu Lys Arg Asp Ser Asp Ile Gln Gln Leu Gln Lys Gln Leu Lys Glu 101 106 111 116				450
gca gaa caa ata ctg gca aca gct gtt tac caa gcg aag gag aaa ctc Ala Glu Gln Ile Leu Ala Thr Ala Val Tyr Gln Ala Lys Glu Lys Leu 117 122 127 132				498
aag tca ata gaa aaa gca aga aaa ggt gct atc tcc tct gaa gaa ata Lys Ser Ile Glu Lys Ala Arg Lys Gly Ala Ile Ser Ser Glu Glu Ile 133 138 143 148				546
att aag tat gca cat agg atc agt gca agt aat gct gta tgt gct cca Ile Lys Tyr Ala His Arg Ile Ser Ala Ser Asn Ala Val Cys Ala Pro 149 154 159 164				594
ctg acc tgg gtt cca ggg gac ccc cgg aga ccc tac cca act gat tta Leu Thr Trp Val Pro Gly Asp Pro Arg Arg Pro Tyr Pro Thr Asp Leu 165 170 175 180				642
gag atg aga agt ggg tta ctg ggt cag atg aac aat cct tcc act aat Glu Met Arg Ser Gly Leu Leu Gly Gln Met Asn Asn Pro Ser Thr Asn 181 186 191 196				690
ggc gtg aat ggc cat tta cca gga gat gca ctt gca gca gga aga ttg Gly Val Asn Gly His Leu Pro Gly Asp Ala Leu Ala Ala Gly Arg Leu 197 202 207 212				738
cca gat gtc ctt gct cca cag tat cca tgg cag tca aat gac atg tcg Pro Asp Val Leu Ala Pro Gln Tyr Pro Trp Gln Ser Asn Asp Met Ser 213 218 223 228				786
atg aat atg tta cca cca aat cat agt agt gac ttt ttg ttg gaa cct Met Asn Met Leu Pro Pro Asn His Ser Ser Asp Phe Leu Leu Glu Pro 229 234 239 244				834
cct ggg cat aat aaa gaa aat gaa gat gat gta gag att atg tca acg Pro Gly His Asn Lys Glu Asn Glu Asp Asp Val Glu Ile Met Ser Thr 245 250 255 260				882
gac tcc tca agc agt agt gag tct gat tga aaaacctt aaaagacaat Asp Ser Ser Ser Ser Ser Glu Ser Asp *261 266 271				933

atacagaatt	gaatactgta	gaattctgtt	tcttaacag	tagcaggaa	atgtaaaacta	993
caggtgacaa	aaaataccca	ggtaaacact	ggcttggta	gaattgtgca	gtcattaaaa	1053
gtcaaaattt	tttgacttc	tttttaaagc	caaagaccat	agtttttagtt	ttaagccact	1113
agtagatat	ttagggaat	agtcaaaatt	tactgtgaa	aaagcagttg	ctatgtgctt	1173
tcttaccctg	ttctgttcca	gttttgcgg	atttgacat	agccattcta	gaaatagagt	1233
tgagggaaat	tatccatata	catactacta	ataggcttct	tgaaattatt	tagaaaagca	1293
tttttaaact	ggcagtggat	gactgaatag	gcatcatatt	tcttttgcg	tgtcattaa	1353
aagtaacaaa	aactgccatt	tgacagtaaa	ggctcttggc	ttctgttgg	ggcatggaa	1413
attgtctcaa	tttgtacagt	ttgttaattgt	aattttgt	aataaatttg	tttgtacatt	1473
aaaaaaaaaa	aaa					1486

<210> 194
 <211> 2353
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (153)..(2309)

<400> 194

ccggaattcc	cgggtcgacg	atttcgtgcg	gaggtcgccg	cgagccgggc	cgagcagtga	60
gggccttagc	ggggccccgag	cggggcccgg	ggcccttaag	ccattcctga	agtcatgggc	120
tggccaggac	atcggtgacc	cgc当地atccg	gt	atg gac gac tgg aag ccc agc		173
				Met Asp Asp Trp Lys Pro Ser		
			1		5	

ccc ctc atc aag ccc ttt ggg gct cgg aag aag cgg agc tgg tac ctt					221
Pro Leu Ile Lys Pro Phe Gly Ala Arg Lys Lys Arg Ser Trp Tyr Leu					
8	13	18	23		

acc tgg aag tat aaa ctg aca aac cag cgg gcc ctg cgg aga ttc tgt					269
Thr Trp Lys Tyr Lys Leu Thr Asn Gln Arg Ala Leu Arg Arg Phe Cys					
24	29	34	39		

cag aca ggg gcc gtg ctt ttc ctg ctg gtg act gtc att gtc aat atc					317
Gln Thr Gly Ala Val Leu Phe Leu Leu Val Thr Val Ile Val Asn Ile					
40	45	50	55		

aag ttg atc ctg gac act cgg cga gcc atc agt gaa gcc aat gaa gac					365
Lys Leu Ile Leu Asp Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp					
56	61	66	71		

gac aac aag gtc ctc aat gtg cct gtg gct gtc att gca ggg aac cga		1085
Asp Asn Lys Val Leu Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg		
296	301	306
311		
ccc aat tac ctg tac agg atg ctg cgc tct ctg ctt tca gcc cag ggg		1133
Pro Asn Tyr Leu Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly		
312	317	322
327		
gtg tct cct cag atg ata aca gtt ttc att gac ggc tac tat gag gaa		1181
Val Ser Pro Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu		
328	333	338
343		
ccc atg gat gtg gtg gca ctg ttt ggt ctg agg ggc atc cag cat act		1229
Pro Met Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr		
344	349	354
359		
ccc atc agc atc aag aat gcc cgc gtg tct cag cac tac aag gcc agc		1277
Pro Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser		
360	365	370
375		
ctc act gcc act ttc aac ctg ttt ccg gag gcc aag ttt gct gtg gtt		1325
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val Val		
376	381	386
391		
ctg gaa gag gac ctg gac att gct gtg gat ttt ttc agt ttc ctg agc		1373
Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe Leu Ser		
392	397	402
407		
caa tcc atc cac cta ctg gag gag gat gac agc ctg tac tgc atc tct		1421
Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr Cys Ile Ser		
408	413	418
423		
gcc tgg aat gac cag ggg tat gaa cac acg gct gag gac cca gca cta		1469
Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu Asp Pro Ala Leu		
424	429	434
439		
ctg tac cgt gtg gag acc atg cct ggg ctg ggc tgg gtg ctc agg agg		1517
Leu Tyr Arg Val Glu Thr Met Pro Gly Leu Gly Trp Val Leu Arg Arg		
440	445	450
455		
tcc ttg tac aag gag gag ctt gag ccc aag tgg cct aca ccg gaa aag		1565
Ser Leu Tyr Lys Glu Glu Leu Glu Pro Lys Trp Pro Thr Pro Glu Lys		
456	461	466
471		
ctc tgg gat tgg gac atg tgg atg cgg atg cct gaa caa cgc cgg ggc		1613
Leu Trp Asp Trp Asp Met Trp Met Arg Met Pro Glu Gln Arg Arg Gly		
472	477	482
487		
cga gag tgc atc atc cct gac gtt tcc cga tcc tac cac ttt ggc atc		1661
Arg Glu Cys Ile Ile Pro Asp Val Ser Arg Ser Tyr His Phe Gly Ile		
488	493	498
503		
gtc ggc ctc aac atg aat ggc tac ttt cac gag gcc tac ttc aag aag		1709
Val Gly Leu Asn Met Asn Gly Tyr Phe His Glu Ala Tyr Phe Lys Lys		
504	509	514
519		
cac aag ttc aac acg gtt cca ggt gtc cag ctc agg aat gtg gac agt		1757

His Lys Phe Asn Thr Val Pro Gly Val Gln Leu Arg Asn Val Asp Ser			
520	525	530	535
ctg aag aaa gaa gct tat gaa gtg gaa gtt cac agg ctg ctc agt gag			1805
Leu Lys Lys Glu Ala Tyr Glu Val Glu Val His Arg Leu Leu Ser Glu			
536	541	546	551
gct gag gtt ctg gac cac agc aag aac cct tgt gaa gac tct ttc ctg			1853
Ala Glu Val Leu Asp His Ser Lys Asn Pro Cys Glu Asp Ser Phe Leu			
552	557	562	567
cca gac aca gag ggc cac acc tac gtg gcc ttt att cga atg gag aaa			1901
Pro Asp Thr Glu Gly His Thr Tyr Val Ala Phe Ile Arg Met Glu Lys			
568	573	578	583
gat gat gac ttc acc acc tgg acc cag ctt gcc aag tgc ctc cat atc			1949
Asp Asp Asp Phe Thr Thr Trp Thr Gln Leu Ala Lys Cys Leu His Ile			
584	589	594	599
tgg gac ctg gat gtg cgt ggc aac cat cgg ggc ctg tgg aga ttg ttt			1997
Trp Asp Leu Asp Val Arg Gly Asn His Arg Gly Leu Trp Arg Leu Phe			
600	605	610	615
cgg aag aag aac cac ttc ctg gtg ggg gtc ccg gct tcc ccc tac			2045
Arg Lys Lys Asn His Phe Leu Val Val Gly Val Pro Ala Ser Pro Tyr			
616	621	626	631
tcg cct ggc tca gaa tct aac cta ttt att gac tgt cct gag ggc ctt			2093
Ser Pro Gly Ser Glu Ser Asn Leu Phe Ile Asp Cys Pro Glu Gly Leu			
632	637	642	647
gaa aac agg ccg aac ctg gag ggc ctg gat ttc ttt ttg ggc tgg aat			2141
Glu Asn Arg Pro Asn Leu Glu Gly Leu Asp Phe Phe Leu Gly Trp Asn			
648	653	658	663
gct gcc ctg agg gtg ggg ctg gct ctt act cag gaa act gct gtg ccc			2189
Ala Ala Leu Arg Val Gly Leu Ala Leu Thr Gln Glu Thr Ala Val Pro			
664	669	674	679
aac cca tgg aca ggc cca gct ggg gcc cac atg ctg aca cag act cac			2237
Asn Pro Trp Thr Gly Pro Ala Gly Ala His Met Leu Thr Gln Thr His			
680	685	690	695
tca gag acc ctt aga cac tgg acc agg cct ctc agc ctt ctc ttt			2285
Ser Glu Thr Leu Arg His Trp Thr Arg Pro Pro Leu Ser Leu Leu Phe			
696	701	706	711
gtc cag att tcc aaa gct gga taa gttggtcatt gataaaaaaaa ggagaagccc			2339
Val Gln Ile Ser Lys Ala Gly *			
712	717		
tcaaaaaaaaaaaaa			2353

<211> 3996
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (52) .. (3996)

<400> 195

gccgacagtc	cctccttgtc	tgttccggg	attcaggcct	ccctccctga	c	atg	gag	57								
						Met	Glu									
						1										
agt	aac	ctg	tct	ggc	ctg	gtg	cct	gct	ggg	ctg	gtg	cct	gct	ctg	105	
Ser	Asn	Leu	Ser	Gly	Leu	Val	Pro	Ala	Ala	Gly	Leu	Val	Pro	Ala	Leu	
3			8				13						18			
cca	cct	gct	gtg	acc	ctg	ggg	ctg	aca	gct	gcc	tac	acc	acc	ctg	tat	153
Pro	Pro	Ala	Val	Thr	Leu	Gly	Leu	Thr	Ala	Ala	Tyr	Thr	Thr	Leu	Tyr	
19				24				29				34				
gcc	ctg=ctc=ttc	ttc	tcc-gtc-tat	gcc	cag	ctc=tgg	ctg	gtg	ctt=ctg						201	
Ala	Leu	Leu	Phe	Phe	Ser	Val	Tyr	Ala	Gln	Leu	Trp	Leu	Val	Leu	Leu	
35					40				45				50			
tat	ggg	cac	aag	cgt	ctc	agc	tat	cag	acg	gtg	ttc	ctg	gcc	ctc	tgt	249
Tyr	Gly	His	Lys	Arg	Leu	Ser	Tyr	Gln	Thr	Val	Phe	Leu	Ala	Leu	Cys	
51					56				61				66			
ctg	ctc	tgg	gcc	ttg	cgt	acc	acc	ctc	ttc	tcc	tac	ttc	cga		297	
Leu	Leu	Trp	Ala	Ala	Leu	Arg	Thr	Thr	Leu	Phe	Ser	Phe	Tyr	Phe	Arg	
67					72				77				82			
gat	act	ccc	cgc	gcc	aac	cgc	ctg	ggg	ccc	ttg	ccc	ttc	tgg	ctt	ctc	345
Asp	Thr	Pro	Arg	Ala	Asn	Arg	Leu	Gly	Pro	Leu	Pro	Phe	Trp	Leu	Leu	
83					88				93				98			
tac	tgc	tgc	ccc	gtc	tgc	cag	ttc	acc	ttg	acg	ctt	atg	aac		393	
Tyr	Cys	Cys	Pro	Val	Cys	Leu	Gln	Phe	Phe	Thr	Leu	Thr	Leu	Met	Asn	
99					104				109				114			
ctc	tac	ttt	gcc	cag	gtg	gtg	ttc	aag	gcc	aag	gtg	aag	cgt	cg	ccg	441
Leu	Tyr	Phe	Ala	Gln	Val	Val	Phe	Lys	Ala	Lys	Val	Lys	Arg	Arg	Pro	
115					120				125				130			
gag	atg	agc	cga	ggc	ttg	ctc	gct	gtc	cga	ggg	gcc	ttt	gtg	ggg	gcc	489
Glu	Met	Ser	Arg	Gly	Leu	Leu	Ala	Val	Arg	Gly	Ala	Phe	Val	Gly	Ala	
131					136				141				146			
tcg	ctg	ctc	ttt	ctg	ctg	gtg	aac	gtg	ctg	tgt	gct	gtg	ctc	tcc	cat	537
Ser	Leu	Leu	Phe	Leu	Leu	Val	Asn	Val	Leu	Cys	Ala	Val	Leu	Ser	His	
147						152			157				162			
cg	cg	cg	gca	cag	ccc	tgg	gcc	ctg	ctt	gtc	cgc	gtc	ctg	gtg		585
Arg	Arg	Arg	Ala	Gln	Pro	Trp	Ala	Leu	Leu	Val	Arg	Val	Leu	Val		
163					168				173				178			

agc gac tcc ctg ttc gtc atc tgc gcg ctg tct ctt gct gcc tgc ctc Ser Asp Ser Leu Phe Val Ile Cys Ala Leu Ser Leu Ala Ala Cys Leu 179 184 189 194	633
tgc ctc gtc gcc agg cgg gcg ccc tcc act agc atc tac ctg gag gcc Cys Leu Val Ala Arg Arg Ala Pro Ser Thr Ser Ile Tyr Leu Glu Ala 195 200 205 210	681
aag ggg acc agt gtg tgc cag gcg gcc gcg atg ggt ggc gcc atg gtc Lys Gly Thr Ser Val Cys Gln Ala Ala Met Gly Gly Ala Met Val 211 216 221 226	729
ctg ctc tat gcc agc cgg gcc tgc tac aac ctg aca gca ctg gcc ttg Leu Leu Tyr Ala Ser Arg Ala Cys Tyr Asn Leu Thr Ala Leu Ala Leu 227 232 237 242	777
gcc ccc cag agc cgg ctg gac acc ttc gat tac gac tgg tac aat gtg Ala Pro Gln Ser Arg Leu Asp Thr Phe Asp Tyr Asp Trp Tyr Asn Val 243 248 253 258	825
tct gac cag gcg gac ctg gtg aat gac ctg ggg aac aaa ggc tac ctg Ser Asp Gln Ala Asp Leu Val Asn Asp Leu Gly Asn Lys Gly Tyr Leu 259 264 269 274	873
gta ttt ggc ctc atc ctc ttc gtg tgg gag cta ctg ccc acc acc ctg Val Phe Gly Leu Ile Leu Phe Val Trp Glu Leu Leu Pro Thr Thr Leu 275 280 285 290	921
ctg gtg ggc ttc ttc cgg gtg cac cgg ccc cca cag gac ctg agc acc Leu Val Gly Phe Phe Arg Val His Arg Pro Pro Gln Asp Leu Ser Thr 291 296 301 306	969
agc cac atc ctc aat ggg cag gtc ttt gcc tct cgg tcc tac ttc ttt Ser His Ile Leu Asn Gly Gln Val Phe Ala Ser Arg Ser Tyr Phe Phe 307 312 317 322	1017
gac cgg gct ggg cac tgt gaa gat gag ggc tgc tcc tgg gag cac agc Asp Arg Ala Gly His Cys Glu Asp Glu Gly Cys Ser Trp Glu His Ser 323 328 333 338	1065
cgg ggt gag agc acc agc tct tgt gac tgt ggc cct ggt cac tgt cct Arg Gly Glu Ser Thr Ser Cys Asp Cys Gly Pro Gly His Cys Pro 339 344 349 354	1113
gag act gac cct gtt tct ctg ctg cag tat gtc ggg cag tct agg ctc Glu Thr Asp Pro Val Ser Leu Leu Gln Tyr Val Gly Gln Ser Arg Leu 355 360 365 370	1161
tgg gag ctg aat acc cag gcc cca gtc ccc ctc acc cta ggc ccc tgt Trp Glu Leu Asn Thr Gln Ala Pro Val Pro Leu Thr Leu Gly Pro Cys 371 376 381 386	1209
gcc aag ttt gtc tgc cgc ttc ttg ccc agg atc ctg ggg gtc gtg gct Ala Lys Phe Val Cys Arg Phe Leu Pro Arg Ile Leu Gly Val Val Ala 387 392 397 402	1257
acc ccc tcc tct ggc cgg ctc ctt gct gct cct gtc ata gac tca ggg	1305

Thr	Pro	Ser	Ser	Gly	Arg	Leu	Leu	Ala	Ala	Pro	Val	Ile	Asp	Ser	Gly	
403					408					413					418	
gca ggg acg ccc cag .ggg cga ctg gcc ggg cggt ggc cac ctc tcg															1353	
Ala	Gly	Thr	Pro	Gln	Gly	Arg	Leu	Ala	Gly	Arg	Gly	Ala	His	Leu	Ser	
419					424					429					434	
cgc gtg ggc gcc tcc ggg agt ggt gtg gcc gcc ggt ccc gcc gcc cgc															1401	
Arg	Val	Gly	Ala	Ser	Gly	Ser	Gly	Val	Ala	Ala	Gly	Pro	Ala	Ala	Arg	
435					440					445					450	
cac gct ccg agg cgt cgc tgt gcg gac gcg ggg gag gcg gtg gga gcg															1449	
His	Ala	Pro	Arg	Arg	Arg	Cys	Ala	Asp	Ala	Gly	Glu	Ala	Val	Gly	Ala	
451					456					461					466	
agc tgc ggg cgc tgc gcg gtg gcc ctg ctg tct ggc gtg tgc acg cta															1497	
Ser	Cys	Gly	Arg	Cys	Ala	Val	Ala	Leu	Leu	Ser	Gly	Val	Cys	Thr	Leu	
467					472					477					482	
gtg tcc aca cac gtg tgc gtg ggc tct ggg tgc cct ggc gcg gcc ggc															1545	
Val	Ser	Thr	His	Val	Cys	Val	Gly	Ser	Gly	Cys	Pro	Gly	Ala	Ala	Gly	
483					488					493					498	
acg ccc atg ggg gcc ggg gat gcc ggg gcg tct gcg gag agt gca gtg															1593	
Thr	Pro	Met	Gly	Ala	Gly	Asp	Ala	Gly	Ala	Ser	Ala	Glu	Ser	Ala	Val	
499					504					509					514	
acg aca gct ccc cag gag ccc ccc gcc cgg ccc ctc cag gcg ggc agt															1641	
Thr	Thr	Ala	Pro	Gln	Glu	Pro	Pro	Ala	Arg	Pro	Leu	Gln	Ala	Gly	Ser	
515					520					525					530	
gga gct ggc ccg gcg cct ggg cgc gcc atg cgc agc acc acg ctc ctg															1689	
Gly	Ala	Gly	Pro	Ala	Pro	Gly	Arg	Ala	Met	Arg	Ser	Thr	Thr	Leu	Leu	
531					536					541					546	
gcc ctg ctg gcg ctg gtc ttg ctt tac ttg gtg tct ggt gcc ctg gtg															1737	
Ala	Leu	Leu	Ala	Leu	Val	Leu	Leu	Tyr	Leu	Val	Ser	Gly	Ala	Leu	Val	
547					552					557					562	
ttc cgg gcc ctg gag cag ccc cac gag cag cag gcc cag agg gag ctg															1785	
Phe	Arg	Ala	Leu	Glu	Gln	Pro	His	Glu	Gln	Gln	Ala	Gln	Arg	Glu	Leu	
563					568					573					578	
ggg gag gtc cga gag aag ttc ctg agg gcc cat ccg tgt gtg agc gac															1833	
Gly	Glu	Val	Arg	Glu	Lys	Phe	Leu	Arg	Ala	His	Pro	Cys	Val	Ser	Asp	
579					584					589					594	
cag gag ctg ggc ctc ctc atc aag gag gtg gct gat gcc ctg gga ggg															1881	
Gln	Glu	Leu	Gly	Leu	Leu	Ile	Lys	Glu	Val	Ala	Asp	Ala	Leu	Gly	Gly	
595					600					605					610	
ggc gcg gac cca gaa acc aac tcg acc agc aac agc agc cac tca gcc															1929	
Gly	Ala	Asp	Pro	Glu	Thr	Asn	Ser	Thr	Ser	Asn	Ser	Ser	His	Ser	Ala	
611					616					621					626	
tgg gac ctg ggc agc gcc ttc ttt ttc tca ggg acc atc atc acc acc															1977	
Trp	Asp	Leu	Gly	Ser	Ala	Phe	Phe	Phe	Ser	Gly	Thr	Ile	Ile	Thr	Thr	

627	632	637	642	
atc ggc tat ggc aat gtg gcc ctg cgc aca gat gcc ggg cgc ctc ttc Ile Gly Tyr Gly Asn Val Ala Leu Arg Thr Asp Ala Gly Arg Leu Phe				2025
643	648	653	658	
tgc atc ttt tat gcg ctg gtg ggg att ccg ctg ttt ggg atc cta ctg Cys Ile Phe Tyr Ala Leu Val Gly Ile Pro Leu Phe Gly Ile Leu Leu				2073
659	664	669	674	
gca ggg gtc ggg gac cg ^g ctg ggc tcc tcc ctg cgc cat ggc atc ggt Ala Gly Val Gly Asp Arg Leu Gly Ser Ser Leu Arg His Gly Ile Gly				2121
675	680	685	690	
cac att gaa gcc atc ttc ttg aag tgg cac gtg cca ccg gag cta gta His Ile Glu Ala Ile Phe Leu Lys Trp His Val Pro Pro Glu Leu Val				2169
691	696	701	706	
aga gtg ctg tcg gcg atg ctt ttc ctg ctg atc ggc tgc ctg ctc ttt Arg Val Leu Ser Ala Met Leu Phe Leu Leu Ile Gly Cys Leu Leu Phe				2217
707	712	717	722	
gtc ctc acg ccc acg ttc gtg ttc tgc tat atg gag gac tgg agc aag Val Leu Thr Pro Thr Phe Val Phe Cys Tyr Met Glu Asp Trp Ser Lys				2265
723	728	733	738	
ctg gag gcc atc tac ttt gtc ata gtg acg ctt acc acc gtg ggc ttt Leu Glu Ala Ile Tyr Phe Val Ile Val Thr Leu Thr Thr Val Gly Phe				2313
739	744	749	754	
ggc gac tat gtg gcc ggc gcg gac ccc agg cag gac tcc ccg gcc tat Gly Asp Tyr Val Ala Gly Ala Asp Pro Arg Gln Asp Ser Pro Ala Tyr				2361
755	760	765	770	
cag ccg ctg gtg tgg ttc tgg atc ctg ctc ggc ctg gct tac ttc gcc Gln Pro Leu Val Trp Phe Trp Ile Leu Leu Gly Leu Ala Tyr Phe Ala				2409
771	776	781	786	
tca gtg ctc acc acc atc ggg aac tgg ctg cga gta gtg tcc cgc cgc Ser Val Leu Thr Thr Ile Gly Asn Trp Leu Arg Val Val Ser Arg Arg				2457
787	792	797	802	
act cgg gca gag atg ggc ggc ctc acg gct cag gct gcc agc tgg act Thr Arg Ala Glu Met Gly Gly Leu Thr Ala Gln Ala Ala Ser Trp Thr				2505
803	808	813	818	
ggc aca gtg aca gcg cgc gtg acc cag cga ggc ggg ccc gcc gcc ccg Gly Thr Val Thr Ala Arg Val Thr Gln Arg Ala Gly Pro Ala Ala Pro				2553
819	824	829	834	
ccg ccg gag aag gag cag cca ctg ctg cct cca ccg ccc tgt cca gcg Pro Pro Glu Lys Glu Gln Pro Leu Leu Pro Pro Pro Pro Cys Pro Ala				2601
835	840	845	850	
cag ccg ctg ggc agg ccc cga tcc cct tcg ccc ccc gag aag gct cag Gln Pro Leu Gly Arg Pro Arg Ser Pro Ser Pro Pro Glu Lys Ala Gln				2649
851	856	861	866	

ccg cct tcc ccg ccc acg gcc tcg gcc ctg gat tat ccc agc gag aac Pro Pro Ser Pro Pro Thr Ala Ser Ala Leu Asp Tyr Pro Ser Glu Asn 867 872 877 882	2697
ctg gcc ttc atc gac gag tcc tcg gat acg cag agc gag cgc ggc tgc Leu Ala Phe Ile Asp Glu Ser Ser Asp Thr Gln Ser Glu Arg Gly Cys 883 888 893 898	2745
ccg ctg ccc cgc gcg ccg aga ggt cgc cgc cca aat ccc ccc agg Pro Leu Pro Arg Ala Pro Arg Gly Arg Arg Pro Asn Pro Pro Arg 899 904 909 914	2793
aag ccc gtg cg ^g ccc cgc ggc ccc ggg cgt ccc cga ^g gac aaa ggc gtg Lys Pro Val Arg Pro Arg Gly Pro Gly Arg Pro Arg Asp Lys Gly Val 915 920 925 930	2841
ccg acc ccc cca agg ctt tct gtg tcg ccc cgg gcg ggt gta tcc Pro Thr Pro Pro Arg Leu Ser Val Ser Leu Pro Arg Ala Gly Val Ser 931 936 941 946	2889
ctc aca gca cct cac gac tgt gcc tca aag cct gca tca ata aat gaa Leu Thr Ala Pro His Asp Cys Ala Ser Lys Pro Ala Ser Ile Asn Glu 947 952 957 962	2937
aac ggt ctg cac cgc tgc ggg cgt gac gct ccc gga cgc gag tgg gtg Asn Gly Leu His Arg Cys Gly Arg Asp Ala Pro Gly Arg Glu Trp Val 963 968 973 978	2985
tgg aat tgc ttt cct cgg gcc acc gtg ggg gca cct ctg gcc tcc cgt Trp Asn Cys Phe Pro Arg Ala Thr Val Gly Ala Pro Leu Ala Ser Arg 979 984 989 994	3033
gac ccc cag gcc gag ggt ccc cgg gca ccc agc ctt ggc tgc ccg cag Asp Pro Gln Ala Glu Gly Pro Arg Ala Pro Ser Leu Gly Cys Pro Gln 995 1000 1005 1010	3081
ccc cca ccc aac ccc acg ttc tac ggg atc ccc aac ccg gcc cgg ctc Pro Pro Pro Asn Pro Thr Phe Tyr Gly Ile Pro Asn Pro Ala Arg Leu 1011 1016 1021 1026	3129
agt tcc cca gcc cgc tct tcc ttc c ^g ctc cag cca tcc gcg acc ctt Ser Ser Pro Ala Arg Ser Ser Phe Pro Leu Gln Pro Ser Ala Thr Leu 1027 1032 1037 1042	3177
ggc tcc ctc ctt gta tgt ggc cca cag gtg tcg ctc aag tct tcc gac Gly Ser Leu Leu Val Cys Gly Pro Gln Val Ser Leu Lys Ser Ser Asp 1043 1048 1053 1058	3225
cgc caa ggc tcg gac gag gag agc gtg cat agc gac act cgg gac ctg Arg Gln Gly Ser Asp Glu Glu Ser Val His Ser Asp Thr Arg Asp Leu 1059 1064 1069 1074	3273
tgg acc acg acc acg ctg tcc cag gca cag ctg aac atg ccg ctg tcc Trp Thr Thr Thr Leu Ser Gln Ala Gln Leu Asn Met Pro Leu Ser 1075 1080 1085 1090	3321

gag gtc tgc gag ggc ttc gac gat gag ggc cgc aac att agc aag acc			3369
Glu Val Cys Glu Gly Phe Asp Asp Glu Gly Arg Asn Ile Ser Lys Thr			
1091	1096	1101	1106
/			
cgc ggg tgg cac agc ccg ggg cg ^g ggc tcg ttg gac gag ggg tac aag			3417
Arg Gly Trp His Ser Pro Gly Arg Gly Ser Leu Asp Glu Gly Tyr Lys			
1107	1112	1117	1122
gcc agc cac aag ccg gag gaa ctg gac gag cac gc ^g ctg gtg gag ctg			3465
Ala Ser His Lys Pro Glu Glu Leu Asp Glu His Ala Leu Val Glu Leu			
1123	1128	1133	1138
gag ttg cac cgc agc tcc atg gaa atc aat ctg ggg gag aag gac			3513
Glu Leu His Arg Gly Ser Ser Met Glu Ile Asn Leu Gly Glu Lys Asp			
1139	1144	1149	1154
act gca tcc cag atc gag gcc gaa aag tct tcc tca atg tca tca ctc			3561
Thr Ala Ser Gln Ile Glu Ala Glu Lys Ser Ser Met Ser Ser Leu			
1155	1160	1165	1170
aat att gc ^g aag cac atg ccc cat cga gc ^g tac tgg gca gag cag cag			3609
-Asn Ile-Ala-Lys His-Met-Pro His Arg-Ala-Tyr Trp-Ala-Glu Gln Gln			
1171	1176	1181	1186
agc agg gtt gga ggg gct ggg gag act ggg cgt ttc ggt ggg ctg cca			3657
Ser Arg Val Gly Gly Ala Gly Glu Thr Gly Arg Phe Gly Gly Leu Pro			
1187	1192	1197	1202
ctg ccc ctg atg gaa ctc atg gag aat gaa gct ctg gaa atc ctc acc			3705
Leu Pro Leu Met Glu Leu Met Glu Asn Glu Ala Leu Glu Ile Leu Thr			
1203	1208	1213	1218
aaa gcc ctc cgg agt aag ctc ccc gc ^g aac ccc caa gaa ctc cca cga			3753
Lys Ala Leu Arg Ser Lys Leu Pro Ala Asn Pro Gln Glu Leu Pro Arg			
1219	1224	1229	1234
cag att ctg gtg gat ttt gca ggg ctg ggg ccc agg ggg aga tgc aaa			3801
Gln Ile Leu Val Asp Phe Ala Gly Leu Gly Pro Arg Gly Arg Cys Lys			
1235	1240	1245	1250
gtt ccc cag gct aac aca gac ctg agt gc ^g ctg cgc tac tgc tac ctc			3849
Val Pro Gln Ala Asn Thr Asp Leu Ser Ala Leu Arg Tyr Cys Tyr Leu			
1251	1256	1261	1266
gaa tca tct gc ^g gtt cct cga atc aca cat gc ^g gc ^g ccc cct ggc tac			3897
Glu Ser Ser Ala Val Pro Arg Ile Thr His Ala Ala Pro Pro Gly Tyr			
1267	1272	1277	1282
cag tta ggg atc ggc agg gac cac ttc ctg act aag gag ctg cag cga			3945
Gln Leu Gly Ile Gly Arg Asp His Phe Leu Thr Lys Glu Leu Gln Arg			
1283	1288	1293	1298
tac atc gaa ggg ctc aag aag cgc cgg agc aag agg ctg tac gtg aat			3993
Tyr Ile Glu Gly Leu Lys Lys Arg Arg Ser Lys Arg Leu Tyr Val Asn			
1299	1304	1309	1314
taa			3996

*
1315

/
|

<210> 196
<211> 1332
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (171)..(920)

<400> 196
actctggAAC gcctgcaggT accggTccgg aattcccggg tcgaccCACG cgtccggggC 60
gcctgacGGA agcggcgGCA gcgggcagCG gctctcgGGC tgcaggCTGG gcagggtccc 120
ctccccacgct cctgccgctg tctcccacgt ccccccaggTG cgccggccacc* atg gcg 176
Met Ala
1
tcc agc gac gag gac ggc acc aac ggc ggc gcc tcg gag gcc ggc gag 224
Ser Ser Asp Glu Asp Gly Thr Asn Gly Gly Ala Ser Glu Ala Gly Glu
3 8 13 18
gac cgg gag gct ccc ggc aag cgg agg cgc ctg ggg ttc ttg gcc acc 272
Asp Arg Glu Ala Pro Gly Lys Arg Arg Arg Leu Gly Phe Leu Ala Thr
19 24 29 34
gcc tgg ctc acc ttc tac gac atc gcc atg acc gcg ggg tgg ttg gtt 320
Ala Trp Leu Thr Phe Tyr Asp Ile Ala Met Thr Ala Gly Trp Leu Val
35 40 45 50
cta gct att gcc atg gta cgt ttt tat atg gaa aaa gga aca cac aga 368
Leu Ala Ile Ala Met Val Arg Phe Tyr Met Glu Lys Gly Thr His Arg
51 56 61 66
ggT tta tat aaa agt att cag aag aca ctt aaa ttt ttc cag aca ttt 416
Gly Leu Tyr Lys Ser Ile Gln Lys Thr Leu Lys Phe Phe Gln Thr Phe
67 72 77 82
gcc ttg ctt gag ata gtt cac tgt tta att gga att gta cct act tct 464
Ala Leu Leu Glu Ile Val His Cys Leu Ile Gly Ile Val Pro Thr Ser
83 88 93 98
gtg att gtg act ggg gtc caa gtg agt tca aga atc ttt atg gtg tgg 512
Val Ile Val Thr Gly Val Gln Val Ser Ser Arg Ile Phe Met Val Trp
99 104 109 114
ctc att act cac agt ata aaa cca atc cag aat gaa gag agt gtg gtg 560
Leu Ile Thr His Ser Ile Lys Pro Ile Gln Asn Glu Glu Ser Val Val
115 120 125 130

ctt ttt ctg gtc gcg tgg act gtg aca gag atc act cgc tat tcc ttc		608
Leu Phe Leu Val Ala Trp Thr Val Thr Glu Ile Thr Arg Tyr Ser Phe		
131	136	141
		146
/		
tac aca ttc agc ctt ctt gac cac ttg cca tac ttc att aaa tgg gcc		656
Tyr Thr Phe Ser Leu Leu Asp His Leu Pro Tyr Phe Ile Lys Trp Ala		
147	152	157
		162
aga tat aat ttt ttt atc atc tta tat cct gtt gga gtt gct ggt gaa		704
Arg Tyr Asn Phe Phe Ile Ile Leu Tyr Pro Val Gly Val Ala Gly Glu		
163	168	173
		178
ctt ctt aca ata tac gct gcc ttg ccg tat gtg aag aaa aca gga atg		752
Leu Leu Thr Ile Tyr Ala Ala Leu Pro Tyr Val Lys Lys Thr Gly Met		
179	184	189
		194
ttt tca ata aga ctt cct aac aaa tac aat gtc tct ttt gac tac tat		800
Phe Ser Ile Arg Leu Pro Asn Lys Tyr Asn Val Ser Phe Asp Tyr Tyr		
195	200	205
		210
tat ttt ctt ctt ata acc atg gca tca tat ata cct ttg ttt cca caa		848
Tyr Phe Leu Leu Ile Thr Met Ala Ser Tyr Ile Pro Leu Phe Pro Gln		
211	216	221
		226
ctc tat ttt cat atg tta cgt caa aga aga aag gtg ctt cat gga gag		896
Leu Tyr Phe His Met Leu Arg Gln Arg Arg Lys Val Leu His Gly Glu		
227	232	237
		242
gtg att gta gaa aag gat gat taa atgatctctg caaacaagggt gcttttcca		950
Val Ile Val Glu Lys Asp Asp *		
243	248	
gaataaccaa gattacctga gtccaaagttt taataacaag aataaacaac tttgtaaaat		1010
atcatggatt gtatggtttc ttaaaatata acttgagaca cgtggtattt gccagtattt		1070
gtgttcctct tgtgccagat ctattttta caagaactgt gcaaatatca gtaacttttgc		1130
ggttaggtatt gattattagg aaaataatta ggtgtattat ctgggggaaa aaaaaacttt		1190
tgctaagttt ttttggaaac atgctcaaag cttttaaat caatatttag aaatttagttt		1250
aacgatttac tattataacct gctagtgata tttatgtgat atttataaat gaaaataaaat		1310
gcaaaaattat aaaaaaaaaa aa		1332

<210> 197
<211> 2128
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (42)..(1031)

<400> 197

taagcttgcg	gccgcgcggc	ctcccgggcg	ggcctacagc	c	atg tcc cgg gac	53									
					Met Ser Arg Asp										
				1											
ccg	ggg	tcg	ggc	tgg	gag	gag	gcc	ccg	cgc	gca	gct	gcc	gcf	ctc	101
Pro	Gly	Ser	Gly	Gly	Trp	Glu	Glu	Ala	Pro	Arg	Ala	Ala	Ala	Leu	
5					10				15					20	
tgc	acc	ctg	tac	cac	gag	gcc	gga	cag	ccg	ctg	cgc	ctg	cag	gac	149
Cys	Thr	Leu	Tyr	His	Glu	Ala	Gly	Gln	Arg	Leu	Arg	Arg	Leu	Gln	Asp
21					26				31					36	
cag	ctc	gct	gcc	cgc	gac	gcc	ctc	atc	gct	ccg	ctc	ccg	gcc	ctg	197
Gln	Leu	Ala	Ala	Arg	Asp	Ala	Leu	Ile	Ala	Arg	Leu	Arg	Ala	Arg	Leu
37					42				47					52	
gcc	gcf	ctg	gag	ggg	gac	gcc	gcf	ccg	tcc	cta	gtg	gac	gcf	ctg	245
Ala	Ala	Leu	Glu	Gly	Asp	Ala	Ala	Pro	Ser	Leu	Val	Asp	Ala	Leu	Leu
53					58				63					68	
gag	cag	gtt	gcf	ccg	ttc	ccg	gag	cag	ctg	cga	agg	cag	gag	ggc	293
Glu	Gln	Val	Ala	Arg	Phe	Arg	Glu	Gln	Leu	Arg	Arg	Gln	Glu	Gly	
69					74				79					84	
gcc	gcc	gag	gcc	cag	atg	ccg	cag	gaa	att	gag	agg	ctg	act	gag	341
Ala	Ala	Glu	Ala	Gln	Met	Arg	Gln	Glu	Ile	Glu	Arg	Leu	Thr	Glu	Arg
85					90				95					100	
cta	gaa	gaa	aaa	gag	agg	gag	atg	cag	cag	ctg	ctg	agc	cag	ccc	389
Leu	Glu	Glu	Lys	Glu	Arg	Glu	Met	Gln	Gln	Leu	Leu	Ser	Gln	Pro	Gln
101					106				111					116	
cac	gag	cga	gag	aag	gaa	gtc	gtc	ctg	cta	ccg	agg	agc	atg	gca	437
His	Glu	Arg	Glu	Lys	Glu	Val	Val	Leu	Leu	Arg	Arg	Ser	Met	Ala	Glu
117					122				127					132	
ggg	gag	ccg	gcc	ccg	gcc	agt	gac	gtc	ctg	tgc	ccg	tcc	ttg	gcc	485
Gly	Glu	Arg	Ala	Arg	Ala	Ala	Ser	Asp	Val	Leu	Cys	Arg	Ser	Leu	Ala
133					138				143					148	
aac	gag	acc	cat	cag	ctg	ccg	agg	acg	ctg	acc	gcc	acc	cac	atg	533
Asn	Glu	Thr	His	Gln	Leu	Arg	Arg	Thr	Leu	Thr	Ala	Thr	Ala	His	Met
149					154				159					164	
tgt	cag	cat	ctg	gcc	aag	tgt	ctg	gat	gaa	cga	cag	cat	gca	caa	agg
Cys	Gln	His	Leu	Ala	Lys	Cys	Leu	Asp	Glu	Arg	Gln	His	Ala	Gln	Arg
165					170				175					180	
aat	gtg	ggg	gag	aga	agt	cct	gac	cag	tgc	gaa	cac	aca	gat	ggg	629
Asn	Val	Gly	Glu	Arg	Ser	Pro	Asp	Gln	Ser	Glu	His	Thr	Asp	Gly	His
181					186				191					196	
acc	tct	gtc	cag	agt	gtt	att	gag	aag	ttg	cag	gaa	aat	cga	ctg	677
Thr	Ser	Val	Gln	Ser	Val	Ile	Glu	Lys	Leu	Gln	Glu	Glu	Asn	Arg	Leu
197					202				207					212	

tta aaa cag aag gtg act cac gtt gaa gac ctc aat gcc aag tgg cag	725
Leu Lys Gln Lys Val Thr His Val Glu Asp Leu Asn Ala Lys Trp Gln	
213 218/ 223 228	
cgc tac aac gcc agc agg gac gaa tac gtg agg ggg ctc cat gcg cag	773
Arg Tyr Asn Ala Ser Arg Asp Glu Tyr Val Arg Gly Leu His Ala Gln	
229 234 239 244	
ctc agg ggg ctg cag atc ccc cac gag ccc gag ctg atg agg aag gag	821
Leu Arg Gly Leu Gln Ile Pro His Glu Pro Glu Leu Met Arg Lys Glu	
245 250 255 260	
atc tcc cg ^g ctc aac aga cag ttg gaa gag aaa at ^a at ^a gac tgt gcc	869
Ile Ser Arg Leu Asn Arg Gln Leu Glu Glu Lys Ile Asn Asp Cys Ala	
261 266 271 276	
gaa gtg aag cag gag ctg gc ^g tcc agg acg gcc cg ^g gat gct gc ^g	917
Glu Val Lys Gln Glu Leu Ala Ala Ser Arg Thr Ala Arg Asp Ala Ala	
277 282 287 292	
ttg gag cg ^g gtg cag atg ctg gaa cag cag gtg tct gtc cct cg ^g gct	965
Leu Glu Arg Val Gln Met Leu Glu Gln Gln Val Ser Val Pro Arg Ala	
293 298 303 308	
ccg gac ggc act gac cag atg tct gct ggc cg ^g tgg tgg cc ^g aaa tca	1013
Pro Asp Gly Thr Asp Gln Met Ser Ala Gly Arg Trp Trp Pro Lys Ser	
309 314 319 324	
tgg gac agg ctg ggc tga aggctt ggtggcactg agtgggcagt ggtcaactgtg	1067
Trp Asp Arg Leu Gly *	
325 330	
gggggtggag aagcctgggg gggcgcttcc tccttccttg agcagaaaatg tgtgtctcgc	1127
ctctcttcag attctcgctt acaaggatga cttcatgtca gaaaggcccgcg atcgggaacg	1187
ggctcaaagt aggattcaag aactggagga aaaggtcgcc tctttgctgc accaggtgtc	1247
ctggagacag gattctcgag agccagacgc cggccggatt cacgctggga gaaaaactgc	1307
caagtatttg gccgcccacg cattagagct tatggtgcct ggtggctgga ggcctgggac	1367
tgggtcccag cagccagaac cccctgcaga gggcgccat cctggcgcgg cccagagagg	1427
ccagggggac ct ^t cagtgcc ct ^t cactgcct gcagtgc ^t tc agtgcacgagc aaggggaaga	1487
gctcctcagg catgtggccg agtgctgcca gtgaccgaga ctcacccgtg cccttgcggc	1547
ctcctggccc ggtgcagctg ccctcaggga cagggtggt gctctcagat gccatgggtt	1607
gagctctact gagagccaag gcccctagaa tagttgcggg gcactctgat cgttcacttt	1667
ggtccctttg gctatggaac aggctgggtc acagggaaact gccagtgagg ctggaggctg	1727
gaggtggaga tggggtcagg aacatctggc agagggaggt cccagtctgt gtctccatca	1787

ggcttaagcc agagctatct ggtgctggtg tgccagcccc tcccccagcc tgcctagaaa	1847
ggggtgtggctg cctgagggag tcacttgtat ggtccccagg gtgggagccc catcctgttc	1907
tatggaataa agcgctcgct ctctgcctcg aaccagtcaa atggagtatt gcggctgcac	1967
gtcacactag ggtggccacc cccgccattg cgagccacat gtctgcactg agaaactgca	2027
tttcagtagc atttgcatac cagccgaaag ttaaagcaca cttattttat tcacctat	2087
ttataataaa cgttcttgct gctgtaaaaa aaaaaaaaaa a	2128

↓

<210> 198
<211> 668
<212> DNA
<213> Homo sapiens

<220>

<221> CDS
<222> (136)..(498)

<400> 198

aggctcgatg tatataacta tctattcgat gatgaagata ccccacccaa cccaaaaaaaaa	60
gagatctctc gaggatccga attcgccggcc gcgtcgaccc cccctacaga agccccccaga	120
gcgcagcacc tcacc atg gac tgc acc tgg agg atc ctc ttc ttg gtg gca	171
Met Asp Cys Thr Trp Arg Ile Leu Phe Leu Val Ala	
1 5 10	

gca gct aca ggc acc cac gcc cag gtc cag ctg gta cag tct ggg gct	219
Ala Ala Thr Gly Thr His Ala Gln Val Gln Leu Val Gln Ser Gly Ala	
13 18 23 28	

gag gtg aag aag cct ggg gcc tca gtg aag gtc tcc tgc aag gtt tcc	267
Glu Val Lys Lys Pro Gly Ala Ser Val Lys Val Ser Cys Lys Val Ser	
29 34 39 44	

gga tac acc ctc act gaa tta tcc atg cac tgg gtg cga cag gct cct	315
Gly Tyr Thr Leu Thr Glu Leu Ser Met His Trp Val Arg Gln Ala Pro	
45 50 55 60	

gga aaa ggg ctt gag tgg atg gga gct ttt gat cct gaa gat ggt gaa	363
Gly Lys Gly Leu Glu Trp Met Gly Ala Phe Asp Pro Glu Asp Gly Glu	
61 66 71 76	

aca atc tac gca cag aag ttc cag ggc aga gtc acc atg acc gag gac	411
Thr Ile Tyr Ala Gln Lys Phe Gln Gly Arg Val Thr Met Thr Glu Asp	
77 82 87 92	

aca tct aca gac aca ggc tac atg ggg ctg agc agc ctg aga tct gag	459
Thr Ser Thr Asp Thr Gly Tyr Met Gly Leu Ser Ser Leu Arg Ser Glu	
93 98 103 108	

gac acg gcc gtg tat tat tgt gca aca gac aca gtg tga aaacccacat	508
Asp Thr Ala Val Tyr Tyr Cys Ala Thr Asp Thr Val *	
109	114
cctgagagcg tcagaaaccc tgaggaatga ggcagctgtg ctgaggctga ggagatgaca	568
ggatttatga agtttaaatc tgtttagaaa atgggtttag taatttagtta aaacagcaat	628
ggaaaaaaaaac gaaatcgcgca cagcgaagtc gaccgggaa	668

<210> 199
 <211> 2310
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (201)..(2105)

<400> 199	
ggcatgcgg taccgctccg gaattaccgg gtcgacgatc tcgagtggct agagctgaaa	60
ggcgaccgct ggtgtcaaac atcttagctc aaatatctgg gaacgattgc gcgctgagga	120
agaccctttg ggactttag ctccactccg gggAACGGAC tcGCCGGAC tgacagttgc	180
cgaaagttag gctgcgggaa atg gcc gct gcg acc atg gct gcg	230
Met Ala Ala Ala Ala Thr Met Ala Ala Ala	
1 5	
gcc cg gaa ctg gtg ttg cg gct ggg acc tca gat atg gag gag gaa	278
Ala Arg Glu Leu Val Leu Arg Ala Gly Thr Ser Asp Met Glu Glu Glu	
11 16 21 26	
gag ggc ccg ctg gcg ggt ggt cct ggg ctc cag gaa cca ctg caa ctt	326
Glu Gly Pro Leu Ala Gly Gly Pro Gly Leu Gln Glu Pro Leu Gln Leu	
27 32 37 42	
ggg gag ttg gat atc act tct gat gaa ttc atc ctg gat gaa gtg gat	374
Gly Glu Leu Asp Ile Thr Ser Asp Glu Phe Ile Leu Asp Glu Val Asp	
43 48 53 58	
gtt cac att cag gca aat ctg gag gat gag tta gta aag gaa gct ctt	422
Val His Ile Gln Ala Asn Leu Glu Asp Glu Leu Val Lys Glu Ala Leu	
59 64 69 74	
aaa acg ggt gta gat ctc cgt cac tat tca aag caa gtt gag ctg gag	470
Lys Thr Gly Val Asp Leu Arg His Tyr Ser Lys Gln Val Glu Leu Glu	
75 80 85 90	
cta cag cag att gaa cag aaa tcc att cgg gat tat att caa gag agt	518
Leu Gln Gln Ile Glu Gln Lys Ser Ile Arg Asp Tyr Ile Gln Glu Ser	
91 96 101 106	

gag aat ata gca tct cta cac aac cag atc aca gcc tgt gat gct gtc		566	
Glu Asn Ile Ala Ser Leu His Asn Gln Ile Thr Ala Cys Asp Ala Val			
107	112	117	122
/			
ctg gag cga atg gag cag atg ttg gga gct ttt cag agt gac ctc agc		614	
Leu Glu Arg Met Glu Gln Met Leu Gly Ala Phe Gln Ser Asp Leu Ser			
123	128	133	138
tcc atc agc tct gag atc cgg aca ctg cag gaa cag tca gga gcc atg		662	
Ser Ile Ser Ser Glu Ile Arg Thr Leu Gln Glu Gln Ser Gly Ala Met			
139	144	149	154
aac att cga ctt cga aat cgc cag gca gtt cgg ggg aaa ctt ggg gag		710	
Asn Ile Arg Leu Arg Asn Arg Gln Ala Val Arg Gly Lys Leu Gly Glu			
155	160	165	170
ctt gtt gat ggt ctg gtg cct tct gct ctg gtc acg gca att ctg		758	
Leu Val Asp Gly Leu Val Val Pro Ser Ala Leu Val Thr Ala Ile Leu			
171	176	181	186
gag gct cca gtg aca gag ccc agg ttc ttg gag cag cta cag gag ctg		806	
Glu Ala Pro Val Thr Glu Pro Arg Phe Leu Glu Gln Leu Gln Glu Leu			
187	192	197	202
gat gcc aag gca gcc gca gtc aga gag cag gaa gct aga ggc aca gca		854	
Asp Ala Lys Ala Ala Val Arg Glu Gln Glu Ala Arg Gly Thr Ala			
203	208	213	218
gcc tgc gca gat gtc aga ggc gtg ctc gat cgg ctc cgg gtc aag gca		902	
Ala Cys Ala Asp Val Arg Gly Val Leu Asp Arg Leu Arg Val Lys Ala			
219	224	229	234
gtg acg aag atc cga gag ttt atc ctc cag aag att tat tcc ttc agg		950	
Val Thr Lys Ile Arg Glu Phe Ile Leu Gln Lys Ile Tyr Ser Phe Arg			
235	240	245	250
aaa ccc atg acc aac tat cag atc ccc cag acg gcc ctg ctg aag tac		998	
Lys Pro Met Thr Asn Tyr Gln Ile Pro Gln Thr Ala Leu Leu Lys Tyr			
251	256	261	266
agg ttc ttc tat cag ttt ctg ctg ggc aat gaa cga gca aca gca aag		1046	
Arg Phe Phe Tyr Gln Phe Leu Leu Gly Asn Glu Arg Ala Thr Ala Lys			
267	272	277	282
gag atc agg gat gaa tat gtg gag acg ctg agc aag att tac ctg tct		1094	
Glu Ile Arg Asp Glu Tyr Val Glu Thr Leu Ser Lys Ile Tyr Leu Ser			
283	288	293	298
tac tac cgc tct tac ctg ggg cgg ctc atg aag gtg cag tat gag gaa		1142	
Tyr Tyr Arg Ser Tyr Leu Gly Arg Leu Met Lys Val Gln Tyr Glu Glu			
299	304	309	314
gtc gct gag aaa gat gat cta atg ggt gtg gaa gat aca gca aag aaa		1190	
Val Ala Glu Lys Asp Asp Leu Met Gly Val Glu Asp Thr Ala Lys Lys			
315	320	325	330
gga ttc ttc tca aag cca tcg ctc cgc agc agg aac acc att ttc acc		1238	

Gly	Phe	Phe	Ser	Lys	Pro	Ser	Leu	Arg	Ser	Arg	Asn	Thr	Ile	Phe	Thr		
331					336				341				346				
ctc	gga	acc	cgc	ggc	tct	gtc	atc	tcc	ccc	act	gaa	ctt	gag	gcc	ccc		1286
Leu	Gly	Thr	Arg	Gly	Ser	Val	Ile	Ser	Pro	Thr	Glu	Leu	Glu	Ala	Pro		
347						352				357				362			
atc	ctg	gtg	cct	cac	aca	gcg	cag	cgc	gga	gag	cag	agg	tat	cca	ttt		1334
Ile	Leu	Val	Pro	His	Thr	Ala	Gln	Arg	Gly	Glu	Gln	Arg	Tyr	Pro	Phe		
363						368				373				378			
gag	gcc	ctc	ttc	cgc	agc	cag	cac	tac	gcc	ctc	cta	gac	aat	tcc	tgc		1382
Glu	Ala	Leu	Phe	Arg	Ser	Gln	His	Tyr	Ala	Leu	Leu	Asp	Asn	Ser	Cys		
379						384				389				394			
cgc	gaa	tac	ctt	ttc	atc	tgt	gaa	ttt	ttt	gtt	gtg	tct	ggc	cca	gct		1430
Arg	Glu	Tyr	Leu	Phe	Ile	Cys	Glu	Phe	Phe	Val	Val	Ser	Gly	Pro	Ala		
395						400				405				410			
gca	cac	gac	ctg	ttc	cat	gct	gtc	atg	ggc	cgt	aca	ctc	agc	atg	acc		1478
Ala	His	Asp	Leu	Phe	His	Ala	Val	Met	Gly	Arg	Thr	Leu	Ser	Met	Thr		
411						416				421				426			
ctg	aaa	cac	ctg	gat	tct	tat	cta	gct	gac	tgc	tac	gat	gcc	att	gct		1526
Leu	Lys	His	Leu	Asp	Ser	Tyr	Leu	Ala	Asp	Gys	Tyr	Asp	Ala	Ile	Ala		
427						432				437				442			
gtt	ttt	ctc	tgt	atc	cac	att	gtt	ctc	cgg	ttc	cgt	aac	att	gca	gca		1574
Val	Phe	Leu	Cys	Ile	His	Ile	Val	Leu	Arg	Phe	Arg	Asn	Ile	Ala	Ala		
443						448				453				458			
aag	agg	gat	gtt	cct	gcc	ctg	gac	agg	tac	tgg	gaa	cag	gtg	ctt	gcc		1622
Lys	Arg	Asp	Val	Pro	Ala	Leu	Asp	Arg	Tyr	Trp	Glu	Gln	Val	Leu	Ala		
459						464				469				474			
ttg	cta	tgg	cca	cgg	ttt	gaa	ctg	atc	ctg	gag	atg	aat	gtt	cag	agc		1670
Leu	Leu	Trp	Pro	Arg	Phe	Glu	Leu	Ile	Leu	Glu	Met	Asn	Val	Gln	Ser		
475						480				485				490			
gtc	cga	agc	act	gac	ccc	cag	cgc	cta	ggg	ggg	ttg	gat	act	cgg	ccc		1718
Val	Arg	Ser	Thr	Asp	Pro	Gln	Arg	Leu	Gly	Gly	Leu	Asp	Thr	Arg	Pro		
491						496				501				506			
cac	tat	atc	aca	cgc	cgc	tat	gca	gag	ttc	tcc	tcc	gct	ctt	gtc	agt		1766
His	Tyr	Ile	Thr	Arg	Arg	Tyr	Ala	Glu	Phe	Ser	Ser	Ala	Leu	Val	Ser		
507						512				517				522			
atc	aac	cag	aca	att	cct	aat	gaa	cgg	acc	atg	caa	ttg	ctg	gga	cag		1814
Ile	Asn	Gln	Thr	Ile	Pro	Asn	Glu	Arg	Thr	Met	Gln	Leu	Leu	Gly	Gln		
523						528				533				538			
ctg	cag	gtg	gag	gtg	gag	aat	ttt	gtc	ctc	cga	gtg	gca	gct	gag	ttc		1862
Leu	Gln	Val	Glu	Val	Glu	Asn	Phe	Val	Leu	Arg	Val	Ala	Ala	Glu	Phe		
539						544				549				554			
tcc	tca	agg	aag	gag	cag	ctt	gtg	ttt	ctg	atc	aac	aac	tat	gac	atg		1910
Ser	Ser	Arg	Lys	Glu	Gln	Leu	Val	Phe	Leu	Ile	Asn	Asn	Tyr	Asp	Met		

ggg gag gtg tta ctc cca gct ctc tat gag gag gaa gag gaa gag gaa		244
Gly Glu Val Leu Leu Pro Ala Leu Tyr Glu Glu Glu Glu Glu Glu Glu		
56 61 66 71		
/		
gag gag gaa gaa gag gtg gaa gaa gaa gaa caa gtg cag aaa ggt		292
Glu Glu Glu Glu Val Glu Glu Glu Glu Gln Val Gln Lys Gly		
72 77 82 87		
ggc agt gtt ggc tct ctg tca gtc aac aag cac cgg gga ctg agc ctc		340
Gly Ser Val Gly Ser Leu Ser Val Asn Lys His Arg Gly Leu Ser Leu		
88 93 98 103		
acg gag aca gag ctg gag gag ctg cgg gct cag gtg ctg cag ctg gtg		388
Thr Glu Thr Glu Leu Glu Leu Arg Ala Gln Val Leu Gln Leu Val		
104 109 114 119		
gca gaa ctg gag gag acc cgg gaa ctg gca ggg cag cat gag gat gac		436
Ala Glu Leu Glu Glu Thr Arg Glu Leu Ala Gly Gln His Glu Asp Asp		
120 125 130 135		
tcc ttg gag cta cag ggg ctc ctg gag gat gaa cgg cta gcc agc gcc		484
Ser Leu Glu Leu Gln Gly Leu Leu Glu Asp Glu Arg Leu Ala Ser Ala		
136 141 146 151		
cag cag gca gag gtg ttc acc aag cag atc cag cag ctc caa ggt gag		532
Gln Gln Ala Glu Val Phe Thr Lys Gln Ile Gln Gln Leu Gln Gly Glu		
152 157 162 167		
ctg cgt tct cta cgg gag gag att tcc ctg tta gag cat gag aaa gaa		580
Leu Arg Ser Leu Arg Glu Glu Ile Ser Leu Leu Glu His Glu Lys Glu		
168 173 178 183		
agc gaa ctt aag gaa ata gaa cag gaa ttg cat ttg gcc cag gct gag		628
Ser Glu Leu Lys Glu Ile Glu Gln Glu Leu His Leu Ala Gln Ala Glu		
184 189 194 199		
atc cag agt ctg cgg caa gca gca gag gat tcc gca act gaa cat gag		676
Ile Gln Ser Leu Arg Gln Ala Ala Glu Asp Ser Ala Thr Glu His Glu		
200 205 210 215		
agt gac ata gca tcc ctg cag gag gat ctc tgc cgg atg cag aat gaa		724
Ser Asp Ile Ala Ser Leu Gln Glu Asp Leu Cys Arg Met Gln Asn Glu		
216 221 226 231		
ctt gaa gac atg gaa cgc att cgg gga gat tat gag atg gag atc gcc		772
Leu Glu Asp Met Glu Arg Ile Arg Gly Asp Tyr Glu Met Glu Ile Ala		
232 237 242 247		
tcc ctc cgt gca gaa atg gaa atg aag agc tct gaa cca tcc ggt agt		820
Ser Leu Arg Ala Glu Met Glu Met Lys Ser Ser Glu Pro Ser Gly Ser		
248 253 258 263		
tta ggt ctc tca gat tac tct ggg tta caa gaa gaa ctg cag gag ctg		868
Leu Gly Leu Ser Asp Tyr Ser Gly Leu Gln Glu Glu Leu Gln Glu Leu		
264 269 274 279		
cgg gaa cgc tac cat ttc ctg aat gag gaa tac cgg gcc ctg cag gag		916

Arg Glu Arg Tyr His Phe Leu Asn Glu Glu Tyr Arg Ala Leu Gln Glu			
280	285	290	295
agc aac agc agc ctc acg ggg cag ctt gca gat ctg gag agt gag agg			964
Ser Asn Ser Ser Leu Thr Gly Gln Leu Ala Asp Leu Glu Ser Glu Arg			
296	301	306	311
aca cag aga gca aca gag aga tgg ctg cag tcc caa aca ctg agt atg			1012
Thr Gln Arg Ala Thr Glu Arg Trp Leu Gln Ser Gln Thr Leu Ser Met			
312	317	322	327
acg tca gca gag tct cag act tca gaa atg gat ttc tta gag cct gat			1060
Thr Ser Ala Glu Ser Gln Thr Ser Glu Met Asp Phe Leu Glu Pro Asp			
328	333	338	343
cct gaa atg cag ttg tta cgg cag cag cta cgg gat gct gaa gag cag			1108
Pro Glu Met Gln Leu Leu Arg Gln Gln Leu Arg Asp Ala Glu Glu Gln			
344	349	354	359
atg cat ggc atg aag aac aag tgt cag gaa ttg tgt tgt gag ttg gaa			1156
Met His Gly Met Lys Asn Lys Cys Gln Glu Leu Cys Cys Glu Leu Glu			
360	365	370	375
gag cta cag cat cat cgc cag gtc agt gag gag gag cag agg cgg ctg			1204
Glu Leu Gln His His Arg Gln Val Ser Glu Glu Glu Gln Arg Arg Leu			
376	381	386	391
cag agg gag ctc aag tgt gct cag aat gag gtg ctt cgg ttt cag acc			1252
Gln Arg Glu Leu Lys Cys Ala Gln Asn Glu Val Leu Arg Phe Gln Thr			
392	397	402	407
tcc cac agt gtc acc cag cgc ttt gag gaa atg gtt gtg aaa gtg ctg			1300
Ser His Ser Val Thr Gln Arg Phe Glu Glu Met Val Val Lys Val Leu			
408	413	418	423
atc aag ctg cag gcg gtg cag gcc atg tac cag ata agc cag gag gaa			1348
Ile Lys Leu Gln Ala Val Gln Ala Met Tyr Gln Ile Ser Gln Glu Glu			
424	429	434	439
cac agc cag ctg caa gag cag atg gaa aag tta ctg gcc aag cag aaa			1396
His Ser Gln Leu Gln Glu Gln Met Glu Lys Leu Leu Ala Lys Gln Lys			
440	445	450	455
gac ctg aag gaa gag ctg gat gcc tgt gaa agg gag ttc aag gag tgc			1444
Asp Leu Lys Glu Glu Leu Asp Ala Cys Glu Arg Glu Phe Lys Glu Cys			
456	461	466	471
atg gaa tgc ctt gaa aag ccc atg gcc ccc cag aac gac aag aat gag			1492
Met Glu Cys Leu Glu Lys Pro Met Ala Pro Gln Asn Asp Lys Asn Glu			
472	477	482	487
aac atg ttt ggg ttg tgg aag cct atg gta ttc ttg gct att gca gct			1540
Asn Met Phe Gly Leu Trp Lys Pro Met Val Phe Leu Ala Ile Ala Ala			
488	493	498	503
gtg gct ctg tat gtg tta ccc aac atg cga cag cag gag tca gag ttc			1588
Val Ala Leu Tyr Val Leu Pro Asn Met Arg Gln Gln Glu Ser Glu Phe			

504	509	514	519	
tgc ctc atg gag tga tggcagacct	tggccagcgc	gagggcagat	ccccagtggc	1643
Cys Leu Met Glu *				/
520				
caccacccctc agctttgggc aggacacact	gtgccagaac	cctccccata	tgttccatgt	1703
gtccccatct cctcagcctc agtcacccag	gctgaaaagg	cttgtggga	gcggctgact	1763
tccatctcct gccttgtgta agaacctgag	ttccttgtaa	ttaaatatca	actgaattac	1823
aaaaaaaaaa aa				1835

<210> 201
 <211> 4029
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (316)..(1842)

<400> 201				
gacggcaagt gccaagctaa aattaaccct ccactaaagg	gaataagctt	gcccggacca		60
tcgactcgcc aacgagagaa ggccctgggg	cacggacacc	gacgggttgc	gactgtgacg	120
tgaggtgttc tcgcgcgcgc	tagcgcgcgt	ctccgggtgc	cgctgacggg	180
tgtcggagc cggaggtggg	ggccgaacca	gccaaggttg	cggggccgc	240
gaagacggag ggcggagccg	ggttcggac	tgcggagact	acacaccgag	300
ggcccgaaagg gagcg atg ctg tgg ttc cag ggc	gcc att ccg	gcc gcc atc		351
Met Leu Trp Phe Gln Gly Ala Ile Pro Ala Ala Ile				
1	5	10		
gcg acg gcc aaa agg agc ggc gcg gtc ttc gtg	gtg ttc gca ggt			399
Ala Thr Ala Lys Arg Ser Gly Ala Val Phe Val Val	Phe Val Ala Gly			
13	18	23	28	
gat gat gaa cag tct aca cag atg gct gca agt	tgg gaa gat gat	aaa		447
Asp Asp Glu Gln Ser Thr Gln Met Ala Ala Ser	Trp Glu Asp Asp Lys			
29	34	39	44	
gtt aca gaa gca tct tca aac agt ttt gtt gct	att aaa atc gat acc			495
Val Thr Glu Ala Ser Ser Asn Ser Phe Val Ala Ile	Lys Ile Asp Thr			
45	50	55	60	
aaa agt gaa gcc tgc cta cag ttt tca caa atc tat	cct gta gtg tgt			543
Lys Ser Glu Ala Cys Leu Gln Phe Ser Gln Ile Tyr	Pro Val Val Cys			
61	66	71	76	

gtt cca tcc agt ttc ttt att gga gac agt gga att ccc ttg gaa gta		591
Val Pro Ser Ser Phe Phe Ile Gly Asp Ser Gly Ile Pro Leu Glu Val		
77	82	87
87		92
ata gca gga agt gtt tct gca gat gag ctt gtt aca aga att cac aag		639
Ile Ala Gly Ser Val Ser Ala Asp Glu Leu Val Thr Arg Ile His Lys		
93	98	103
103		108
gtc cga cag atg cat ttg cta aaa agt gaa aca tca gta gca aat ggc		687
Val Arg Gln Met His Leu Leu Lys Ser Glu Thr Ser Val Ala Asn Gly		
109	114	119
119		124
agt cag tca gaa agt tca gtg tct act cca tct gcg tca ttt gaa cct		735
Ser Gln Ser Glu Ser Val Ser Thr Pro Ser Ala Ser Phe Glu Pro		
125	130	135
135		140
aac aac act tgt gaa aac tct cag tcc aga aat gca gag ctt tgt gag		783
Asn Asn Thr Cys Glu Asn Ser Gln Ser Arg Asn Ala Glu Leu Cys Glu		
141	146	151
151		156
ata cca ccc act tct gat aca aag tca gat act gca aca gga gga gaa		831
Ile Pro Pro Thr Ser Asp Thr Lys Ser Asp Thr Ala Thr Gly Gly Glu		
157	162	167
167		172
agt gca ggc cat gcc act tcc tct cag gag cct agt gga tgc tca gat		879
Ser Ala Gly His Ala Thr Ser Ser Gln Glu Pro Ser Gly Cys Ser Asp		
173	178	183
183		188
cag aga cct gca gag gac ctc aac atc cga gtg gaa aga cta aca aaa		927
Gln Arg Pro Ala Glu Asp Leu Asn Ile Arg Val Glu Arg Leu Thr Lys		
189	194	199
199		204
aaa ctt gaa gaa agg aga gaa gag aaa aga aaa gag gaa gaa cag aga		975
Lys Leu Glu Glu Arg Arg Glu Glu Lys Arg Lys Glu Glu Glu Gln Arg		
205	210	215
215		220
gaa att aag aag gaa att gag agg aga aaa act gga aaa gaa atg ttg		1023
Glu Ile Lys Lys Glu Ile Glu Arg Arg Lys Thr Gly Lys Glu Met Leu		
221	226	231
231		236
gat tat aaa aga aaa caa gaa gaa tta aca aaa aga atg ctg gag		1071
Asp Tyr Lys Arg Lys Gln Glu Glu Glu Leu Thr Lys Arg Met Leu Glu		
237	242	247
247		252
gaa aga aac aga gag aaa gca gaa gat agg gca gct cga gaa cgt ata		1119
Glu Arg Asn Arg Glu Lys Ala Glu Asp Arg Ala Ala Arg Glu Arg Ile		
253	258	263
263		268
aaa cag cag att gca ttg gac cgt gca gag aga gct gct cgt ttt gca		1167
Lys Gln Gln Ile Ala Leu Asp Arg Ala Glu Arg Ala Ala Arg Phe Ala		
269	274	279
279		284
aag aca aag gaa gta gag gct gcc aaa gct gct gcc ttg cta gca		1215
Lys Thr Lys Glu Glu Val Glu Ala Ala Lys Ala Ala Leu Leu Ala		
285	290	295
295		300
aaa cag gca gaa atg gaa gtc aag agg gaa tct tat gca aga gaa aga		1263

Lys	Gln	Ala	Glu	Met	Glu	Val	Lys	Arg	Glu	Ser	Tyr	Ala	Arg	Glu	Arg	
301																311
																316
agc	act	gtt	gca	aga	att	caa	tcc	cgt	ctt	cct	gat	ggt	tct	tcc	ttt	1311
Ser	Thr	Val	Ala	Arg	Ile	Gln	Phe	Arg	Leu	Pro	Asp	Gly	Ser	Ser	Phe	
317																322
																327
																332
aca	aat	cag	tcc	cct	tct	gat	gct	cct	cta	gaa	gag	gca	agg	cag	ttt	1359
Thr	Asn	Gln	Phe	Pro	Ser	Asp	Ala	Pro	Leu	Glu	Glu	Ala	Arg	Gln	Phe	
333																338
																343
																348
gct	gca	cag	act	gtt	ggc	aac	act	tac	ggt	aat	ttt	tcg	tta	gca	acc	1407
Ala	Ala	Gln	Thr	Val	Gly	Asn	Thr	Tyr	Gly	Asn	Phe	Ser	Leu	Ala	Thr	
349																354
																359
																364
atg	ttt	ccc	agg	agg	gaa	ttt	acc	aaa	gaa	gat	tat	aaa	aag	aag	tta	1455
Met	Phe	Pro	Arg	Arg	Glu	Phe	Thr	Lys	Glu	Asp	Tyr	Lys	Lys	Lys	Leu	
365																370
																375
																380
ctg	gat	ttg	gaa	ctt	gcc	cca	agc	gct	tcg	gtg	gta	ctg	ttg	cca	gca	1503
Leu	Asp	Leu	Glu	Leu	Ala	Pro	Ser	Ala	Ser	Val	Val	Leu	Leu	Pro	Ala	
381																386
																391
																396
gga	aga	cca	act	gca	tcc	att	gta	cac	tct	tcc	agc	gga	gac	att	tgg	1551
Gly	Arg	Pro	Thr	Ala	Ser	Ile	Val	His	Ser	Ser	Ser	Gly	Asp	Ile	Trp	
397																402
																407
																412
acc	ttg	ttg	gga	aca	gtg	ctt	tat	cca	tcc	ctt	gcc	atc	tgg	aga	tta	1599
Thr	Leu	Leu	Gly	Thr	Val	Leu	Tyr	Pro	Phe	Leu	Ala	Ile	Trp	Arg	Leu	
413																418
																423
																428
att	agc	aat	tcc	ttg	ttt	agt	aat	ccg	cct	ccc	aca	cag	act	tca	gtg	1647
Ile	Ser	Asn	Phe	Leu	Phe	Ser	Asn	Pro	Pro	Pro	Pro	Thr	Gln	Thr	Ser	
429																434
																439
																444
aga	gta	aca	tcg	tca	gaa	ccc	cca	aac	cct	gca	tca	tct	agc	aaa	tca	1695
Arg	Val	Thr	Ser	Ser	Glu	Pro	Pro	Asn	Pro	Ala	Ser	Ser	Ser	Lys	Ser	
445																450
																455
																460
gaa	aaa	agg	gaa	cca	gtg	aga	aaa	aga	gtg	ctg	gaa	aaa	cgt	gga	gac	1743
Glu	Lys	Arg	Glu	Pro	Val	Arg	Lys	Arg	Val	Leu	Glu	Lys	Arg	Gly	Asp	
461																466
																471
																476
gac	ttt	aaa	aag	gag	ggg	aaa	att	tat	aga	tta	agg	act	caa	gat	gat	1791
Asp	Phe	Lys	Lys	Glu	Gly	Lys	Ile	Tyr	Arg	Leu	Arg	Thr	Gln	Asp	Asp	
477																482
																487
																492
ggt	gaa	gat	gaa	aac	aac	act	tgg	aat	gga	aat	tcc	act	caa	cag	atg	1839
Gly	Glu	Asp	Glu	Asn	Asn	Thr	Trp	Asn	Gly	Asn	Ser	Thr	Gln	Gln	Met	
493																498
																503
																508
tag	tgtg	acaagtataa	tatgtgcaat	aatcattgtt	tctcttatga	tttaattcaa										1896
*																
509																
ctaaaattct	actggagaag	tgggactgct	ttatattttc	caactggct	ataaaatgtc											1956

tctttattcc	tgcttagtgg	gtgtgggttg	aagggtttta	actcagaaaa	gaaaagacag	2016
gaaataactc	tctgcttagt	ccttgcttat	atggcaacca	ctgctagaac	cctaaaagaa	2076
ccaaaaatct	gccacagcct	gcctccatca	gcttcttatt	tagtatttca	tatgccatt	2136
agccctatgc	ttcagatgac	acgtttgtt	tagagctact	ttgctccaag	actcttaagc	2196
ccaaagtaac	tggtatgtca	ctgagtaact	tgactcggtg	tcagagcatt	ttaactagcc	2256
actcagatga	gaatttatgt	ttaacttctc	tttttactca	tcagctgcaa	gcaaaatctt	2316
gtagtttta	atcttaaaca	ctgaataaaaa	aaactttccc	ctaaattgga	atgatcttag	2376
tttgctttg	agttttgtta	tctagcatct	ttttgttgca	cagggctcta	ttgaggtcct	2436
atgtctctga	ttttttttt	ccccagtatt	gccctggagc	tgtctctgga	aagtagctgg	2496
cgaggttacc	ttaactatca	ctgaagaaaag	aaattttctg	acacactgat	ggcatgtgac	2556
ttgtctccta	agtcagttag	gcatcacttt	gtttgcataa	agtatacgg	ttgttaaggc	2616
ctttgttctt	gtgagatgca	aaacagctgc	tagtctgcaa	cctagtttc	cctctcacct	2676
ttaactgacg	ttttgtcctc	aataattaca	caaggacqta	gagtacctat	aggacaaaaaa	2736
gtatagaata	aaaatatgcc	tttagtcatt	tggtttttct	taaaaaagttg	agattcttaa	2796
tctgacttac	atgttacttt	atccgtatgt	ctttgttagt	ggagaccgct	aaactaatga	2856
tgtttgaaaa	cagttcctct	gttttagatt	ggaagatagc	actctagagt	ggacatacgg	2916
aaagactgtg	actttatttt	gtaatgggag	gaagaaattt	tctcagagca	aactttctat	2976
tttttacctg	tgaataaca	gtgactttt	aaaatggtga	cagtgttggc	aaggaaacag	3036
caacacaggg	tgcgctgttg	gtaggagtga	aaaccagtat	aattcttctg	aaaaacattt	3096
atcagaaaact	taaaatattt	cataccgttt	gatccagtag	cttcttctaa	atcataaatg	3156
cagacaatgt	ttaggtaaag	acatactcat	taagtgttat	ttatttact	caagaactgg	3216
aaaccaacta	aatgccttct	atagaagtaa	tttttgcata	ggagaaaatgg	tacaatacta	3276
attaacaact	tggtttaaca	tgtttactga	gcatctgtta	agtgttgggg	gaaaaagcag	3336
caggatccag	agctataagg	acagtgtgat	ctcagtttg	caaacacatt	ttctacatag	3396
atagtactag	gtattaatag	atatgtaaag	aaagaaatca	caccattaat	aatggtaaga	3456
ttggtttatg	tgattttagt	ggtatttttg	gcacccttat	atatgttttc	caaactttca	3516
gcagtgatat	tattccata	actaaaaag	tgagttgaa	aaagaaaatc	tccagcaagc	3576
atctcattta	aataaagggtt	tgtcatctt	aaaaatacag	caatatgtga	ctttttaaaa	3636
aagctgtcaa	ataggtgtga	ccctactaat	aattattaga	aatacattta	aaaacatcga	3696

gtacctcaag tcagttgcc ttgaaaaata tcaaataaa ctcttagaga aatgtacata	3756
aaagaatgct tcgtaattt ggagtaggag gttccctcct caatttgtt tttttaaaaa	3816
gtacatggta aaaaaaaaaa ttcacaacag tatataaggc tgtaaaatga gaattctgcc	3876
ccctcaccc ttaccccagt actattctcc agaggtatac tattaacaat ttcttatgtt	3936
atttcaaga aatttgtatg cgtatataag caaatatgtt atctttatTT tttaaataaa	3996
tgggatcata ttatataattc taaaaaaaaaaa aaa	4029

<210> 202
 <211> 914
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (182)..(568)

<400> 202	
cctgctctgt agagccggcg gcaaccgggt agcttgccca ggttgtgagg aaccgcagcg	60
cccgcaggac cgggccccgtg agcctgcagc cgccccgcgc cgtgacctgc gaccctagac	120
cccgactccc tttggctcag cccgcgcgccc ccaggccccgg cccggggcggc gcgacgggag	180
g atg agc ggc ggg cgc gga agg agg agc cgc ctc agc cgc agc tgg	226
Met Ser Gly Gly Arg Arg Arg Ser Arg Arg Leu Ser Arg Ser Trp	
1 5 10	
cca acg ggg ccc tca aag tct ccg tct gga gta agg tgc tgc gga cga	274
Pro Thr Gly Pro Ser Lys Ser Pro Ser Gly Val Arg Cys Cys Gly Arg	
16 21 26 31	
cgc gcc tgg gag gat aag gat gaa ttt tta gat gtg atc tac tgg ttc	322
Arg Ala Trp Glu Asp Lys Asp Glu Phe Leu Asp Val Ile Tyr Trp Phe	
32 37 42 47	
cga cag atc att gct gtg gtc ctg ggt gtc att tgg gga gtt ttg cca	370
Arg Gln Ile Ile Ala Val Val Leu Gly Val Ile Trp Gly Val Leu Pro	
48 53 58 63	
tta cga ggg ttc ttg gga ata gca gga ttc tgc ctg atc aat gca gga	418
Leu Arg Gly Phe Leu Gly Ile Ala Gly Phe Cys Leu Ile Asn Ala Gly	
64 69 74 79	
gtc ctg tac ctc tac ttc agc aat tac cta cag att gat gag gaa gaa	466
Val Leu Tyr Leu Tyr Phe Ser Asn Tyr Leu Gln Ile Asp Glu Glu Glu	
80 85 90 95	
tat ggt ggc acg tgg gag ctc acg aag gaa ggg ttt atg acc tct ttt	514

Tyr Gly Gly Thr Trp Glu Leu Thr Lys Glu Gly Phe Met Thr Ser Phe
 96 101 106 111
 gcc ttg ttc atg gtc att tgg atc atc ttt tac act gcc atc cat tat 562
 Ala Leu Phe Met Val Ile Trp Ile Ile Phe Tyr Thr Ala Ile His Tyr
 112 117 122 127
 gac tga tgggttacag ctcccaagtg ctccctatcc agtccaaagg accctttga 618
 Asp *
 128
 ttacagcaca ggaacttgat cgttgggaa ccccagcccc ttggacttg gaagaccggt 678
 gtttccttggaa ccgcgaatca gtgtgttggg catcagtgtt ttcttgcagg gttgtgacct 738
 gaaaacttttt aaaaacccccc cccctttggg gaagcatttt tgaatttatac catccccaaac 798
 catttttttt tggataccat caagtaaacag ctattatgg ccaagtggag ctgtcattta 858
 attttagtgc cctctggatt cagatgaaac attaaattgt tttcctcgat tttcaa 914

 <210> 203
 <211> 1131
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> CDS
 <222> (93)..(1082)

 <400> 203
 tttgaacgcc ttgaggtacc ggtccggaat tcccggtcg acccacgcgt ccggaaagct 60
 tggttacaac ccgggacacc cggagcttca gg atg gtt cgt act aag aca tgg 113
 Met Val Arg Thr Lys Thr Trp
 1 5

 acc ctg aag aag cac ttt gtt ggc tat cct act aat agt gac ttt gag 161
 Thr Leu Lys Lys His Phe Val Gly Tyr Pro Thr Asn Ser Asp Phe Glu
 8 13 18 23

 ttg aag aca gct gag ctc cca ccc tta aaa aat gga gag gtc ctg ctt 209
 Leu Lys Thr Ala Glu Leu Pro Pro Leu Lys Asn Gly Glu Val Leu Leu
 24 29 34 39

 gaa gct ttg ttc ctc acc gtg gat ccc tac atg aga gtg gca gcc aaa 257
 Glu Ala Leu Phe Leu Thr Val Asp Pro Tyr Met Arg Val Ala Ala Lys
 40 45 50 55

 aga ttg aag gaa ggt gat aca atg atg ggg cag caa gtg gcc aaa gtt 305
 Arg Leu Lys Glu Gly Asp Thr Met Met Gly Gln Gln Val Ala Lys Val
 56 61 66 71

 gtg gaa agt aaa aat gta gcc cta cca aaa gga act att gta ctg gct 353

Val	Glu	Ser	Lys	Asn	Val	Ala	Leu	Pro	Lys	Gly	Thr	Ile	Val	Leu	Ala	
72					77				82				87			
tct	cca	ggc	tgg	aca	acg	cac	tcc	att	tct	,gat	ggg	aaa	gat	ctg	gaa	401
Ser	Pro	Gly	Trp	Thr	Thr	His	Ser	Ile	Ser	Asp	Gly	Lys	Asp	Leu	Glu	
88														98	103	
aag	ctg	ctg	aca	gag	tgg	cca	gac	aca	ata	cca	ctg	tct	ttg	gct	ctg	449
Lys	Leu	Leu	Thr	Glu	Trp	Pro	Asp	Thr	Ile	Pro	Leu	Ser	Leu	Ala	Leu	
104														114	119	
ggg	aca	gtt	ggc	atg	cca	ggc	ctg	act	gcc	tac	ttt	ggc	cta	ctt	gaa	497
Gly	Thr	Val	Gly	Met	Pro	Gly	Leu	Thr	Ala	Tyr	Phe	Gly	Leu	Leu	Glu	
120														130	135	
atc	tgt	gtt	gtg	aag	ggt	gga	gaa	aca	gtg	atg	gtt	aat	gca	gca	gct	545
Ile	Cys	Gly	Val	Lys	Gly	Gly	Glu	Thr	Val	Met	Val	Asn	Ala	Ala	Ala	
136														146	151	
gga	gct	gtg	ggc	tca	gtc	gtg	ggg	cag	att	gca	aag	ctc	aag	ggc	tgc	593
Gly	Ala	Val	Gly	Ser	Val	Val	Gly	Gln	Ile	Ala	Lys	Leu	Lys	Gly	Cys	
152														157	162	167
aaa	gtt	gtt	gga	gca	gta	ggg	tct	gat	gaa	aag	gtt	gcc	tac	ctt	caa	641
Lys	Val	Val	Gly	Ala	Val	Gly	Ser	Asp	Glu	Lys	Val	Ala	Tyr	Leu	Gln	
168														173	178	183
aag	ctt	gga	ttt	gat	gtc	gtc	ttt	aac	tac	aag	acg	gta	gag	tct	ttg	689
Lys	Leu	Gly	Phe	Asp	Val	Val	Phe	Asn	Tyr	Lys	Thr	Val	Glu	Ser	Leu	
184														189	194	199
gaa	gaa	acc	ttg	aag	aaa	gcg	tct	cct	gat	ggt	tat	gat	tgt	tat	ttt	737
Glu	Glu	Thr	Leu	Lys	Lys	Ala	Ser	Pro	Asp	Gly	Tyr	Asp	Cys	Tyr	Phe	
200														205	210	215
gat	aat	gta	ggt	gga	gag	ttt	tca	aac	act	gtt	atc	ggc	cag	atg	aag	785
Asp	Asn	Val	Gly	Gly	Glu	Phe	Ser	Asn	Thr	Val	Ile	Gly	Gln	Met	Lys	
216														221	226	231
aaa	ttt	gga	agg	att	gcc	ata	tgt	gga	gcc	atc	tct	aca	tat	aac	aga	833
Lys	Phe	Gly	Arg	Ile	Ala	Ile	Cys	Gly	Ala	Ile	Ser	Thr	Tyr	Asn	Arg	
232														237	242	247
acc	ggc	cca	ctt	ccc	cca	ggc	cca	ccc	cca	gag	att	gtt	atc	tat	cag	881
Thr	Gly	Pro	Leu	Pro	Pro	Gly	Pro	Pro	Pro	Glu	Ile	Val	Ile	Tyr	Gln	
248														253	258	263
gag	ctt	cgc	atg	gaa	gct	ttt	gtc	gtc	tac	cgc	tgg	caa	gga	gat	gcc	929
Glu	Leu	Arg	Met	Glu	Ala	Phe	Val	Val	Tyr	Arg	Trp	Gln	Gly	Asp	Ala	
264														269	274	279
cgc	caa	aaa	gct	ctg	aag	gac	ttg	ctg	aaa	tgg	gtc	tta	gag	ggt	aaa	977
Arg	Gln	Lys	Ala	Leu	Lys	Asp	Leu	Leu	Lys	Trp	Val	Leu	Glu	Gly	Lys	
280														285	290	295
atc	cag	tac	aag	gaa	tat	atc	att	gaa	gga	ttt	gaa	aac	atg	cca	gct	1025
Ile	Gln	Tyr	Lys	Glu	Tyr	Ile	Ile	Glu	Gly	Phe	Glu	Asn	Met	Pro	Ala	

296	301	306	311	
gca ttt atg gga atg ctg aaa gga gat aat ttg ggg aag aca ata gtg Ala Phe Met Gly Met Leu Lys Gly Asp Asn Leu Gly Lys Thr Ile Val				1073
312	317	322	327	
aaa gca tga aaaagag gacacatgga atctggaggc catttagatg attagttaat Lys Ala *				1129
328				
tg				1131
<210> 204 <211> 1854 <212> DNA <213> Homo sapiens				
<220> <221> CDS <222> (142)..(1758)				
<400> 204 tcatccaggc ttccgcaggc cagtctccgg cagcttctcg cggcttcgca agccccttcc 60				
cgtgatgccc cgccgcctggc tgtcgcgggtt gccgggcaac gcgctgtcca tgtcgcgggc 120				
ctcgctggga ctccctggga g atg agg ccg cga ggt ctc ccg ccg ctc ctg 171 Met Arg Pro Arg Gly Leu Pro Pro Leu Leu ' 1 5				
gtg gtg ctc ctg ggc tgc tgg gcc tcc gtg agc gcc cag acc gat gcc 219 Val Val Leu Leu Gly Cys Trp Ala Ser Val Ala Gln Thr Asp Ala 11 16 21 26				
acc ccg gcg gtg acg aca gag ggc ctc aac tcc acc gag gca gcc ctg 267 Thr Pro Ala Val Thr Glu Gly Leu Asn Ser Thr Glu Ala Ala Leu 27 32 37 42				
gcc acc ttc gga act ttc ccg tcg acc agg ccc ccc ggg act ccc agg 315 Ala Thr Phe Gly Thr Phe Pro Ser Thr Arg Pro Pro Gly Thr Pro Arg 43 48 53 58				
gct cca ggg ccc tcc tcc ggc ccc agg cct acc cca gtc acg gac gtt 363 Ala Pro Gly Pro Ser Ser Gly Pro Arg Pro Thr Pro Val Thr Asp Val 59 64 69 74				
gct gtt ctc tgt gtc tgt gac tta tcc cca gca cag tgt gac atc aac 411 Ala Val Leu Cys Val Cys Asp Leu Ser Pro Ala Gln Cys Asp Ile Asn 75 80 85 90				
tgc tgc tgt gat ccc gac tgc agc tcc gtg gat ttc agt gtc ttt tct 459 Cys Cys Cys Asp Pro Asp Cys Ser Ser Val Asp Phe Ser Val Phe Ser 91 96 101 106				

gcc tgc tca gtt cca gtt gtc acg ggc gac agc cag ttt tgt agt caa Ala Cys Ser Val Pro Val Val Thr Gly Asp Ser Gln Phe Cys Ser Gln	507
107 112 117 122	
 aaa gca gtc atc tat tca ttg aat ttt aca gca aac cca cct caa aga Lys Ala Val Ile Tyr Ser Leu Asn Phe Thr Ala Asn Pro Pro Gln Arg	555
123 128 133 138	
 gta ttt gaa ctt gtt gac cag att aat cca tct att ttc tgc att cat Val Phe Glu Leu Val Asp Gln Ile Asn Pro Ser Ile Phe Cys Ile His	603
139 144 149 154	
 att aca aac tat aaa cct gca tta tcc ttt att aat cca gaa gta cct Ile Thr Asn Tyr Lys Pro Ala Leu Ser Phe Ile Asn Pro Glu Val Pro	651
155 160 165 170	
 gat gaa aac aat ttt gat aca ttg atg aaa aca tct gat ggt ttt aca Asp Glu Asn Asn Phe Asp Thr Leu Met Lys Thr Ser Asp Gly Phe Thr	699
171 176 181 186	
 ttg aat gct gaa tca tat gtt tcc ttc aca acc aaa ctg gat att cct Leu Asn Ala Glu Ser Tyr Val Ser Phe Thr Thr Lys Leu Asp Ile Pro	747
187 192 197 202	
 act gct gct aaa tat gag tat ggg gtt cct ctg cag act tca gat tcg Thr Ala Ala Lys Tyr Glu Tyr Gly Val Pro Leu Gln Thr Ser Asp Ser	795
203 208 213 218	
 ttt ctg aga ttt cct tcg tcc ctg aca tca tct ctg tgc act gat aat Phe Leu Arg Phe Pro Ser Ser Leu Thr Ser Ser Leu Cys Thr Asp Asn	843
219 224 229 234	
 aac cct gca gcg ttt ctg gtg aac cag gct gtt aag tgc acc aga aaa Asn Pro Ala Ala Phe Leu Val Asn Gln Ala Val Lys Cys Thr Arg Lys	891
235 240 245 250	
 ata aat tta gaa cag tgt gaa gaa att gaa gcc ctc agc atg gct ttt Ile Asn Leu Glu Gln Cys Glu Glu Ile Glu Ala Leu Ser Met Ala Phe	939
251 256 261 266	
 tac agc agc ccg gaa att ctg agg gta cct gat tca aga aaa aag gtc Tyr Ser Ser Pro Glu Ile Leu Arg Val Pro Asp Ser Arg Lys Lys Val	987
267 272 277 282	
 cct atc act gtt cag tcc atc gtc att cag tct cta aat aaa acg ctc Pro Ile Thr Val Gln Ser Ile Val Ile Gln Ser Leu Asn Lys Thr Leu	1035
283 288 293 298	
 acc cga cgg gag gac act gat gtg ctg cag ccg act ctc gtc aac gct Thr Arg Arg Glu Asp Thr Asp Val Leu Gln Pro Thr Leu Val Asn Ala	1083
299 304 309 314	
 gga cac ttt agc ctt tgc gtg aat gtt gtt ctt gag gta aag tac agc Gly His Phe Ser Leu Cys Val Asn Val Val Leu Glu Val Lys Tyr Ser	1131
315 320 325 330	
 ctc aca tac aca gat gca ggt gaa gtc acc aaa gct gat ctc tca ttc	1179

Leu Thr Tyr Thr Asp Ala Gly Glu Val Thr Lys Ala Asp Leu Ser Phe			
331	336	341	346
gtt ctg ggg aca gtt agc agc gta gtg gtc cca ctg cag caa aag ttt			1227
Val Leu Gly Thr Val Ser Ser Val Val Val Pro Leu Gln Gln Lys Phe			
347	352	357	362
gaa att cat ttt ctt cag gaa aat acc cag cca gtc cct ctc agt gga			1275
Glu Ile His Phe Leu Gln Glu Asn Thr Gln Pro Val Pro Leu Ser Gly			
363	368	373	378
aac cct ggt tat gtc gtg ggg ctc cca tta gct gct gga ttc cag cct			1323
Asn Pro Gly Tyr Val Val Gly Leu Pro Leu Ala Ala Gly Phe Gln Pro			
379	384	389	394
cat aag ggt gga gct ctc ccg tgt cag ctc gta gca cag aag gtg aag			1371
His Lys Gly Gly Ala Leu Pro Cys Gln Leu Val Ala Gln Lys Val Lys			
395	400	405	410
agc ctg ctg tgg ggc cag ggc ttc cca gat tac gtg gcc cct ttt gga			1419
Ser Leu Leu Trp Gly Gln Gly Phe Pro Asp Tyr Val Ala Pro Phe Gly			
411	416	421	426
aat tcc cag gcc cag gac atg ctg gac tgg gtg ccc atc cac ttc atc			1467
Asn Ser Gln Ala Gln Asp Met Leu Asp Trp Val Pro Ile His Phe Ile			
427	432	437	442
acc cag tca ttc aac agg aag gat tcc tgc cag ctc cca ggg gct ttg			1515
Thr Gln Ser Phe Asn Arg Lys Asp Ser Cys Gln Leu Pro Gly Ala Leu			
443	448	453	458
gtt ata gaa gtg aag tgg act aaa tac gga tcc ctg ctg aat cca cag			1563
Val Ile Glu Val Lys Trp Thr Lys Tyr Gly Ser Leu Leu Asn Pro Gln			
459	464	469	474
gcc aaa ata gtc aat gta act gca aat cta att tca tcc tcc ttt cct			1611
Ala Lys Ile Val Asn Val Thr Ala Asn Leu Ile Ser Ser Ser Phe Pro			
475	480	485	490
gag gcc aac tca gga aat gaa agg acg att ctt att tcc act gcg gtt			1659
Glu Ala Asn Ser Gly Asn Glu Arg Thr Ile Leu Ile Ser Thr Ala Val			
491	496	501	506
act ttt gtg gat gtg tct gca cct gca gag gca ggc ttc aga gct cca			1707
Thr Phe Val Asp Val Ser Ala Pro Ala Glu Ala Gly Phe Arg Ala Pro			
507	512	517	522
cca gcc atc aat gcc agg ctg ccc ttt aac ttc ttc ttc ccg ttt gtt			1755
Pro Ala Ile Asn Ala Arg Leu Pro Phe Asn Phe Phe Pro Phe Val			
523	528	533	538
tga caat gctcagatgc atcagttcct taatatacac gtgaaaatttg aaaactgtac			1812
*			
539			
attcggtagatc attaaatttt atatacaact aaaaaaaaaaa aa			1854

<210> 205
<211> 2785
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (402)..(2282)

<400> 205
caaggtagtgcgg cgggttagtgt actcattcga aggagaatac ccccaattca ctagacgagc 60
ccctaattgg gggtaggtgcggcc tctttctcc cccttccac cagcactgcc 120
ctcagttctg cttctagcca cgcccttcg cgttcacgtc cagcgccctg gcgggattga 180
tttgaggacg actggactgc cattgcgcct gcgcaggag cccaggcaa gagccgctag 240
gctgcctgc ccgaagggtc caactgtcag tgagcctgcg caggaggcca ataggctgcc 300
aataactcctt ggactccccg ccagggccct gctgtcagtgc cgccctgcgcg cgggtccggc 360
gccgagggttc ttgactgctg tgccggacgc caggtgtagc c atg cag cga gcc 413
Met Gln Arg Ala
1
gat tcc gag cag ccc tcc aag cgt ccc cgt tgc gat gac agc ccg aga 461
Asp Ser Glu Gln Pro Ser Lys Arg Pro Arg Cys Asp Asp Ser Pro Arg
5 10 15 20
acc ccc tca aac acc cct tcc gca gag gca gac tgg tcc ccg ggc ctg 509
Thr Pro Ser Asn Thr Pro Ser Ala Glu Ala Asp Trp Ser Pro Gly Leu
21 26 31 36
gaa ctc cat ccc gac tac aag aca tgg ggt ccg gag cag gtg tgc tcc 557
Glu Leu His Pro Asp Tyr Lys Thr Trp Gly Pro Glu Gln Val Cys Ser
37 42 47 52
ttc ctc agg cgc ggt ggc ttt gaa gag ccg gtg ctg ctg aag aac atc 605
Phe Leu Arg Arg Gly Gly Phe Glu Glu Pro Val Leu Leu Lys Asn Ile
53 58 63 68
cga gaa aat gaa atc aca ggc gca tta ctg cct tgt ctt gat gag tct 653
Arg Glu Asn Glu Ile Thr Gly Ala Leu Leu Pro Cys Leu Asp Glu Ser
69 74 79 84
cgt ttt gaa aat ctt gga gta agt tcc ttg ggg gag agg aag aag ctg 701
Arg Phe Glu Asn Leu Gly Val Ser Ser Leu Gly Glu Arg Lys Lys Leu
85 90 95 100
ctt agt tat atc cag cga ttg gtt caa atc cac gtt gat aca atg aag 749
Leu Ser Tyr Ile Gln Arg Leu Val Gln Ile His Val Asp Thr Met Lys
101 106 111 116

gta att aat gat cct atc cat ggc cac att gag ctc cac cct ctc ctc			797
Val Ile Asn Asp Pro Ile His Gly His Ile Glu Leu His Pro Leu Leu			
117	122	127	132
gtc cga atc att gat aca cct caa ttt caa cgt ctt cga tac atc aaa			845
Val Arg Ile Ile Asp Thr Pro Gln Phe Gln Arg Leu Arg Tyr Ile Lys			
133	138	143	148
cag ctg gga ggt ggt tac tat gtt ttt cca gga gct tca cac aat cga			893
Gln Leu Gly Gly Tyr Tyr Val Phe Pro Gly Ala Ser His Asn Arg			
149	154	159	164
ttt gag cat agt cta ggg gtg ggg tat cta gca gga tgt cta gtt cac			941
Phe Glu His Ser Leu Gly Val Gly Tyr Leu Ala Gly Cys Leu Val His			
165	170	175	180
gca ctg ggt gaa aaa caa cca gag ctg cag ata agt gaa cga gat gtt			989
Ala Leu Gly Glu Lys Gln Pro Glu Leu Gln Ile Ser Glu Arg Asp Val			
181	186	191	196
ctc tgt gtt cag att gct gga ctt tgt cat gat ctc ggt cat ggg cca			1037
Leu Cys Val Gln Ile Ala Gly Leu Cys His Asp Leu Gly His Gly Pro			
197	202	207	212
ttt tct cac atg ttt gat gga cga ttt att cca ctt gct cgc ccg gag			1085
Phe Ser His Met Phe Asp Gly Arg Phe Ile Pro Leu Ala Arg Pro Glu			
213	218	223	228
gtg aaa tgg acg cat gaa caa ggc tca gtt atg atg ttt gag cac ctt			1133
Val Lys Trp Thr His Glu Gln Gly Ser Val Met Met Phe Glu His Leu			
229	234	239	244
att aat tct aat gga att aag cct gtc atg gaa caa tat ggt ctc atc			1181
Ile Asn Ser Asn Gly Ile Lys Pro Val Met Glu Gln Tyr Gly Leu Ile			
245	250	255	260
cct gaa gaa gat att tgc ttt ata aag gaa caa att gta gga cca ctt			1229
Pro Glu Glu Asp Ile Cys Phe Ile Lys Glu Gln Ile Val Gly Pro Leu			
261	266	271	276
gaa tca cct gtc gaa gat tca ttg tgg cca tat aaa ggg cgt cct gaa			1277
Glu Ser Pro Val Glu Asp Ser Leu Trp Pro Tyr Lys Gly Arg Pro Glu			
277	282	287	292
aac aaa agc ttc ctt tat gag ata gta tct aat aaa aga aat ggc att			1325
Asn Lys Ser Phe Leu Tyr Glu Ile Val Ser Asn Lys Arg Asn Gly Ile			
293	298	303	308
gat gtg gac aaa tgg gat tat ttt gcc agg gac tgc cat cat ctt gga			1373
Asp Val Asp Lys Trp Asp Tyr Phe Ala Arg Asp Cys His His Leu Gly			
309	314	319	324
atc caa aat aat ttt gat tac aag cgc ttt att aag ttt gcc cgt gtc			1421
Ile Gln Asn Asn Phe Asp Tyr Lys Arg Phe Ile Lys Phe Ala Arg Val			
325	330	335	340
tgt gaa gta gac aat gag ttg cgt att tgt gct aga gat aag gaa gtt			1469

Cys Glu Val Asp Asn Glu Leu Arg Ile Cys Ala Arg Asp Lys Glu Val			
341	346	351	356
gga aat ctg tat gac atg ttc cac act cgc aac tct tta cac cgt aga			1517
Gly Asn Leu Tyr Asp Met Phe His Thr Arg Asn Ser Leu His Arg Arg			
357	362	367	372
gct tat caa cac aaa gtt ggc aac att att gat aca atg att aca gat			1565
Ala Tyr Gln His Lys Val Gly Asn Ile Ile Asp Thr Met Ile Thr Asp			
373	378	383	388
gct ttc ctc aaa gca gat gac tac ata gag att aca ggt gct gga gga			1613
Ala Phe Leu Lys Ala Asp Asp Tyr Ile Glu Ile Thr Gly Ala Gly Gly			
389	394	399	404
aaa aag tat cgc att tct aca gca att gac gac atg gaa gcc tat act			1661
Lys Lys Tyr Arg Ile Ser Thr Ala Ile Asp Asp Met Glu Ala Tyr Thr			
405	410	415	420
aag ctg aca gat aac att ttt ctg gag att tta tac tct act gat ccc			1709
Lys Leu Thr Asp Asn Ile Phe Leu Glu Ile Leu Tyr Ser Thr Asp Pro			
421	426	431	436
aaa ttg aaa gac gca cga gag att tta aaa caa att gaa tac cgt aat			1757
Lys Leu Lys Asp Ala Arg Glu Ile Leu Lys Gln Ile Glu Tyr Arg Asn			
437	442	447	452
cta ttc aag tat gtg ggt gag acg cag cca aca gga caa ata aag att			1805
Leu Phe Lys Tyr Val Gly Glu Thr Gln Pro Thr Gly Gln Ile Lys Ile			
453	458	463	468
aaa agg gag gac tat gaa tct ctt cca aaa gag gtt gcc agt gct aaa			1853
Lys Arg Glu Asp Tyr Glu Ser Leu Pro Lys Glu Val Ala Ser Ala Lys			
469	474	479	484
ccc aaa gta ttg cta gac gtg aaa ctg aag gct gaa gat ttt ata gtg			1901
Pro Lys Val Leu Leu Asp Val Lys Leu Lys Ala Glu Asp Phe Ile Val			
485	490	495	500
gat gtt atc aac atg gat tat gga atg caa gaa aag aat cca att gat			1949
Asp Val Ile Asn Met Asp Tyr Gly Met Gln Glu Lys Asn Pro Ile Asp			
501	506	511	516
cat gtt agc ttc tat tgt aag act gcc ccc aac aga gca atc agg att			1997
His Val Ser Phe Tyr Cys Lys Thr Ala Pro Asn Arg Ala Ile Arg Ile			
517	522	527	532
act aaa aac cag gtt tca caa ctt ctg cca gag aaa ttt gca gag cag			2045
Thr Lys Asn Gln Val Ser Gln Leu Leu Pro Glu Lys Phe Ala Glu Gln			
533	538	543	548
ctg att cga gta tat tgt aag aag gtg gac aga aag agt ttg tat gcc			2093
Leu Ile Arg Val Tyr Cys Lys Val Asp Arg Lys Ser Leu Tyr Ala			
549	554	559	564
gca aga caa tat ttt gtt cag tgg tgt gca gac aga aat ttc acc aag			2141
Ala Arg Gln Tyr Phe Val Gln Trp Cys Ala Asp Arg Asn Phe Thr Lys			

tccactttaa tacattcatg ctcctgagc ctgtggaaat tcaagaggaa cagaaccaga	300
aataattgaa ccataactgc ctttggcat, cttgcctctt ctgggaggct taatttctta	360
caaatatgtg gctctgcttt tcaaatacttta gtttgatgat tttctcttct tcnttttca	420
ggtttcccc ccacgacctg accgtgtcg tatagtgacg ggagggacag atggcattgg	480
ctattctaca gccaagcattc tggcgagact tggcatgcat gttatcatag ctggaaataa	540
tgacagcaaa gccaaacaag ttgtaagcaa aataaaagaa gaaaccttga acgacaaaga	600
gacgtgagtc ttgctgtgtt gcccgggctg gctttgcctc tgaaactcaa gcgatcctcc	660
cacccatcgcc tctcgaggag ctggactac aggcgtgcac catcattcc tcctaaaatt	720
tggaattttt atactgtgac ttggcttcc atg act tcc atc cgg cag ttt gtg Met Thr Ser Ile Arg Gln Phe Val	773
1 5	

cag-aag-ttc-aag-atg aag aag-att-cct=ctc-cat-gtc ctg atc-aac-aat	821
Gln Lys Phe Lys Met Lys Lys Ile Pro Leu His Val Leu Ile Asn Asn	
9 14 19 24	
gct ggg gtg atg atg gtc cct cag agg aaa acc aga gat gga ttc gaa	869
Ala Gly Val Met Met Val Pro Gln Arg Lys Thr Arg Asp Gly Phe Glu	
25 30 35 40	
gaa cat ttc ggc ctg aac tac cta ggg cac ttc ctg ctg acc aac ctt	917
Glu His Phe Gly Leu Asn Tyr Leu Gly His Phe Leu Leu Thr Asn Leu	
41 46 51 56	
ctc ttg gat acg ctg aaa gag tct ggg tcc cct ggc cac agt gcg agg	965
Leu Leu Asp Thr Leu Lys Glu Ser Gly Ser Pro Gly His Ser Ala Arg	
57 62 67 72	
gtg gtc acc gtc tcc tct gcc acc cat tac gtc gct gag ctg aac atg	1013
Val Val Thr Val Ser Ser Ala Thr His Tyr Val Ala Glu Leu Asn Met	
73 78 83 88	
gat gac ctt cag agc agt gcc tgc tac tca ccc cac gca gcc tac gcc	1061
Asp Asp Leu Gln Ser Ser Ala Cys Tyr Ser Pro His Ala Ala Tyr Ala	
89 94 99 104	
cag agc aag ctg gcc ctt gtc ctg ttc acc tac cac ctc cag cgg ctg	1109
Gln Ser Lys Leu Ala Leu Val Leu Phe Thr Tyr His Leu Gln Arg Leu	
105 110 115 120	
ctg gcg gct gag gga agc cac gtg acc gcc aac gtg gtg gac ccc ggg	1157
Leu Ala Ala Glu Gly Ser His Val Thr Ala Asn Val Val Asp Pro Gly	
121 126 131 136	
gtg gtc aac acg gac gtc tac aag cac gtg ttc tgg gcc acc cgt ctg	1205
Val Val Asn Thr Asp Val Tyr Lys His Val Phe Trp Ala Thr Arg Leu	
137 142 147 152	

g _c g a _a g a _a g c _t t c _t c g _g c t _g g t _t g c _t t t _t c a _a g a _c c c _{cc} c g _a t g _a a g _g a Ala Lys Lys Leu Leu Gly Trp Leu Leu Phe Lys Thr Pro Asp Glu Gly 153 158 163 168	1253
g _c g t _g g a _c t t _c c a _t c t _a c g _c a g _c a g _t c a _c c c _{ca} a g _a g c _t g g _a a g _g a g _t t Ala Trp Thr Ser Ile Tyr Ala Ala Val Thr Pro Glu Leu Glu Gly Val 169 174 179 184	1301
g _g t g _g c c _a t t _a c c _t a t _a c a _a c a _a g a _a a g _a g a _c c a _a g t _c c c _t c c _a c g _t c Gly Gly His Tyr Leu Tyr Asn Lys Lys Glu Thr Lys Ser Leu His Val 185 190 195 200	1349
a _c c t _a c a _a c c _a g a _a a c _t g c _a g c _a g c _t g t _g g t _c t a _a g a _{gt} t _g t g _a g Thr Tyr Asn Gln Lys Leu Gln Gln Leu Trp Ser Lys Ser Cys Glu 201 206 211 216	1397
a _t g a _c t g _g g g _t c c _t t g _a t g _t g a _c c c _t g t _g a t atcctgtctc aggatacgctg Met Thr Gly Val Asp Val Thr Leu * 217 222	1448
ctgccccaaag aaacacattt cacctgccaa tagcttgtgg gtctgtgaag actgcggtgt tttagttctt cacacccacc tgcccacagg gctctgtctt ctattttga gacagctgcc tcaacctctg cagaacttca agaagccaaa taaacatttt ggaggataat caccctaagt ggtcttcaac cataaacttt gttgattccaa agtgcccagt tgtcacaggt gccataaata attacatttt ccaacataaa tttttttttt tccttgcgc gttataataaa ctgagttacaa aagttccaag agagatgctc tcttttcagg ggctgcaatg tcctctctga gacctagtgg tggatgaggt ctcctgtttt atttttttcc ttgcactcaact catttttcca gagacccagc tgtgattcac aggtgtcaga catggggagg tgtgagcctt gcttgctaca gcctgttagga ttagtttgc acgtttttttt gttttttttt ttccatgtttttaaacccatcaatg gttttttttt aagtgaagca tgccactgtc aaatccgaga atgtaaaccg ctgaacagct atggatcaaa tggtagccct caaaagatat gttcatgccc taaccctcag aacctataaa tattacttta tttggaaaag aatcttttgc gatagaatta agaattttga gatgggtcat tatggatcat cccagtgaac ctaatgccat tcacgagggt tcttatncag aggacaggtt gaggggagat ttggagtaca gaaggacaag atatncgtg tggatggtgg cagacagaga ngggagttga tggccaccac aggccaggca tg	1508 1568 1628 1688 1748 1808 1868 1928 1988 2048 2108 2168 2228 2288 2310

<210> 207
 <211> 1341
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1145)

<400> 207

gcacgagggc	gcgcttaggc	aggcggtggc	gcggctggag	tgccgcgggg	aggctgtgc	60	
cggttgc	ttt ctgcagccgc	atctcggcca	gcttcctcg	ccgtccccgg	ggcgctgtgc	120	
gtctccagtc	cgggaccgaa	gccgcctgcc	gtagcggcg	gccagatccg	cgtccgcct	180	
cagcggccgg	aggacatgcg	ggagagaga	atg agc cag agg gac acg ctg gtg			233	
			Met Ser Gln Arg Asp Thr Leu Val				
			1	5			
cat ctg ttt	gcc gga	tgt ggt	ggt aca	gtg gga	gct att	ctg aca	281
His Leu	Phe Ala	Gly Gly	Cys Gly	Gly Thr	Val Gly	Ala Ile Leu Thr	
9	14		19		24		
tgt cca	ctg gaa	gtt gta	aaa aca	cga ctg	cag tca	tct tct	329
Cys Pro	Leu Glu	Val Val	Lys Thr	Arg Leu	Gln Ser	Ser Ser Val	
25	30		35		40		
ctt tat att	tct gaa	gtt cag	ctg aac	acc atg	gct gga	gcc agt gtc	377
Leu Tyr	Ile Ser	Glu Val	Gln Leu	Asn Thr	Met Ala	Gly Ala Ser Val	
41	46		51		56		
aac cga	gta gtg	tct ccc	gga cct	ctt cat	tgc cta	aag gtg atc ttg	425
Asn Arg	Val Val	Ser Pro	Gly Pro	Leu His	Cys Leu	Lys Val Ile Leu	
57	62		67		72		
gaa aaa	gaa ggg	cct cgt	tcc ttg	ttt aga	gga cta	ggc ccc aat tta	473
Glu Lys	Glu Gly	Pro Arg	Ser Leu	Phe Arg	Gly Leu	Gly Pro Asn Leu	
73	78		83		88		
gtg ggg	gta gcc	cct tcc	aga gca	ata tac	ttt gct	gct tat tca aac	521
Val Gly	Val Ala	Pro Ser	Arg Ala	Ile Tyr	Phe Ala	Ala Tyr Ser Asn	
89	94		99		104		
tgc aag	gaa aag	ttg aat	gat gta	ttt gat	cct gat	tct acc caa gta	569
Cys Lys	Glu Lys	Leu Asn	Asp Val	Phe Asp	Pro Asp	Ser Thr Gln Val	
105	110		115		120		
cat atg	att tca	gct gca	atg gca	ggt ttt	act gca	atc aca gca acc	617
His Met	Ile Ser	Ala Ala	Met Ala	Gly Phe	Thr Ala	Ile Thr Ala Thr	
121	126		131		136		
aac ccc	att tgg	ctt ata	aag act	cgg tta	cag ctt	gat gca agg aac	665
Asn Pro	Ile Trp	Leu Ile	Lys Thr	Arg Leu	Gln Leu	Asp Ala Arg Asn	
137	142		147		152		
cgc ggg	gaa agg	cga atg	ggt gct	ttt gaa	tgt cgt	aaa gtg tat	713
Arg Gly	Glu Arg	Arg Met	Gly Ala	Phe Glu	Cys Val	Arg Lys Val Tyr	
153	158		163		168		
cag aca	gat gga	cta aaa	gga ttt	tat agg	ggc atg	tct gct tca tat	761

Gln	Thr	Asp	Gly	Leu	Lys	Gly	Phe	Tyr	Arg	Gly	Met	Ser	Ala	Ser	Tyr	
169																184
gct ggt ata tcà gag act gtt atc cat ttt gtt att tat gaa agt ata															809	
Ala	Gly	Ile	Ser	Glu	Thr	Val	Ile	His	Phe	Val	Ile	Tyr	Glu	Ser	Ile	
185																200
aaa caa aaa cta ctg gaa tat aag act gct tct aca atg gaa aat gat															857	
Lys	Gln	Lys	Leu	Leu	Glu	Tyr	Lys	Thr	Ala	Ser	Thr	Met	Glu	Asn	Asp	
201																216
gaa gag tct gtg aaa gaa gca tca gat ttt gtg gga atg atg cta gct															905	
Glu	Glu	Ser	Val	Lys	Glu	Ala	Ser	Asp	Phe	Val	Gly	Met	Met	Leu	Ala	
217																232
gct gcc acc tca aaa act tgt gcc aca act ata gca tat cca cat gaa															953	
Ala	Ala	Thr	Ser	Lys	Thr	Cys	Ala	Thr	Thr	Ile	Ala	Tyr	Pro	His	Glu	
233																248
gtt gta aga aca aga cta cgt gaa gag gga aca aaa tac aga tct ttt															1001	
Val	Val	Arg	Thr	Arg	Leu	Arg	Glu	Glu	Gly	Thr	Lys	Tyr	Arg	Ser	Phe	
249																264
ttt cag act cta tct ttg ctt gtt caa gaa gaa ggt tat ggg tct ctt															1049	
Phe	Gln	Thr	Leu	Ser	Leu	Leu	Val	Gln	Glu	Glu	Gly	Tyr	Gly	Ser	Leu	
265																280
tat cgt ggt ctg aca act cat cta gtg aga cag att cca aac aca gcc															1097	
Tyr	Arg	Gly	Leu	Thr	His	Leu	Val	Arg	Gln	Ile	Pro	Asn	Thr	Ala		
281																296
att atg atg gcc acc tat gaa ttg gtg gtt tac cta ctc aat gga tag															1145	
Ile	Met	Met	Ala	Thr	Tyr	Glu	Leu	Val	Val	Tyr	Leu	Leu	Asn	Gly	*	
297																312
cagcacgagg actgctgtac tgcaaaaaaa gaagacaaa agattacagt ggaccatgg															1205	
atacagaagc cagcatggca gacagaagaa aaatagttt ggaacatgta actattctaa															1265	
gtggaagttt tggtagga attatagtaa tcacaccaca ttacttgcc tttcggtaat															1325	
gtgaaaaaaaa aaaaaaa															1341	

<210> 208
 <211> 1262
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (210)..(1067)

<400> 208
 gcacgagggc gcgcttaggc aggcggtggc gcggtggag tgccgcgggg agggctgtgc

60

cggttgcttt	ctgcagccgc	atctcggcca	gctctcctcg	ccgtccccgg	ggcgctgtgc	120										
gtctccagtc	cgggaccgaa	gccgcctgcc	gtagcggcg	gccagatccg	cgtcccgct	180										
cagcggccgg	aggacatgcg	ggagagaga	atg	agc	cag	1										
			agg	gac	acg	5										
			Met	Ser	Gln	Arg	Asp	Thr	Leu	Val	233					
cat	ctg	ttt	gcc	gga	tgt	ggt	aca	gtg	gga	gct	att	ctg	aca	281		
His	Leu	Phe	Ala	Gly	Gly	Cys	Gly	Gly	Thr	Val	Gly	Ala	Ile	Leu	Thr	
9		14							19				24			
tgt	cca	ctg	gaa	gtt	gta	aaa	aca	cga	ctg	cag	tca	tct	tct	gtg	acg	329
Cys	Pro	Leu	Glu	Val	Val	Lys	Thr	Arg	Leu	Gln	Ser	Ser	Ser	Val	Thr	
25		30							35				40			
ctt	tat	att	tct	gaa	gtt	cag	ctg	aac	acc	atg	gct	gga	gcc	agt	gtc	377
Leu	Tyr	Ile	Ser	Glu	Val	Gln	Leu	Asn	Thr	Met	Ala	Gly	Ala	Ser	Val	
41		46							51				56			
aac	cga	gta	gtg	tct	ccc	gga	cct	ctt	cat	tgc	cta	aaa	gca	ata	tac	425
Asn	Arg	Val	Val	Ser	Pro	Gly	Pro	Leu	His	Cys	Leu	Lys	Ala	Ile	Tyr	
57		62							67				72			
ttt	gct	gct	tat	tca	aac	tgc	aag	gaa	aag	ttg	aat	gat	gta	ttt	gat	473
Phe	Ala	Ala	Tyr	Ser	Asn	Cys	Lys	Glu	Lys	Leu	Asn	Asp	Val	Phe	Asp	
73		78							83				88			
cct	gat	tct	acc	caa	gta	cat	atg	att	tca	gct	gca	atg	gca	ggt	ttt	521
Pro	Asp	Ser	Thr	Gln	Val	His	Met	Ile	Ser	Ala	Ala	Met	Ala	Gly	Phe	
89		94							99				104			
act	gca	atc	aca	gca	acc	aac	ccc	att	tgg	ctt	ata	aag	act	cgg	tta	569
Thr	Ala	Ile	Thr	Ala	Thr	Asn	Pro	Ile	Trp	Leu	Ile	Lys	Thr	Arg	Leu	
105									110				115		120	
cag	ctt	gat	gca	agg	aac	cgc	ggg	gaa	agg	cga	atg	ggt	gct	ttt	gaa	617
Gln	Leu	Asp	Ala	Arg	Asn	Arg	Gly	Glu	Arg	Arg	Met	Gly	Ala	Phe	Glu	
121									126				131		136	
tgt	gtt	cgt	aaa	gtg	tat	cag	aca	gat	gga	cta	aaa	gga	ttt	tat	agg	665
Cys	Val	Arg	Lys	Val	Tyr	Gln	Thr	Asp	Gly	Leu	Lys	Gly	Phe	Tyr	Arg	
137									142				147		152	
ggc	atg	tct	gct	tca	tat	gct	ggt	ata	tca	gag	act	gtt	atc	cat	ttt	713
Gly	Met	Ser	Ala	Ser	Tyr	Ala	Gly	Ile	Ser	Glu	Thr	Val	Ile	His	Phe	
153									158				163		168	
gtt	att	tat	gaa	agt	ata	aaa	caa	aaa	cta	ctg	gaa	tat	aag	act	gct	761
Val	Ile	Tyr	Glu	Ser	Ile	Lys	Gln	Lys	Leu	Leu	Glu	Tyr	Lys	Thr	Ala	
169									174				179		184	
tct	aca	atg	gaa	aat	gat	gaa	gag	tct	gtg	aaa	gaa	gca	tca	gat	ttt	809
Ser	Thr	Met	Glu	Asn	Asp	Glu	Glu	Ser	Val	Lys	Glu	Ala	Ser	Asp	Phe	
185									190				195		200	

gtg gga atg atg cta gct gct gcc acc tca aaa act tgt gcc aca act	857
Val Gly Met Met Leu Ala Ala Ala Thr Ser Lys Thr Cys Ala Thr Thr	
201 206 211 216	
ata gca tat cca cat gaa gtt gta aga aca aga cta cgt gaa gag gga	905
Ile Ala Tyr Pro His Glu Val Val Arg Thr Arg Leu Arg Glu Glu Gly	
217 222 227 232	
aca aaa tac aga tct ttt ttt cag act cta tct ttg ctt gtt caa gaa	953
Thr Lys Tyr Arg Ser Phe Phe Gln Thr Leu Ser Leu Leu Val Gln Glu	
233 238 243 248	
gaa ggt tat ggg tct ctt tat cgt ggt ctg aca act cat cta gtg aga	1001
Glu Gly Tyr Gly Ser Leu Tyr Arg Gly Leu Thr Thr His Leu Val Arg	
249 254 259 264	
cag att cca aac aca gcc att atg atg gcc acc tat gaa ttg gtg gtt	1049
Gln Ile Pro Asn Thr Ala Ile Met Met Ala Thr Tyr Glu Leu Val Val	
265 270 275 280	
tac cta ctc aat gga tag cagcac gaggactgct gtactgcaaa aaaagaagac	1103
Tyr Leu Leu Asn Gly *	
281 286	
caaaaagatta cagtggacca tgggatacag aagccagcat ggcagacaga agaaaaatag	1163
tttgggaaca tgtaactatt ctaagtggaa gttttgttgt aggaattata gtaatcacac	1223
cacattactt ggccttcgg taatgtgaaa aaaaaaaaaa	1262
<210> 209	
<211> 2038	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (102)..(1364)	
<400> 209	
gcacaggctg agatgtggtt ctgcgcgtgt gcggacggct gtctgttaac tccgcggta	60
gttccccggac tggtggtctgg tctgcagggt tgacctgcgc a atg cag agg ctg	113
Met Gln Arg Leu	
1	
cag gta gtg ctg ggc cac ctg agg ggt ccg gcc gat tcc ggc tgg atg	161
Gln Val Val Leu Gly His Leu Arg Gly Pro Ala Asp Ser Gly Trp Met	
5 10 15 20	
ccg cag gcc gcg cct tgc ctg agc ggt gcc ccg cag gcc tcg gcc gcg	209
Pro Gln Ala Ala Pro Cys Leu Ser Gly Ala Pro Gln Ala Ser Ala Ala	
21 26 31 36	

gat	gtg	gtg	gtg	cac	ggg	cgg	cgc	acg	gcc	atc	tgc	cgg	gct	ggc		257
Asp	Val	Val	Val	Val	His	Gly	Arg	Arg	Thr	Ala	Ile	Cys	Arg	Ala	Gly	
37															52	
/																
cgc	ggc	ggc	ttc	aag	gac	acc	acc	ccc	gac	gag	ctt	ctc	tcg	gca	gtc	305
Arg	Gly	Gly	Phe	Lys	Asp	Thr	Thr	Pro	Asp	Glu	Leu	Leu	Ser	Ala	Val	
53															68	
atg	acc	gct	gtt	ctc	aag	gac	gtg	aat	ctg	agg	ccg	gaa	cag	ctg	ggg	353
Met	Thr	Ala	Val	Leu	Lys	Asp	Val	Asn	Leu	Arg	Pro	Glu	Gln	Leu	Gly	
69															84	
gac	atc	tgt	gtc	gga	aat	gtg	ctg	cag	cct	ggg	gcc	ggg	gca	atc	atg	401
Asp	Ile	Cys	Val	Gly	Asn	Val	Leu	Gln	Pro	Gly	Ala	Gly	Ala	Ile	Met	
85															100	
gcc	cga	atc	gcc	cag	ttt	ctg	agt	gac	atc	ccg	gag	act	gtg	cct	ttg	449
Ala	Arg	Ile	Ala	Gln	Phe	Leu	Ser	Asp	Ile	Pro	Glu	Thr	Val	Pro	Leu	
101															116	
tcc	act	gtc	aat	aga	cag	tgt	tcg	tcg	ggg	cta	cag	gca	gtg	gcc	agc	497
Ser	Thr	Val	Asn	Arg	Gln	Cys	Ser	Ser	Gly	Leu	Gln	Ala	Val	Ala	Ser	
117															132	
ata	gca	ggg	gtc	atc	aga	aat	ggg	tct	tat	gac	att	ggc	atg	gcc	tgt	545
Ile	Ala	Gly	Gly	Ile	Arg	Asn	Gly	Ser	Tyr	Asp	Ile	Gly	Met	Ala	Cys	
133															148	
ggg	gtg	gag	tcc	atg	tcc	ctg	gct	gac	aga	ggg	aac	cct	gga	aat	att	593
Gly	Val	Glu	Ser	Met	Ser	Leu	Ala	Asp	Arg	Gly	Asn	Pro	Gly	Asn	Ile	
149															164	
act	tcg	cgc	ttg	atg	gag	aag	gag	aag	gcc	aga	gat	tgc	ctg	att	cct	641
Thr	Ser	Arg	Leu	Met	Glu	Lys	Glu	Lys	Ala	Arg	Asp	Cys	Leu	Ile	Pro	
165															180	
atg	ggg	ata	acc	tct	gag	aat	gtg	gct	gag	cgg	ttt	ggc	att	tca	cgg	689
Met	Gly	Ile	Thr	Ser	Glu	Asn	Val	Ala	Glu	Arg	Phe	Gly	Ile	Ser	Arg	
181															196	
gag	aag	cag	gat	acc	ttt	gcc	ctg	gct	tcc	cag	cag	aag	gca	gca	aga	737
Glu	Lys	Gln	Asp	Thr	Phe	Ala	Leu	Ala	Ser	Gln	Gln	Lys	Ala	Ala	Arg	
197															212	
gcc	cag	agc	aag	ggc	tgt	ttc	caa	gct	gag	att	gtg	cct	gtg	acc	acc	785
Ala	Gln	Ser	Lys	Gly	Cys	Phe	Gln	Ala	Glu	Ile	Val	Pro	Val	Thr	Thr	
213															228	
acg	gtc	cat	gat	gac	aag	ggc	acc	aag	agg	agc	atc	act	gtg	acc	cag	833
Thr	Val	His	Asp	Asp	Lys	Gly	Thr	Lys	Arg	Ser	Ile	Thr	Val	Thr	Gln	
229															244	
gat	gag	ggg	atc	cgc	ccc	agc	acc	acc	atg	gag	ggc	ctg	gcc	aaa	ctg	881
Asp	Glu	Gly	Ile	Arg	Pro	Ser	Thr	Thr	Met	Glu	Gly	Leu	Ala	Lys	Leu	
245															260	
aag	cct	gcc	ttc	aag	aaa	gat	ggt	tct	acc	aca	gct	gga	aac	tct	agc	929

Lys Pro Ala Phe Lys Lys Asp Gly Ser Thr Thr Ala Gly Asn Ser Ser			
261	266	271	276
cag gtg agt gat ggg gca gct gcc atc/ctg ctg gcc cg agg tcc aag			977
Gln Val Ser Asp Gly Ala Ala Ala Ile Leu Leu Ala Arg Arg Ser Lys			
277	282	287	292
gca gaa gag ttg ggc ctt ccc atc ctt ggg gtc ctg agg tct tat gca			1025
Ala Glu Glu Leu Gly Leu Pro Ile Leu Gly Val Leu Arg Ser Tyr Ala			
293	298	303	308
gtg gtt ggg gtc cca cct gac atc atg .ggc att gga cct gcc tat gcc			1073
Val Val Gly Val Pro Pro Asp Ile Met Gly Ile Gly Pro Ala Tyr Ala			
309	314	319	324
atc cca gta gct ttg caa aaa gca ggg ctg aca gtg agt gac gtg gac			1121
Ile Pro Val Ala Leu Gln Lys Ala Gly Leu Thr Val Ser Asp Val Asp			
325	330	335	340
atc ttc gag atc aat gag gcc ttt gca agc cag gct gcc tac tgt gtg			1169
Ile Phe Glu Ile Asn Glu Ala Phe Ala Ser Gln Ala Ala Tyr Cys Val			
341	346	351	356
gag aag cta cga ctc ccc cct gag aag gtg aac ccc ctg ggg ggt gca			1217
Glu Lys Leu Arg Leu Pro Pro Glu Lys Val Asn Pro Leu Gly Gly Ala			
357	362	367	372
gtg gcc tta ggg cac cca ctg ggc tgc act ggg gca cga cag gtc atc			1265
Val Ala Leu Gly His Pro Leu Gly Cys Thr Gly Ala Arg Gln Val Ile			
373	378	383	388
acg ctg cca tcc tgc tgg ccc gga gtc caa ggc aga aga gtt ggg cct			1313
Thr Leu Pro Ser Cys Trp Pro Gly Val Gln Gly Arg Arg Val Gly Pro			
389	394	399	404
tcc cat cct tgg ggt cct gag gtc tta tgc agt ggt tgg ggt ccc acc			1361
Ser His Pro Trp Gly Pro Glu Val Leu Cys Ser Gly Trp Gly Pro Thr			
405	410	415	420
tga catc atgggcattg gacctgccta tgccatcccc gtagcttgc aaaaagcagg			1418
*			
421			
gctgacagtg agtgacgtgg acatcttcga gatcaatgag gcctttgcaa gccaggctgc			1478
ctactgtgtg gagaagctac gactcccccc tgagaagggtg aaccccccgg ggggtgcagt			1538
ggccttaggg cacccactgg gctgcactgg ggcacgacag gtcatacacgc tgctcaatga			1598
gctgaagcgc cgtggaaaga gggcatacgg agtgggtgtcc atgtgcatacg ggactggaat			1658
gggagccgct gccgtctttg aataccctgg gaactgagtg aggtcccagg ctggaggcgc			1718
tacgcagaca gtcctgctgc tctagcagca aggcagtaac accacaaaaag caaaaccaca			1778
tggaaaaact cagcactggt ggtggggca gtggacagat caaggcactt caactcattt			1838

ggaaaatgtg aacactgatg acatggata ggagtgggtg ggggttgag ccaccatca	1898
gaccctctt agctgtcaa gataaaagca gcctgggtca cccaggccac aaggccatgg	1958
ttaattctta aggcaaggca aatccatgga tgagaagtgc aatgggcata gtaaaagtgc	2018
atgaatttaa aaaaaaaaaa	2038

<210> 210
 <211> 2022
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (133)..(1548)

<400> 210					
tagtgccaat tggttcggtg tcataactat ctattcgatg atgaagatac cccacccaaac	60				
ccaaaaaaaaag agatctctcg aggatccgaa ttgcggccg cgtcgaccac aaaggcaaaa	120				
acaaaggagc tg atg gca aag aag gta gct gtg att gga gct ggg gtc	168				
Met Ala Lys Lys Val Ala Val Ile Gly Ala Gly Val					
1 5 10					
agt ggc cta att tct ctg aag tgc tgt gtg gat gag gga ctt gag ccc	216				
Ser Gly Leu Ile Ser Leu Lys Cys Cys Val Asp Glu Gly Leu Glu Pro					
13 18 23 28					
act tgc ttt gag aga act gaa gat att gga gga gtg tgg agg ttc aaa	264				
Thr Cys Phe Glu Arg Thr Glu Asp Ile Gly Gly Val Trp Arg Phe Lys					
29 34 39 44					
gag aat gtg gaa gat ggc cga gca agt atc tat caa tct gtc gtt acc	312				
Glu Asn Val Glu Asp Gly Arg Ala Ser Ile Tyr Gln Ser Val Val Thr					
45 50 55 60					
aac acc agc aaa gaa atg tcc tgt ttc agt gac ttt cca atg cct gaa	360				
Asn Thr Ser Lys Glu Met Ser Cys Phe Ser Asp Phe Pro Met Pro Glu					
61 66 71 76					
gat ttt cca aac ttc ctg cat aat tct aaa ctt ctg gaa tat ttc agg	408				
Asp Phe Pro Asn Phe Leu His Asn Ser Lys Leu Leu Glu Tyr Phe Arg					
77 82 87 92					
att ttt gct aaa aaa ttt gat ctg cta aaa tat att cag ttc cag aca	456				
Ile Phe Ala Lys Lys Phe Asp Leu Leu Lys Tyr Ile Gln Phe Gln Thr					
93 98 103 108					
act gtc ctt agt gtg aga aaa tgt cca gat ttc tca tcc tct ggc caa	504				
Thr Val Leu Ser Val Arg Lys Cys Pro Asp Phe Ser Ser Ser Gly Gln					
109 114 119 124					

tgg aag gtt gtc act cag agc aac ggc aag gag cag agt gct gtc ttt Trp Lys Val Val Thr Gln Ser Asn Gly Lys Glu Gln Ser Ala Val Phe	125	130	135	140	552
gac gca gtt atg gtt tgc agt ggc cac cac att cta cct cat atc cca Asp Ala Val Met Val Cys Ser Gly His His Ile Leu Pro His Ile Pro	141	146	151	156	600
ctg aag tca ttt cca ggt atg gag agg ttc aaa ggc caa tat ttc cat Leu Lys Ser Phe Pro Gly Met Glu Arg Phe Lys Gly Gln Tyr Phe His	157	162	167	172	648
agc cgc caa tac aag cat cca gat gga ttt gag gga aaa cgc atc ctg Ser Arg Gln Tyr Lys His Pro Asp Gly Phe Glu Gly [#] Lys Arg Ile Leu	173	178	183	188	696
gtg att gga atg gga aac tca ggc tca gat att gct gtt gag ctg agt Val Ile Gly Met Gly Asn Ser Gly Ser Asp Ile Ala Val Glu Leu Ser	189	194	199	204	744
aag aat gct gct cag gtt ttt atc agc acc agg cat ggc acc tgg gtc Lys Asn Ala Ala Gln Val Phe Ile Ser Thr Arg His Gly Thr Trp Val	205	210	215	220	792
atg agc cgt atc tct gaa gat ggc tat cct tgg gac tca gtg ttc cac Met Ser Arg Ile Ser Glu Asp Gly Tyr Pro Trp Asp Ser Val Phe His	221	226	231	236	840
acc cgg ttt cgt tct atg ctc cgc aat gta ctg cca cga aca gct gta Thr Arg Phe Arg Ser Met Leu Arg Asn Val Leu Pro Arg Thr Ala Val	237	242	247	252	888
aaa tgg atg ata gaa caa cag atg aat cgg tgg ttc aac cat gaa aat Lys Trp Met Ile Glu Gln Gln Met Asn Arg Trp Phe Asn His Glu Asn	253	258	263	268	936
tat ggc ctt gag cct caa aac aaa tac att atg aag gaa cct gta cta Tyr Gly Leu Glu Pro Gln Asn Lys Tyr Ile Met Lys Glu Pro Val Leu	269	274	279	284	984
aat gat gat gtc cca agt cgt cta ctc tgt gga gcc atc aag gtg aaa Asn Asp Asp Val Pro Ser Arg Leu Leu Cys Gly Ala Ile Lys Val Lys	285	290	295	300	1032
tct aca gtg aaa gag ctc aca gaa act tct gcc atc ttt gag gat gga Ser Thr Val Lys Glu Leu Thr Glu Thr Ser Ala Ile Phe Glu Asp Gly	301	306	311	316	1080
aca gtg gag gag aac att gat gtc atc att ttt gca aca gga tat agt Thr Val Glu Glu Asn Ile Asp Val Ile Ile Phe Ala Thr Gly Tyr Ser	317	322	327	332	1128
ttc tct ttt ccc ttc ctt gaa gat tca ctc gtt aaa gta gag aat aat Phe Ser Phe Pro Phe Leu Glu Asp Ser Leu Val Lys Val Glu Asn Asn	333	338	343	348	1176
atg gtc tca ctg tat aaa tac ata ttc ccc gct cac ctg gac aag tca					1224

Met Val Ser Leu Tyr Lys Tyr Ile Phe Pro Ala His Leu Asp Lys Ser			
349	354	359	364
acc ctc gcg tgc att ggt ctc atc cag ccc cta ggt tcc att ttc cca			1272
Thr Leu Ala Cys Ile Gly Leu Ile Gln Pro Leu Gly Ser Ile Phe Pro			
365	370	375	380
act gct gaa ctt caa gct cgt tgg gtg aca aga gtt ttc aaa ggc ttg			1320
Thr Ala Glu Leu Gln Ala Arg Trp Val Thr Arg Val Phe Lys Gly Leu			
381	386	391	396
tgt agc ctg ccc tca gag aga act atg atg atg gac att atc aaa agg			1368
Cys Ser Leu Pro Ser Glu Arg Thr Met Met Asp Ile Ile Lys Arg			
397	402	407	412
aat gaa aaa aga att gac ctg ttt gga gaa agc cag agc cag acg ttg			1416
Asn Glu Lys Arg Ile Asp Leu Phe Gly Glu Ser Gln Ser Gln Thr Leu			
413	418	423	428
cag acc aat tat gtt gac tac ttg gac gag ctc gcc tta gag ata ggt			1464
Gln Thr Asn Tyr Val Asp Tyr Leu Asp Glu Leu Ala Leu Glu Ile Gly			
429	434	439	444
gcg aag cca gat ttc tgc tct ctc ttg ttc aaa gat cct aaa ctg gct			1512
Ala Lys Pro Asp Phe Cys Ser Leu Leu Phe Lys Asp Pro Lys Leu Ala			
445	450	455	460
gtg aga ctc tat ttc gga ccc tgc aac tcc tat tag tatac gcctgggtgg			1562
Val Arg Leu Tyr Phe Gly Pro Cys Asn Ser Tyr *			
461	466	471	
gcctggcaa tggaaaggag ccagaaatgc catcttacc cagaaacaaa gaatactgaa			1622
gccactcaag actcggccc tgaaggattc atctaatttc tcagttctt ttctgtgaa			1682
aatcctggc cttcttgctg ttgttgtgc cttttttgc caacttcaat ggtccatgc			1742
agcataatgc tttgggctt attatctgt cagtcactac ctcctaaaga aaaaaaaaaa			1802
ggctaaaaaa aaaaacatta cattcatgtt ctaattataa attttaaagt tagtactac			1862
aggcaggggg gaaattgtaa agaatttagca aaatttaggt tatgtacaaa accaaaaattt			1922
ggccatgaaa tttgcctt ccatgcttcc ctcagttcac caaagttacc aaaatgtaaa			1982
ataaaataaa actggctcag gtaagtaggg ctgccaaccc			2022

<210> 211
<211> 2843
<212> DNA
<213> Homo sapiens

<220>
<221> CDS

<222> (286)..(1725)

<400> 211

gtgctggctt	gatgtaccta	tctattcgat	gatgaagata	ccccaccaaa	cccaaaaaaa	60
gagatctctc	gaggatccga	attcgccgc	gcgtcgacca	aggtcctcca	gcgttcctag	120
agcggagaag	aaagcgctcc	gaagagctag	agctgacact	cggcgatgag	ctaagacgct	180
gttcagagc	gtttgggtcc	tctgaggccc	cttgaccagg	agtgtctctg	aagatacagt	240
ccaaagaaag	ttctccaaaa	caaggagagc	agtctgaagc	tgggg	atg gca aca	294
					Met Ala Thr	
				1		
gca ttg	gtg agt	gcc cat	tcc ctg	gct ccc	ctg aat	342
Ala Leu	Val Ser	Ala His	Ser Leu	Ala Pro	Leu Asn	Lys Lys Glu
4	9	14	19			
ggg ctt	cgg gta	gtg agg	gag gat	cac tac	tct act	390
Gly Leu	Arg Val	Val Arg	Glu Asp	His Tyr	Ser Thr	Trp Glu Gln Gly
20	25	30	35			
ttc aag	ctg caa	gga aac	agt aaa	ggc ctt	gga cag	438
Phe Lys	Leu Gln	Gly Asn	Ser Lys	Gly Leu	Gly Gln	Glu Pro Leu Cys
36	41	46	51			
aaa caa	ttc agg	cag ttg	cgt tat	gaa gag	acc aca	486
Lys Gln	Phe Arg	Gln Leu	Arg Tyr	Glu Glu	Thr Thr	Gly Pro Arg Glu
52	57	62	67			
gca cta	agt cgg	ctc cgg	gag ctc	tgt caa	cag tgg	534
Ala Leu	Ser Arg	Leu Arg	Glu Leu	Cys Gln	Trp Leu	Gln Pro Glu
68	73	78	83			
acc cat	acc aag	gag cag	atc ctg	gag ctg	ctg gag	582
Thr His	Thr Lys	Glu Gln	Ile Leu	Glu Leu	Leu Val	Glu Gln Phe
84	89	94	99			
ctg atc	atc ctg	cct aag	gag ctc	cag gcc	cgg gtg	630
Leu Ile	Ile Leu	Pro Lys	Glu Leu	Gln Ala	Arg Val	Gln Glu His His
100	105	110	115			
cca gag	agc agg	gag gac	gtg gtt	gtt ctg	gag gat	678
Pro Glu	Ser Arg	Glu Asp	Val Val	Val Val	Leu Glu	Asp Leu Gln Leu
116	121	126	131			
gat ctt	gga gaa	aca gga	caa cag	gtg gac	cca gac	726
Asp Lys	Leu Gly	Glu Thr	Gly Gln	Gln Val	Asp Pro	Asp Gln Pro Lys Lys
132	137	142	147			
caa aaa	ata ctt	gtg gag	gag atg	gcc cct	ctg aaa	774
Gln Lys	Ile Leu	Val Glu	Glu Met	Ala Pro	Leu Lys	Gly Val Gln Glu
148	153	158	163			
cag cag	gtt cgg	cat gag	tg gaa	aca aag	cct gag	822
Gln Gln	Val Arg	His Glu	Cys Glu	Val Thr	Lys Pro	Glu Lys

164	169	174	179	
ggt gag gag aca agg att gag aat ggg aag ctt att gta gta aca gac Gly Glu Glu Thr Arg Ile Glu Asn Gly Lys Leu Ile Val Val Thr Asp 180 185 190 195				870
tct tgt gga aga gta gag tca tct ggg aaa ata tct gaa ccc atg gag Ser Cys Gly Arg Val Glu Ser Ser Gly Lys Ile Ser Glu Pro Met Glu 196 201 206 211				918
gct cat aat gag ggc tct aac ttg gaa agg cat cag gcc aag ccc aaa Ala His Asn Glu Gly Ser Asn Leu Glu Arg His Gln Ala Lys Pro Lys 212 217 222 227				966
gag aag att gag tat aaa tgc tca gaa cgt gag cag aga ttc atc cag Glu Lys Ile Glu Tyr Lys Cys Ser Glu Arg Glu Gln Arg Phe Ile Gln 228 233 238 243				1014
cac ttg gac ctg att gaa cat gcg agt aca cac acg gga aag aaa tcc His Leu Asp Leu Ile Glu His Ala Ser Thr His Thr Gly Lys Lys Ser 244 249 254 259				1062
tgc gag tct gat gtg tgt cag agt tcc agt ctt aca gga cat aag aaa Cys Glu Ser Asp Val Cys Gln Ser Ser Ser Leu Thr Gly His Lys Lys 260 265 270 275				1110
gtc ctc tct aga gag aaa ggt cat cag tgt cat gag tgt ggg aaa gcc Val Leu Ser Arg Glu Lys Gly His Gln Cys His Glu Cys Gly Lys Ala 276 281 286 291				1158
ttt cag agg agt tca cac ctc gtc aga cat cag aaa atc cat ctt ggt Phe Gln Arg Ser Ser His Leu Val Arg His Gln Lys Ile His Leu Gly 292 297 302 307				1206
gag aag cct tat cag tgc aat gag tgt ggc aaa gtc ttt agc cag aat Glu Lys Pro Tyr Gln Cys Asn Glu Cys Gly Lys Val Phe Ser Gln Asn 308 313 318 323				1254
gca ggc ctt ttg gaa cat ctc aga att cat act gga gag aaa cct tat Ala Gly Leu Leu Glu His Leu Arg Ile His Thr Gly Glu Lys Pro Tyr 324 329 334 339				1302
cta tgt atc cat tgt gga aaa aat ttt agg cgc agc tct cac ctt aat Leu Cys Ile His Cys Gly Lys Asn Phe Arg Arg Ser Ser His Leu Asn 340 345 350 355				1350
cga cat cag aga att cac agt cag gag gag ccc tgt gag tgc aag gag Arg His Gln Arg Ile His Ser Gln Glu Glu Pro Cys Glu Cys Lys Glu 356 361 366 371				1398
tgt gga aaa acc ttt agt cag gcc tta ctc ctc acc cac cat cag aga Cys Gly Lys Thr Phe Ser Gln Ala Leu Leu Leu Thr His His Gln Arg 372 377 382 387				1446
atc cat agt cac tcc aaa agc cat caa tgt aac gag tgt gga aaa gct Ile His Ser His Ser Lys Ser His Gln Cys Asn Glu Cys Gly Lys Ala 388 393 398 403				1494

ttc agt ttg acc tca gac ctt att cga cac cac aga att cat act gga	1542
Phe Ser Leu Thr Ser Asp Leu Ile Arg His His Arg Ile His Thr Gly	
404 / 409 . 414 . 419	
gaa aaa cct ttc aag tgt aac ata tgc cag aaa gcc ttc cga cta aac	1590
Glu Lys Pro Phe Lys Cys Asn Ile Cys Gln Lys Ala Phe Arg Leu Asn	
420 . 425 . 430 . 435	
tca cac ctt gct cag cat gta aga atc cac aat gaa gaa aaa ccc tat	1638
Ser His Leu Ala Gln His Val Arg Ile His Asn Glu Glu Lys Pro Tyr	
436 . 441 . 446 . 451	
cag tgt agt gaa tgt gga gaa gcc ttc agg caa agg tca ggt ctt ttt	1686
Gln Cys Ser Glu Cys Gly Glu Ala Phe Arg Gln Arg Ser Gly Leu Phe	
452 . 457 . 462 . 467	
caa cat cag aga tat cac cac aaa gac aaa ctg gct tga tgagggtttc	1735
Gln His Gln Arg Tyr His His Lys Asp Lys Leu Ala *	
468 . 473 . 478	
tctccttgta gaacatcaga gaaggcacat tgactagcaa acagcacttt agaaaaagtc	1795
accgttagccc actgtggcat cagaaaattc ttggggctg agttggaggc tccctgcctc	1855
tattctctct ccttgctt cttgaagtc agcttggac cacaataatt tcactgtaga	1915
tgatatgcta ggatcaaagt taaacagcat tcttcaactgc aggacatctc agagcatgta	1975
acataactgc atgattatat actctaagca atagagagct tcatgactga gtaagagttt	2035
tgaagtcagc agtgaatcaa gtccccacag atttgcaggc ttaagcagaa caagggaaaga	2095
ttgatatttt tggatatgct atagcagctt tctcctatga aataaaaactg atgatgtttg	2155
gaagtataact actctcaaag gtgtcttaa agtacaggtt aatggtgaac atttcccccc	2215
agtggcttca cctcattcct cccactggcc ttaccccttc ctcccccagt ggaagcattt	2275
tcaaaagcaa agataatttt cgctggtaa cttcagaact tgccttcagg gttagctca	2335
tgtaatttta ccatttcca tccccattcc ccaccacatt atgtcaagat tcaagttata	2395
aattaacgtt ttacttagac tttgaaagag atttcatgag taatttgaat gaaccttgct	2455
gaatataatct gaatagaacac tgtctgactt gataactcca gtgccagttt agtggctgct	2515
gcatacgacac tattcagtaa atgtctgatg aaagaaattt gacttttcc cttaataact	2575
gatgatgcaa ttttggaaatg ttgcttgcctc tggaataactt cggaaagttaa acaataaaagt	2635
cagcttggag aggagatcat gatcttata ctgtgaatag cagaatgtca cagatgaaga	2695
atattaaaat tagggcgtc cactccaaaa catatcacca gagtgacaac ttcagccctc	2755
agcctctgca atccatatat atcctggctc tgggagtc tagaataactg tttccttcta	2815

ataaaggttt caaacaaaaaa aaaaaaat

2843

<210> 212

<211> 3134

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (110)..(2812)

<400> 212

gcccccggtcc atatgaggca atggagaccc tgcagtaccg gtccggatt cccgggtcga 60

cccacgcgtc cgccgggttcc ggttgcataca gcgaggatt cacggcgaa atg aga 115
Met Arg
1

ctg ttc gtg agt gat ggc gtc ccg ggt tgc ttg ccg gtg ctg gcc 163
Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu Ala Ala
3 8 13 18

gcc ggg aga gcc cgg ggc aga gca gag gtg ctc atc agc act gta ggc 211
Ala Gly Arg Ala Arg Gly Arg Ala Glu Val Leu Ile Ser Thr Val Gly
19 24 29 34

ccg gaa gat tgt gtg gtc ccg ttc ctg acc ccg cct aag gtc cct gtc 259
Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val Pro Val
35 40 45 50

ttg cag ctg gat agc ggc aac tac ctc ttc tcc act agt gca atc tgc 307
Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys
51 56 61 66

cga tat ttt ttt ttg tta tct ggc tgg gag caa gat gac ctc act aac 355
Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn
67 72 77 82

cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct 403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala
83 88 93 98

gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt 451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu
99 104 109 114

ggc tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt 499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg
115 120 125 130

cag aac tgt cct ttc ctg gct ggg gag aca gaa tct cta gcc gac att 547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Thr Glu Ser Leu Ala Asp Ile
131 136 141 146

gtt ttg tgg gga gcc cta tac cca tta ctg caa gat ccc gcc tac ctc		595
Val Leu Trp Gly Ala Leu Tyr Pro Leu Leu Gln Asp Pro Ala Tyr Leu		
147	152	157
		162
cct gag gag ctg agt gcc ctg cac agc tgg ttc cag aca ctg agt acc		643
Pro Glu Glu Leu Ser Ala Leu His Ser Trp Phe Gln Thr Leu Ser Thr		
163	168	173
		178
cag gaa cca tgt cag cga gct gca gag act gta ctg aaa cag caa ggt		691
Gln Glu Pro Cys Gln Arg Ala Ala Glu Thr Val Leu Lys Gln Gln Gly		
179	184	189
		194
gtc ctg gct ctc cgg cct tac ctc caa aag cag ccc cag ccc agc ccc		739
Val Leu Ala Leu Arg Pro Tyr Leu Gln Lys Gln Pro Gln Pro Ser Pro		
195	200	205
		210
gct gag gga agg gct gtc acc aat gag cct gag gag gag ctg gct		787
Ala Glu Gly Arg Ala Val Thr Asn Glu Pro Glu Glu Glu Leu Ala		
211	216	221
		226
acc cta tct gag gag gag att gct atg gct gtt act gct tgg gag aag		835
Thr Leu Ser Glu Glu Ile Ala Met Ala Val Thr Ala Trp Glu Lys		
227	232	237
		242
ggc cta gaa agt ttg ccc ccg ctg cgg ccc cag cag aat cca gtg ttg		883
Gly Leu Glu Ser Leu Pro Pro Leu Arg Pro Gln Gln Asn Pro Val Leu		
243	248	253
		258
cct gtg gct gga gaa agg aat gtg ctc atc acc agt gcc ctc cct tac		931
Pro Val Ala Gly Glu Arg Asn Val Leu Ile Thr Ser Ala Leu Pro Tyr		
259	264	269
		274
gtc aac aat gtc ccc cac ctt ggg aac atc att ggt tgt gtg ctc agt		979
Val Asn Asn Val Pro His Leu Gly Asn Ile Ile Gly Cys Val Leu Ser		
275	280	285
		290
gcc gat gtc ttt gcc agg tac tct cgc ctc cgc cag tgg aac acc ctc		1027
Ala Asp Val Phe Ala Arg Tyr Ser Arg Leu Arg Gln Trp Asn Thr Leu		
291	296	301
		306
tat ctg tgt ggg aca gat gag tat ggt aca gca aca gag acc aag gct		1075
Tyr Leu Cys Gly Thr Asp Glu Tyr Gly Thr Ala Thr Glu Thr Lys Ala		
307	312	317
		322
ctg gag gag gga cta acc ccc cag gag atc tgc gac aag tac cac atc		1123
Leu Glu Glu Gly Leu Thr Pro Gln Glu Ile Cys Asp Lys Tyr His Ile		
323	328	333
		338
atc cat gct gac atc tac cgc tgg ttt aac att tcg ttt gat att ttt		1171
Ile His Ala Asp Ile Tyr Arg Trp Phe Asn Ile Ser Phe Asp Ile Phe		
339	344	349
		354
ggt cgc acc acc act cca cag cag acc aaa atc acc cag gac att ttc		1219
Gly Arg Thr Thr Pro Gln Gln Thr Lys Ile Thr Gln Asp Ile Phe		
355	360	365
		370
cag cag ttg ctg aaa cga ggt ttt gtg ctg caa gat act gtg gag caa		1267

Gln Gln Leu Leu Lys Arg Gly Phe Val Leu Gln Asp Thr Val Glu Gln			
371	376	381	386
ctg cga tgt gag cac tgt gct cgc ttc ctg gct gac cgc ttc gtg gag			1315
Leu Arg Cys Glu His Cys Ala Arg Phe Leu Ala Asp Arg Phe Val Glu			
387	392	397	402
ggc gtg tgt ccc ttc tgt ggc tat gag gag gct cgg ggt gac cag tgt			1363
Gly Val Cys Pro Phe Cys Gly Tyr Glu Glu Ala Arg Gly Asp Gln Cys			
403	408	413	418
gac aag tgt ggc aag ctc atc aat gct gtc gag ctt aag aag cct cag			1411
Asp Lys Cys Gly Lys Leu Ile Asn Ala Val Glu Leu Lys Lys Pro Gln			
419	424	429	434
tgt aaa gtc tgc cga tca tgc cct gtg gtg cag tcg agc cag cac ctg			1459
Cys Lys Val Cys Arg Ser Cys Pro Val Val Gln Ser Ser Gln His Leu			
435	440	445	450
ttt ctg gac ctg cct aag ctg gag aag cga ctg gag gag tgg ttg ggg			1507
Phe Leu Asp Leu Pro Lys Leu Glu Lys Arg Leu Glu Glu Trp Leu Gly			
451	456	461	466
agg aca ttg cct ggc agt gac tgg aca ccc aat gcc cag ttt atc acc			1555
Arg Thr Leu Pro Gly Ser Asp Trp Thr Pro Asn Ala Gln Phe Ile Thr			
467	472	477	482
cgt tct tgg ctt cgg gat ggc ctc aag cca cgc tgc ata acc cga gac			1603
Arg Ser Trp Leu Arg Asp Gly Leu Lys Pro Arg Cys Ile Thr Arg Asp			
483	488	493	498
ctc aaa tgg gga acc cct gta ccc tta gaa ggt ttt gaa gac aag gta			1651
Leu Lys Trp Gly Thr Pro Val Pro Leu Glu Gly Phe Glu Asp Lys Val			
499	504	509	514
ttc tat gtc tgg ttt gat gcc act att ggc tat ctg tcc atc aca gcc			1699
Phe Tyr Val Trp Phe Asp Ala Thr Ile Gly Tyr Leu Ser Ile Thr Ala			
515	520	525	530
aac tac aca gac cag tgg gag aga tgg tgg aag aac cca gag caa gtg			1747
Asn Tyr Thr Asp Gln Trp Glu Arg Trp Trp Lys Asn Pro Glu Gln Val			
531	536	541	546
gac ctg tat cag ttc atg gcc aaa gac aat gtt cct ttc cat agc tta			1795
Asp Leu Tyr Gln Phe Met Ala Lys Asp Asn Val Pro Phe His Ser Leu			
547	552	557	562
gtc ttt cct tgc tca gcc cta gga gct gag gat aac tat acc ttg gtc			1843
Val Phe Pro Cys Ser Ala Leu Gly Ala Glu Asp Asn Tyr Thr Leu Val			
563	568	573	578
agc cac ctc att gct aca gag tac ctg aac tat gag gat ggg aaa ttc			1891
Ser His Leu Ile Ala Thr Glu Tyr Leu Asn Tyr Glu Asp Gly Lys Phe			
579	584	589	594
tct aag agc cgc ggt gtg gga gtg ttt ggg gac atg gcc cag gac acg			1939
Ser Lys Ser Arg Gly Val Gly Val Phe Gly Asp Met Ala Gln Asp Thr			

595	600	605	610	
ggg atc cct gct gac atc tgg cgc ttc tat ctg ctg tac att cgg cct Gly Ile Pro Ala Asp Ile Trp Arg Phe Tyr Leu Leu Tyr Ile Arg Pro				1987
611	616	621		626
gag ggc cag gac agt gct ttc tcc tgg acg gac ctg ctg ctg aag aat Glu Gly Gln Asp Ser Ala Phe Ser Trp Thr Asp Leu Leu Leu Lys Asn				2035
627	632	637		642
aat tct gag ctg ctt aac aac ctg ggc aac ttc atc aac aga gct ggg Asn Ser Glu Leu Leu Asn Leu Gly Asn Phe Ile Asn Arg Ala Gly				2083
643	648	653		658
atg ttt gtg tct aag ttc ttt ggg ggc tat gtg cct gag atg gtg ctc Met Phe Val Ser Lys Phe Phe Gly Gly Tyr Val Pro Glu Met Val Leu				2131
659	664	669		674
acc cct gat gat cag cgc ctg ctg gcc cat gtc acc ctg gag ctc cag Thr Pro Asp Asp Gln Arg Leu Leu Ala His Val Thr Leu Glu Leu Gln				2179
675	680	685		690
cac tat cac cag cta ctt gag aag gtt cgg atc cgg gat gcc ttg cgc His Tyr His Gln Leu Leu Glu Lys Val Arg Ile Arg Asp Ala Leu Arg				2227
691	696	701		706
agt atc ctc acc ata tct cga cat ggc aac caa tat att cag gtg aat Ser Ile Leu Thr Ile Ser Arg His Gly Asn Gln Tyr Ile Gln Val Asn				2275
707	712	717		722
gag ccc tgg aag cgg att aaa ggc agt gag gct gac agg caa cgg gca Glu Pro Trp Lys Arg Ile Lys Gly Ser Glu Ala Asp Arg Gln Arg Ala				2323
723	728	733		738
gga aca gtg act ggc ttg gca gtg aat ata qct gcc ttg ctc tct gtc Gly Thr Val Thr Gly Leu Ala Val Asn Ile Ala Ala Leu Leu Ser Val				2371
739	744	749		754
atg ctt cag cct tac atg ccc acg gtt agt gcc aca atc cag gcc cag Met Leu Gln Pro Tyr Met Pro Thr Val Ser Ala Thr Ile Gln Ala Gln				2419
755	760	765		770
ctg cag ctc cca cct cca gcc tgc agt atc ctg ctg aca aac ttc ctg Leu Gln Leu Pro Pro Ala Cys Ser Ile Leu Leu Thr Asn Phe Leu				2467
771	776	781		786
tgt acc tta cca gca gga cac cag att ggc aca gtc agt ccc ttg ttc Cys Thr Leu Pro Ala Gly His Gln Ile Gly Thr Val Ser Pro Leu Phe				2515
787	792	797		802
caa aaa ttg gaa aat gac cag att gaa agt tta agg cag cgc ttt gga Gln Lys Leu Glu Asn Asp Gln Ile Glu Ser Leu Arg Gln Arg Phe Gly				2563
803	808	813		818
ggg ggc cag gca aaa acg tcc ctg aag cca gca gtt gta gag act gtt Gly Gly Gln Ala Lys Thr Ser Leu Lys Pro Ala Val Val Glu Thr Val				2611
819	824	829		834

aca aca gcc aag cca cag cag ata caa gcg ctg atg gat gaa gtg aca	2659
Thr Thr Ala Lys Pro Gln Gln Ile Gln Ala Leu Met Asp Glu Val Thr	
835 840 845 850	/
aaa caa gga aac att gtc cga gaa ctg aaa gca caa aag gca gac aag	2707
Lys Gln Gly Asn Ile Val Arg Glu Leu Lys Ala Gln Lys Ala Asp Lys	
851 856 861 866	
aac gag gtt gct gcg gag gtg gcg aaa ctc ttg gat cta aag aaa cag	2755
Asn Glu Val Ala Ala Glu Val Ala Lys Leu Leu Asp Leu Lys Lys Gln	
867 872 877 882	
ttg gct gta gct gag ggg aaa ccc cct gaa gcc cct aaa ggc aag aag	2803
Leu Ala Val Ala Glu Gly Lys Pro Pro Glu Ala Pro Lys Gly Lys Lys	
883 888 893 898	
aaa aag taa aagacct tggctcatag aaagtcaactt taatagatag ggacagtaat	2859
Lys Lys *	
899	
aaataaatgt acaatctcta tataacaagct gagaccctttc cttttgtcta ctccaaggct	2919
tccccctgcg tatgtggat tgagggcac atcattggca ctatgtgagag gtagtcagt	2979
agccacttct gggaaaggtg gtagtgtgg cccaaatgggg ggactgtatgc tcccaagtgc	3039
acgcggccgg atatattaata gtagtagtcg acccgaaaaat tccggaccgg tacctgcaag	3099
gcgtaccagc tttcccaat agtgaattcg tatta	3134
<210> 213	
<211> 3059	
<212> DNA	
<213> Homo sapiens	
<220>	
<221> CDS	
<222> (110)..(2737)	
<400> 213	
gccccccgtcc atatgaggca atggagaccc tgcagtaccg gtccggaaatt cccgggtcga	60
cccacgcgtc cgcccggttcc ggttgcataca gcgaggatt cacggcgaa atg aga	115
Met Arg	
1	
ctg ttc gtg agt gat ggc gtc ccg ggt tgc ttg ccg gtg ctg gcc gcc	163
Leu Phe Val Ser Asp Gly Val Pro Gly Cys Leu Pro Val Leu Ala Ala	
3 8 13 18	
gcc ggg aga gcc cgg ggc aga gca gag gtg ctc atc agc act gta ggc	211
Ala Gly Arg Ala Arg Gly Arg Ala Glu Val Leu Ile Ser Thr Val Gly	
19 24 29 34	

ccg gaa gat tgt gtg gtc ccg ttc ctg acc cgg cct aag gtc cct gtc			259
Pro Glu Asp Cys Val Val Pro Phe Leu Thr Arg Pro Lys Val Pro Val			
35	40	45	50
ttg cag ctg gat agc ggc aac tac ctc ttc tcc act agt gca atc tgc			307
Leu Gln Leu Asp Ser Gly Asn Tyr Leu Phe Ser Thr Ser Ala Ile Cys			
51	56	61	66
cga tat ttt ttt ttg tta tct ggc tgg gag caa gat gac ctc act aac			355
Arg Tyr Phe Phe Leu Leu Ser Gly Trp Glu Gln Asp Asp Leu Thr Asn			
67	72	77	82
cag tgg ctg gaa tgg gaa gcg aca gag ctg cag cca gct ttg tct gct			403
Gln Trp Leu Glu Trp Glu Ala Thr Glu Leu Gln Pro Ala Leu Ser Ala			
83	88	93	98
gcc ctg tac tat tta gtg gtc caa ggc aag aag ggg gaa gat gtt ctt			451
Ala Leu Tyr Tyr Leu Val Val Gln Gly Lys Lys Gly Glu Asp Val Leu			
99	104	109	114
ggt tca gtg cgg aga gcc ctg act cac att gac cac agc ttg agt cgt			499
Gly Ser Val Arg Arg Ala Leu Thr His Ile Asp His Ser Leu Ser Arg			
115	120	125	130
cag aac tgt cct ttc ctg gct ggg gag gag ctg agt gcc ctg cac agc			547
Gln Asn Cys Pro Phe Leu Ala Gly Glu Glu Leu Ser Ala Leu His Ser			
131	136	141	146
tgg ttc cag aca ctg agt acc cag gaa cca tgt cag cga gct gca gag			595
Trp Phe Gln Thr Leu Ser Thr Gln Glu Pro Cys Gln Arg Ala Ala Glu			
147	152	157	162
act gta ctg aaa cag caa ggt gtc ctg gct ctc cgg cct tac ctc caa			643
Thr Val Leu Lys Gln Gln Gly Val Leu Ala Leu Arg Pro Tyr Leu Gln			
163	168	173	178
aag cag ccc cag ccc agc ccc gct gag gga agg gct gtc acc aat gag			691
Lys Gln Pro Gln Pro Ser Pro Ala Glu Gly Arg Ala Val Thr Asn Glu			
179	184	189	194
cct gag gag gag ctg gct acc cta tct gag gag gag att gct atg			739
Pro Glu Glu Glu Leu Ala Thr Leu Ser Glu Glu Glu Ile Ala Met			
195	200	205	210
gct gtt act gct tgg gag aag ggc cta gaa agt ttg ccc ccc ctg cgg			787
Ala Val Thr Ala Trp Glu Lys Gly Leu Glu Ser Leu Pro Pro Leu Arg			
211	216	221	226
ccc cag cag aat cca gtg ttg cct gtg gct gga gaa agg aat gtg ctc			835
Pro Gln Gln Asn Pro Val Leu Pro Val Ala Gly Glu Arg Asn Val Leu			
227	232	237	242
atc acc agt gcc ctc cct tac gtc aac aat gtc ccc cac ctt ggg aac			883
Ile Thr Ser Ala Leu Pro Tyr Val Asn Asn Val Pro His Leu Gly Asn			
243	248	253	258

atc att ggt tgt gtg ctc agt gcc gat gtc ttt gcc agg tac tct cgc Ile Ile Gly Cys Val Leu Ser Ala Asp Val Phe Ala Arg Tyr Ser Arg 259 264 269 274	931
/	
ctc cgc cag tgg aac acc ctc tat ctg tgt ggg aca gat gag tat ggt Leu Arg Gln Trp Asn Thr Leu Tyr Leu Cys Gly Thr Asp Glu Tyr Gly 275 280 285 290	979
aca gca aca gag acc aag gct ctg gag gag gga cta acc ccc cag gag Thr Ala Thr Glu Thr Lys Ala Leu Glu Glu Gly Leu Thr Pro Gln Glu 291 296 301 306	1027
atc tgc gac aag tac cac atc atc cat gct gac atc tac cgc tgg ttt Ile Cys Asp Lys Tyr His Ile Ile His Ala Asp Ile Tyr Arg Trp Phe 307 312 317 322	1075
aac att tcg ttt gat att ttt ggt cgc acc acc act cca cag cag acc Asn Ile Ser Phe Asp Ile Phe Gly Arg Thr Thr Pro Gln Gln Thr 323 328 333 338	1123
aaa atc acc cag gac att ttc cag cag ttg ctg aaa cga ggt ttt gtg Lys Ile Thr Gln Asp Ile Phe Gln Gln Leu Leu Lys Arg Gly Phe Val 339 344 349 354	1171
ctg caa gat act gtg gag caa ctg cga tgt gag cac tgt gct cgc ttc Leu Gln Asp Thr Val Glu Gln Leu Arg Cys Glu His Cys Ala Arg Phe 355 360 365 370	1219
ctg gct gac cgc ttc gtg gag ggc gtg tgt ccc ttc tgt ggc tat gag Leu Ala Asp Arg Phe Val Glu Gly Val Cys Pro Phe Cys Gly Tyr Glu 371 376 381 386	1267
gag gct cgg ggt gac cag tgt gac aag tgt ggc aag ctc atc aat gct Glu Ala Arg Gly Asp Gln Cys Asp Lys Cys Gly Lys Leu Ile Asn Ala 387 392 397 402	1315
gtc gag ctt aag aag cct cag tgt aaa gtc tgc cga tca tgc cct gtg Val Glu Leu Lys Pro Gln Cys Lys Val Cys Arg Ser Cys Pro Val 403 408 413 418	1363
gtg cag tcg agc cag cac ctg ttt ctg gac ctg cct aag ctg gag aag Val Gln Ser Ser Gln His Leu Phe Leu Asp Leu Pro Lys Leu Glu Lys 419 424 429 434	1411
cga ctg gag gag tgg ttg ggg agg aca ttg cct ggc agt gac tgg aca Arg Leu Glu Glu Trp Leu Gly Arg Thr Leu Pro Gly Ser Asp Trp Thr 435 440 445 450	1459
ccc aat gcc cag ttt atc acc cgt tct tgg ctt cgg gat ggc ctc aag Pro Asn Ala Gln Phe Ile Thr Arg Ser Trp Leu Arg Asp Gly Leu Lys 451 456 461 466	1507
cca cgc tgc ata acc cga gac ctc aaa tgg gga acc cct gta ccc tta Pro Arg Cys Ile Thr Arg Asp Leu Lys Trp Gly Thr Pro Val Pro Leu 467 472 477 482	1555
gaa ggt ttt gaa gac aag gta ttc tat gtc tgg ttt gat gcc act att	1603

Glu	Gly	Phe	Glu	Asp	Lys	Val	Phe	Tyr	Val	Trp	Phe	Asp	Ala	Thr	Ile		
483				488					493				498				
ggc	tat	ctg	tcc	atc	aca	gcc	aac	tac	aca	gac	cag	tgg	gag	aga	tgg	1651	
Gly	Tyr	Leu	Ser	Ile	Thr	Ala	Asn	Tyr	Thr	Asp	Gln	Trp	Glu	Arg	Trp		
499					504				509				514				
tgg	aag	aac	cca	gag	caa	gtg	gac	ctg	tat	cag	ttc	atg	gcc	aaa	gac	1699	
Trp	Lys	Asn	Pro	Glu	Gln	Val	Asp	Leu	Tyr	Gln	Phe	Met	Ala	Lys	Asp		
515						520			525			530					
aat	gtt	cct	ttc	cat	agc	tta	gtc	ttt	cct	tgc	tca	gcc	cta	gga	gct	1747	
Asn	Val	Pro	Phe	His	Ser	Leu	Val	Phe	Pro	Cys	Ser	Ala	Leu	Gly	Ala		
531						536			541			546					
gag	gat	aac	tat	acc	ttg	gtc	agc	cac	ctc	att	gct	aca	gag	tac	ctg	1795	
Glu	Asp	Asn	Tyr	Thr	Leu	Val	Ser	His	Leu	Ile	Ala	Thr	Glu	Tyr	Leu		
547						552			557			562					
aac	tat	gag	gat	ggg	aaa	ttc	tct	aag	agc	cgc	ggt	gtg	gga	gtg	ttt	1843	
Asn	Tyr	Glu	Asp	Gly	Lys	Phe	Ser	Lys	Ser	Arg	Gly	Val	Gly	Val	Phe		
563						568			573			578					
ggg	gac	atg	gcc	cag	gac	acg	ggg	atc	cct	gct	gac	atc	tgg	cgc	ttc	1891	
Gly	Asp	Met	Ala	Gln	Asp	Thr	Gly	Ile	Pro	Ala	Asp	Ile	Trp	Arg	Phe		
579						584			589			594					
tat	ctg	ctg	tac	att	cg	cct	gag	ggc	cag	gac	agt	gct	ttc	tcc	tgg	1939	
Tyr	Leu	Leu	Tyr	Ile	Arg	Pro	Glu	Gly	Gln	Asp	Ser	Ala	Phe	Ser	Trp		
595						600			605			610					
acg	gac	ctg	ctg	ctg	aag	aat	aat	tct	gag	ctg	ctt	aac	aac	ctg	ggc	1987	
Thr	Asp	Leu	Leu	Leu	Lys	Asn	Asn	Ser	Glu	Leu	Leu	Asn	Asn	Leu	Gly		
611						616			621			626					
aac	ttc	atc	aac	aga	gct	ggg	atg	ttt	gtg	tct	aag	ttc	ttt	ggg	ggc	2035	
Asn	Phe	Ile	Asn	Arg	Ala	Gly	Met	Phe	Val	Ser	Lys	Phe	Phe	Gly	Gly		
627						632			637			642					
tat	gtg	cct	gag	atg	gtg	ctc	acc	cct	gat	gat	cag	cgc	ctg	ctg	gcc	2083	
Tyr	Val	Pro	Glu	Met	Val	Leu	Thr	Pro	Asp	Asp	Gln	Arg	Leu	Leu	Ala		
643						648			653			658					
cat	gtc	acc	ctg	gag	ctc	cag	cac	tat	cac	cag	cta	ctt	gag	aag	gtt	2131	
His	Val	Thr	Leu	Glu	Leu	Gln	His	Tyr	His	Gln	Leu	Leu	Glu	Lys	Val		
659						664			669			674					
cgg	atc	cgg	gat	gcc	ttg	cgc	agt	atc	ctc	acc	ata	tct	cga	cat	ggc	2179	
Arg	Ile	Arg	Asp	Ala	Leu	Arg	Ser	Ile	Leu	Thr	Ile	Ser	Arg	His	Gly		
675						680			685			690					
aac	caa	tat	att	cag	gtg	aat	gag	ccc	tgg	aag	cgg	att	aaa	ggc	agt	2227	
Asn	Gln	Tyr	Ile	Gln	Val	Asn	Glu	Pro	Trp	Lys	Arg	Ile	Lys	Gly	Ser		
691						696			701			706					
gag	gct	gac	agg	caa	cg	gca	gga	aca	gtg	act	ggc	ttg	gca	gtg	aat	2275	
Glu	Ala	Asp	Arg	Gln	Ala	Gly	Thr	Val	Thr	Gly	Leu	Ala	Val	Asn			